anyın	GBA	sympol	gene Name	feco	heco	teco	fpr8	hpr8	tpr8	ican	mcan	tcan
V00594_at	V00594	mt2a	Metallothionein isoform 2	1683.1	1698.4	143.4	371.1	414.5	107.8	3.3	261	74.2
X64177_f_at_	X64177	mt1h	Metallothionein	761.9	728.2	93.6	73.7	6.99	27.4	10.4	27.4	14.9
M21121 at	M21121	rantes	SCYAE Small individual outside AS (DANIES)	7 90 7		000		2000	-	113	07.7	Ç
1416.1.16.1.01.	1416.146.1	Idilico	(SOLAS SILIBILITIDACIDIE CYTONITE AS (NAIN ES)	/707/	100	53.4		390.0	115.3	113.0	87.4	43.7
X04500_at_	X04500	illb	IL1B interleukin 1, beta	199.3	598.3	184.4	9.1	12.6	20.2	24	11.1	48.7
M13755_at_	M13755	isg15	G1P2 Interferon, alpha-inducible protein (clone IFI.15K)	214.1	545.6	57.4	253	662	100.2	302.7	208.8	34.3
J03910_rna1 _at_	J03910	mt1g	(clone 14VS) metallothionein (G (MT1G) gene	602.9		138.9				0	27	0
X04602_s_at_	X04602	9li	IL6 Interleukin 6 (B cell stimulatory factor 2)	408.5	1	-		76.5	269.4	14.6	43	111
U33017_at_	U33017	slam	Signaling lymphocytic activation molecule (SLAM) mRNA	320.7	343.9	685.7	4.8	25.8	ю	2.7	24.4	84.5
V00594_s_at_	V00594	mt2a	Metallothionein isoform 2	167.1	337.3	15	64.9	122.8	34.8	69.4	52.2	9.4
M65290_at	M65290	i12b/p40	IL12B Natural killer cell stimulatory factor (IL12B)	71.2	261.5	825.7	0	2.3	4.7	32.8	76	412.7
Y00787_s_at_	Y00787	81	INTERLEUKIN-8 PRECURSOR	89.1	234.5	40.9	9.6	13.1	8.4	8.2	10.8	10.5
X57579_s_at_		activinba	Activin beta-A subunit (exon 2)	166.9	233.7	47.2	22.8	16.8	9.4	14.1	19.3	24.6
X02910_at_	X02910	tnfa	TNF Tumor necrosis factor	144.1	225.5	115.7	73.8	58.6	48.5	27.2	81.1	43.2
L11329_at_	L11329	dusp2	DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1	52.1	177.6	16.1	16.2	14.7	2.4	7.9	1.4	2.9
			MX1 Myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein									
M33882_at_	M33882	mx1	p78)	61.1	1668	84 7	90.3	152.2	86.8	34	397.3	102
M31165_at_	M31165	tnfaip6	TUMOR NECROSIS FACTOR INDUCIBLE PROTEIN TSG-6 PRECURSOR	172.2	163.5	624.1	9.09	100.2	101.8	7.1	5.6	58.6
M59465_at_	M59465	a20	TNFAIP1 Tumor necrosis factor alpha inducible protein A20	87	158.7	41.1	65.3	73.5	22.9	2,6	5.9	9.6
L19779_at_	L19779	h2a	Histone H2A.2 mRNA	53.2	154	83.4		122.8	1	7.9	10.8	33.4

Figure 1A

	m	0	vi -	∞ آرد	1		<u> </u>																
	9 109.3	604	'	22.8	\perp		'		"	9.5	0.6	116 5	179.1	0.2	20.9	56.3	7 0		7.5	13.4	43.2	39.3	
	35.	212.1	1	14.6	4.0	0	1	1		6.1	0	17	8.3	9.0	2.5	11	5.6		20.8	4	39.4	15.8	
	10.6	50		51.4	0.4	7.4	·	0 00	2	97	2.3	6.6	4	× C	5.5	26.5	4.9	-	55.9	4:4	19.8	0.5	
	86.3	498.1	7	49.2	0.4	8.5	87.4	32.2	3	0.00	0.2	91.6	17.5	0	122.2	83.5	0.7		30.3		50.4	95.7	1
	86.3	192.2	٠,	72.5	0	73.8	13.8	8.4	ά	2	4	92.1	35.7 1	+	7	03.0	8:7	1	11.7	-	82.3	22.4 9	
	143.7	265.8	6.0	38.8	0.5	52.8	15.3	2	2		6.0	_	1 40.7	-	21 2		1.2	0 21		_	40.9	39.5	
	204	618.8	644.5	46	147.8	11.4	9.809	703.3	333.5	-	303.7		63.6	-	98.23	+	31	13.1	\perp	ļ.,	٥		
-	149.2	143.4	130.6	130	127.2	125	120.8 6	114.4					٦	ľ			6	_	2		+ 4 Z	3 1281.1	
-		- 1			- 1		- 1		3 107.8	106 5		104.1			× ×		84	84	76.	7		71.8	
	233.7	136.8	49.6	42.6	74.3	73.8	110	39.1	109.8	45.8		1053	50.2	00	58.1		14.6	13	57	2.		144.3	
SOD.2 gene for manganese superoxide	INTERFERONALPHA INDUCED 11.5 KD PROTEIN		Interferon regulatory factor 7 (humids)	MMP1 Matrix metalloproteinase 1 (interstitial	MACROPHAGE INFLAMMATORY PROTEIN 1.	THE CORNOR	Cycloxygenase-2 (hCox-2) gene	GRUZ GROZ oncogene	Interleukin 8 (1L8) gene	Cystic fibrosis antigen mRNA	SOD2 Superovide district	Bci-2 related (Bfi-1) mRNA	PTX3 Pentaxin-related gene (hMT-le)	IL-1 beta	MMP12 Matrix metallo	(macrophage elastace)	RPS3 Bihamara	Protein tyrosipe phosphat	MX2 Myxovirus (influenza) resistance 2	homolog of murine	IL6 Interleukin 6 /B cell stimulate	CC con summatory lactor 2)	į
sod2	ifi27	gro1	irf7	mmo1	mip1a	Cxoz	Groo	01:	9	cagb	sod2	bcl2a1 mt1e		ptx3		mmp12	ıfıtm2	dusp5		TXZ	116		
X65965	X67325	X54489	U53830	X54925	M23178	U04636	M57731	M28130	106211	1150311		U29680 M10942	7511CM			73808		U15932	M30819				
X65965_s_at_	X67325_at_			X54925_at					11_s_at	T	\neg	M10942_at_M	M31166 at	7		1	<u></u>	U15932_at_ U1	M30818 at M3		Y00081_s_at_ Y00081		

89.6	132		t	50.5	20.7	33.8	5.2 E	35.3	83.6	T '	ارم	e	70 5		55.9		116.1	7	<u> </u>	41.3	0	28.7	Г	5.5	۲: ₂	15.7
248.6	34.9	-		0.01	ΣĮ.	0.0	29.3		74	7		9.0	23.0	1	34				, , , , , , , , , , , , , , , , , , ,		4.6	12		9.0		17.3
18.6 2	12		121	1.0.1	5.0	*	20.3		\perp	0	3	1.7	8	-	22.7			1.4	-	-	6.6	3 1		200	2	24.6 17
141.1	20.8	_	127	10	1 0	2	21.2	1	44.4	0		5.4	47.9		5		0 00	5.1	47.7		6.5	34			;}	
266 14	9.9		97 1			-	26.7 2	45.6 7	\mathbf{I}	5.7	-	5.2	82.6		3.7 31	82 10	5	4.4	~	,		89			1	-
	6.1		70.6		L	-	22 2	1	3.2	4.7		7	6	_	m			0.4	1 53		51	31		38	1	3 19.7
	68.3		5.8 7			-					-	7	3 42.		2	3 372.7	1 27.2		3 76.1	L		20.5	17	-		ر ار
	7			m					212.3	72.2	0,0		26.3	(62.	19.3	191	78.3	48.3		5.7	104.2	38.5	5.2	171	7
71.6	8.0/		68.2	99	64.4		58.9	57.2	55.5	55.4	σ.	0110	51	0	40.0	44.6	43.7	43.6	42.3	3	42.2	33.7	39.6	39.5	7 08	7. 6
19.8	32.4		115.3	40.2	46.3	0	23.2	χ.ς. ₂		47.3	0		51.9	- 74	1	164.9	34.6	30.7	34.3	6	201.9	5.53	43.5	22.4	49.2	25.1
IF156 Interferon induced protein 56 CD38 CD38 antigen (p45)	6.16 gene (interferon inducible peptide	precursor) extracted from Human interferon.	TRYPTOPHANYI TBNA SVNTILET SE	BF B-factor properdin	Interferon-induced leucine vinne	(IFP35) mRNA, partial cds	RPS3 Ribosomal protein S3 /wrong name	IL15RA Interleukin 15 recentor alpha chain	PI Protease inhibitor 1 (anti-elastase), alpha-1.	antitypsin	GRO3 GRO3 oncogene	MCP-0 gene	יייין אמיוט	IAP homolog C (MIHC) mRNA	SCYA4 Small inducible cytokine A4	HEM45 mRNA		DDI11 DNA damage inducible transcript 1 TAP1 Transporter 1, ABC (ATP binding	SCYA4 Small inclurible addition as	(homologous to mouse Mip.1b)	B94 PROTEIN		TXN Thioradocia	Mitogen induced miclear organic	(MINOR) mRNA	IKIG-G mRNA
g10p1 cd38	-	g1p3	wars	bf		ifi35	ifi17	il15ra	+ c c		gro3	mcp2		ciap2	min 1 h	hem45	1000	ganuto.	tap1	mip1b	thraip2	rd155	txn		minor	11164
D84276		j	X59892	L15702		U72882	104164	031628	K01396		X53800	98866X		03/546	M69203	U88964	M5097A	VEZEOO	73676	J04130	HG3415	HT3598	X77584		U12767	22525
D84276_at	U22970 rna1	s at	X59892_at	L15/02 at	U/2882_s_at	104164 00	304104 at	021020 dl	K01396 at	00000				M69203 s at		1-1	MOUS/4_s_at	X57522 at		04130 s at W92357 at		at	X77584_atx		U12/6/_atU52513_at	1

Γ		~1	_	ī	6	0	_	2	<u> </u>		.O.	-(~	_	ਨਜ		~ 1	<u>~_</u>	_	т	~ ,						
		20.1	ζ						23.2		1.6	65.6	Ц.	318.2		7	6.6	10.4		9.3		1	-		ı	-
		1.5	11.3	1	10.5	0.2			11.5	•	6.0	2.1		109.1		30.1	11.7	4.5	ľ	9		α	1.0	90	5	
	(0.5	10.4		3.6	1.1		22.2	6		Σ.Τ	11	-	5.7	Ú	0 0	3.5	5.6	(9.5		-	0	250	-	
	(43.2	5.3		0.3	2.1		7.6	15	ı	0	16.2	0	590.2	0 70	77.7		-	,	4.6		5	7 6	74	0.7	
	(19.8	6.2		7.4	m	ı	5.5	13.7	0	70.7	2.2		730.1	126	100	ò	2	;	1		24.1	3.6	17	26.5	
		17.7	10.8		4.5	٦	1	5.3	2/.5	C	0.0	7.9	-	2/1/3	3	o c	0.0	1.9	o c	9	_	14	0.8	22	4.3	
-	0,00	124.0	44.9		35.3	χ.	Č	2	22.0	0	9	71.9	20,01	104.0	2000	7 00	†.	8.5	7 00	7.07		27	25.9	48.8	3.5	
	000	30.6	38	00	88 1	4.75	- , , ,	1./0	20.0	35.2	3	34.8	2	7:15	34.1	325	0.50	32.4	30.6	7,1		32.2	31.6	31.1	30.9	
	22.0	53.3	126.1	Ļ	12	, , ,	0 / 0	0 1	01.7	0		29.8	14.7) 	16.9	25.2		2.5	70.6	2		23.7	3.9	43.8	13.2	,
PUE4B Phosphodiesterase 4B, cAMP specific	(dunce (Drosophila)-homolog phosphodiesterase E4)	GOS2 gene extracted from Human GOS2 gene,	5' flank and cds	AK3 mRNA for adenvlate kinase 3	MT1L Metallothionein 11	Thyroid receptor interactor (TRIP10) mPNA 2	end of cds	IL7R Interleukin 7 recentor		Proline-Rich Protein Prb4, Allele	PTGIR Prostaglandin I2 (prostacyclin) receptor	TNF.related appropriationalization	mRNA	C1NH Complement component 1 inhibitor	(angioedema, hereditary)	L-kynurenine hydrolase mRNA	P2x Durinocentor mBNA	ICAM1 Intercellular adhoring	(CD54), human rhinovirus receptor	NFKB2 Nuclear factor of kappa light	polypeptide gene enhancer in B-cells 2	(p49/p100)	LIMIK-Z	INIDIATION MENA	rc-epsilon-receptor gamma-chain mRNA	NFKB1 Nuclear factor of kappa light
	dpde4	0000	2505	ak3	mt11		trip10	il7r		prb4	oteir		trail		c1nh	kynu	p2x4		icam1		((nrko p52	niink2	10021	166118	nfkbn50
	L20971	7000774	IM / 2885	X60673	X76717		L40379	M29696	HG4490-	HT4876	D38128		U37518		M13690	17//60	AF000234		M24283		000000	3/0036 D/15906				M58603
	L20971_at_		X60673 rna1		X76717_at			M29696_at	HG4490.	HT4876_f_at_ HT4876	D38128 at	Т	\rightarrow	M13690_s_at	10220	-	AF000234_at		M24283_at_ N			045906 at F	- 1	Ţ	1	M58603 at M58603

Figure 1D

10101	010101											
HT1612 at	HG1612.											
	7101	inaciliar CRS	Macmarcks	19.2	30	44.7	7.	30.2	16.0	,		
X02875_s_at_	X02875	oasl	OIAS (2'.5') oligoadenvlate synthetase		1			3	600	40	× -	15.6
D28915_at	D28915	mtan44	Hepatitis C-associated microtubular aggregate	10./	9	48.7	41.5	58.8	117.7	4.2	20.5	4.08
U48807_at	U48807	dusp4	Divelli p44	8.5	29.6	53.6	10.7	47.1	44.3	1.3	15	0
U03891_at	U03891	unknown	Phorbolin I many martial and	5.6	29.6	7.4	2.4	3.1	86	200	200	2 10
			GBP1 Grandate binding	43.8	28.9	21.9	189.3	58.3	23.3	4.4	0 0	200
M55542_at_	M55542	gbp1	doi 1 duaiyiate binding protein I, interferon. inducible, 67kD						22		0	39.3
U50648_s_at			Interferon inducible RNA-dependent protein	38.4	78.4	99.4	34.6	20	99	1.5	26.4	75.9
D30755 at	050648	pkr	kinase (Pkr) gene	9	άζ	, ,		(-	
1159286 at	D30/33	NAF I	VIM Vimentin	56 3	0.000	10.6	Σ, ζ	200	22.1	40.1	24.8	19.1
MANAEE	023200	itac	Beta-R1 mRNA, partial cds	27.0	27.6	13.0	13.5	4.9	5.9	14.1	5.3	7.9
1020E7	INI34455	ldo	IDO Indole 2,3 dioxygenase	273.7	27.0	23/3	201.6	207.8	340.8	3.8	74.4	389.7
00000/at	/50500	snl	Actin bundling protein mRNA	2,3.7	6.72	213.8	2/9.5	89.2	97.8	1.5	3.4	106
760001			Urokinase type plasminogen activator recentor	03.0	6:/2	8.4	4.1	10.4	14.1	32	13.4	2.3
S_at_	1009937	plaur	gene extracted from Human urokinase-type			_						
			BIG1 Broell translocation	17	26.9	14.5	12.5	10.7	2.4	~	ر ب	,
X61123_at	X61123	btg1	proliferative				-			,	?;	5
U02020_at_	U02020	pbef	Pre-B cell enhancing factor (PRFE) mBNA	30.4	26.8	14.4	8.4	4.6	4.4	3.6	7.4	7.6
000				50.5	26.4	37.4	6.9	11.9	14.5	5.9	1.4	8.5
X53296_s_at_X53296	X53296		ILIRN Interleukin 1 receptor antagonist	7.7.7.	7 90	(_	-	-	
M10943 at	M10943	f	Metallothionein-If gene (hMT-If)	. L	4.02	9.9	78.7	14.4	4.6	4.3	7.7	4
359049 at	559049	ier1	RGS1 Regulator of G-protein signalling 1	0.0	70.1	20.0	0	0	2.7	1	6.0	0
M14660_at_	M14660	g10p2	ISG-54K gene (interferon stimulated gene)	ř	6.03	15.9	2.2	2.8	9.1	6.6	10.8	8
U66711_rna1			checoning a 34 kUA protein, exon 2	5.9	25	27.9	109	312.4	206	C	u	-, ((
_s_at_	U66711	ly6e	Ly-6-related protein (9804) gene	0	- [1	7	4.00.4
11 05072 s at 11 05072	05070			0.0	24.7	4.7	6.1	13.6	2.4	2.4	1.7	4
2 2 2	-030/Z	111	IRF1 Interferon regulatory factor 1	48.2	24.5	63	63.7	2000	700	~		L C
, C			(prostaglandin G/H synthase and	_							7.1	000
L13320_S_at_ L1532b		cox2	cyclooxygenase)	39.5	23.7	92.4	7	1.2	9			,
									,	1 1 1	5	† i

Figure 1E

U19523_at_	U19523		dystonia) (alternative products)	001	0 00							
M86849_at_	M86849	cx26	Connexin 26 (GJB2) mRNA	0.00	0.22	139.7	15.8	20.5	50.5	4.0	22.4	132.8
M21005_at_	M21005	caga	CAI GRANIII IN A	6.3	0.77	31.0	0.2	1.4	2.4	0.4	0.1	4.5
			Down syndrome oritical cariation	4.0	77.7	165.6	0	1.4	9.6	0.8	0	6.0
U28833_at_	U28833	dscrl	mRNA		Ç	(,					
M90657_at	M90657	m3s1	TUMOR-ASSOCIATED ANTIGEN I 6	10.	47.77	2.9	0.4	3.2	0.2	2.9	1.3	1.2
U66838_at_	U66838		Cyclin A1 mRNA	18.5	77.7	90.1	0.3	0.3	0	0	0	0
M16750_s_at				2.3	22.1	53.5	12.3	23.5	65.7	1.1	1.9	23.6
		pim1	PIM1 Pim·1 oncogene	700	5	;	•					
X68486_at_	X68486	adora2a	ADENOSINE AZA RECEPTOR	20.7	0.17	δί.	4.2	3./	9.4	3	5.9	8.2
D86967_at	D86967		KIAA0212 pene	8.0		49.3	3.4	3.5	20.3	3.2	1.6	8.6
				29.9	21.4	5.7	0.4	6.7	0.3	0.8	2.1	4.9
L13391_at_	L13391	g0s8	REGULATOR OF G.PROTEIN SIGNALLING 2	4	- [,	1	-,				
			TNFR2 Tumor necrosis factor recentor 2	5	7.17	5)	Ö	4.2	12.8	0.7	0.5	2.1
M32315_at	M32315	tnfr2	(75kD)	70	7 00	0	- (- (,	_		
X66401_cds1			LMP2 gene extracted from H.sapiens genes	2	7.7	607	ار در	0.5	0.6	5.4	~	2.5
at	X66401	tap2	TAP1, TAP2, LMP2, LMP7 and DOB	30.6	30.6	200	-	((
M62831_at	M62831	etr101	Transcription factor ETR101 mRNA	0.00	20.00	36.4	14:3	0.0	6.3	6.1	23.6	31.9
U64197_at_	U64197	mip3a/larc	CC chemokine I ARC predictor	0 0	4.02	2	9.3	16.6	11.2	9.0	0.5	1.2
D14874_at_	D14874	adm	ADM Adrenomedullin	10.8	20.5	164.2	1.7	12.2	16.1	0	3.9	6.4
M36284_s_at				18	20.1	46.2	3.4	4.5	10.4	2.5	5.2	16.1
1	M36284	ge	GYPC Glycophorin C (Gerbich blood group)	0		1						
L19871_at_	L19871	atf3	ATF3 Activating transcription factor 3	10.6	10.7	1.	100	6.5	7	1.6	6.0	2.3
X78710_at_	X78710	mtf1	MTF-1 mRNA for metal-regulatory transcription factor			0.0	70.1	201	12.4	5.4	1.5	3.9
			MAJOR HISTOCOMPATIBILITY COMPLEY	œ'	19.7	8.9	2.9	2	1.1	0	1.5	2.3
M69043_at_	M69043	ikba	ENHANCER-BINDING PROTEIN MAD3	23.0	10.6							
U08021 at	008021	+	Nicotinamide N-methyltransferase (NNMT)				0.41	0.0	4.	4.3	3.7	8.4
13210 at	113210	man Ohn	ייייין פיייין	3.7	19.6	1.7	0.3	6	Ċ	α	C	_
	2222	יוומרבטט	Mac-z binding protein mRNA	9	19.5	21	5.6	72	110	27.5	5 0	1 C
106797 5 34	707901	,	PROBABLE G PROTEIN-COUPLED RECEPTOR				-	?}	?!	6./3	0.11	34.5
- 10-10-10-10-10-10-10-10-10-10-10-10-10-1	100131	באכול	LCKI HOMOLOG	12.7	19.2	30.6	80	7.9	9	14 9		7 00
D17357_at	D17357	actbA	Activin Deta-A gene, regulatory sequence of						:		7	30.7
				29.4	18.8	10.8	0.2	6.0	7.3	r o	-	-

Figure 1F

7.3_at	Caspase-like apoptosis regulatory protein 2 (Clarp) mRNA, alternatively spliced	7 8 1	2 2 2	37.0	-			L	
39 at 579639 ext1 63_at_ D50663 tctel1 00_at_ U60800 sema4d 3445_at AF008445 plscr1 48_at_ D45248 pa28b 60_at_ U15460 batf 27_s_at X65724 ndp 10_at L78440 stat4 27_s_at M87503 isgf3 33_at_ M65543 GBP2 33_at_ M65543 GBP2 33_at_ M66633 pscdbp 6_rnal M87504 tagln 1 at_ X88277 dusp1 1 at_ A88277 dusp1 1 at_ A88277 dusp1 1 at_ A88277 dusp1 1 at_ A88277 dusp1 1 at_ A88481 mmp14 if 1 at_ A8516 ecgf if 6_rnal M3724 ecgf if 6_rnal M3724 ecgf if 6_rnal M3544 ecgf if 6_rnal M3544 ecgf if 6_rnal M3544 ecgf if 6_rnal M3546 gcsf if 6_rnal X03656 gcsf if 6_rnal X03656 gcsf					1		λ.		18.4
63.at D50663 tctell 00.at U60800 semadd 3445_at AF008445 plscr1 48.at D45248 pa28b 60.at U15460 batf 24_at X65724 ndp 27_s_at U50527 23_at M87503 isgf3 33_at U6633 pscdbp 77_at X68277 duspl 11_at D21261 tagln2 6_rnal 11_at D21261 tagln2 11_at D31261 tagln2 11_at D31040 tacl2 11_at D31040 tacl2 11_at X03656 tagln2 11_at X03656 tagln2		1	10.4			2		2.1	41.5
00_at_ U60800 sema4d 3445_at AF008445 piscr1 48_at_ D45248 pa28b 60_at_ U15460 batf 24_at_ X65724 ndp 27_s_at N65724 ndp 27_s_at L78440 stat4 27_s_at U50527 gBP2 33_at_ M87503 isgf3 13_at_ L06633 pscdbp 7_at_ X68277 dusp1 6_mal D21261 tagin2 1a_t_ D21261 tagin2 1a_t_ D21261 tagin2 1a_t_ D21261 tagin2 6_mal X85116 epb72 1a_t_ L48411 taf1 1a_t_ U19261 taf1 1a_t_ U19261 taf2 6_mat_ D10040 taci2 6_mat_ X03656 gcsf 6_mat_ X60417 xccof			1		_		3.5	6.0	5.3
445_at 46_at 478440 4844 487503 48875 48875 48875 48877 48810 488116 488116 488116 488116 488116 488116 48611 4861	7		- 1	9	-	3.3 15.	1 5.1	13.5	30.8
AF008445 plscr1		5.1	17.6	3.7 4	4.3 13	3.5 8.	1 0.6	14.5	20.5
48 at D45248 pa28b 60 at U15460 baff 24 at X65724 ndp 24 at X65724 ndp 27 sat L78440 stat4 27 sat U50527 sgf3 33 at M87503 isgf3 73 at X68277 dusp1 73 at X68277 dusp1 13 at D21261 tagin2 24 at M31724 ptp1b 6 crnal X85116 epb72 1 at Z48481 mmp14 1 at HG544 ecgf 6 crnal HT544 ecgf 6 crnal X03656 gcsf 6 crnal X6315 gcsf				_					
60 at U15460 baff 24 at X65724 ndp 10 at L78440 stat4 27 s. at U50527 stat4 23 at M87503 isgf3 13 at M6533 pscdbp 7 at X68277 dusp1 11 at D21261 tagin2 24 at M31724 ptp1b 6 -rna1 X85116 epb72 1 at 248481 mmp14 1 at L48481 raf1 1 at L48481 raf1 1 at L48481 raf1 1 at L019261 raf1 1 at L019261 raf1 6 at D10040 fac12 6 at D10040 fac12 6 at X03656 gcsf 1 at X60417 ccross	1	\perp	21	1.	2	m	3 1.2	6.3	88.5
24_at_ X65724	+	7	7.2	7		8.2 5.	7 34.3		5.5
10_at L78440 stat4 27_s_at U50527 03_at M87503 isgf3 13_at M87503 isgf3 13_at L06633 pscdbp 13_at L06633 pscdbp 11_at D21261 tagln2 24_at M31724 ptp1b 6_rna1 X85116 epb72 1_at Z48481 mmp14 1_at Z48481 mmp14 1_at U19261 traf1 1_at U19261 traf1 1_at U19261 traf1 6_rat D10040 facl2 6_rna1 X03656 gcsf 6_rna1 X60415 gcsf					1.5 0	0.4 0.	9	3.3	=
27_s_at	<u> </u>	33.4	7.1 39	39.4	1	.2	0 3.5	0.5	2.5
27_s_at U50527 03_at	מוסו סו	7							
0.50527 0.3.at M87503 isgf3 1.2.at M55543 GBP2 3.3.at L06633 pscdbp 1.3.at L06633 pscdbp 1.3.at D21261 tagin2 24.at M31724 ptp1b 6.rna1 X85116 epb72 if 1.3.at 248481 mmp14 if 1.3.at 248481 mmp14 if 1.3.at U19261 traf1 if 6.rna1 X6344 ecgf if 6.rna1 X63656 gcsf (6.7.at X03656 gcsf (6.7.at X0365		1	10.4	40.6	0	1.4 6.9	5 3.1	2.4	7.8
M87503 isgf3 M55543 GBP2 L06633 pscdbp X68277 dusp1 D21261 tagln2 M31724 ptp1b X85116 epb72 X85116 epb72 Z48481 mmp14 if U19261 traf1 H5544 ecgf H7544 ecgf D10040 faci2 f									
13_at_ M87503 isgf3 13_at_ M55543 GBP2 3_at_ L06633 pscdbp 13_at_ D6633 pscdbp 11_at_ D2124 ptp1b 13_at_ M31724 ptp1b 13_at_ Z48481 mmp14 if 11_at_ U19261 traf1		<u></u>	10.4	/6.1	1	3.3 18.	4 3.3	13.9	50.7
13_at_ M55543 GBP2 3_at_ L06633 pscdbp 17_at_ X6877 dusp1 11_at_ D21261 tagln2 124_at_ M31724 ptp1b f 6_rna1 X85116 epb72 i 11_at_ Z48481 mmp14 i 11_at_ U19261 traf1 i 11_at_ U		5.4	α	-0					
3-at_ L06633 pscdbp 7_at_ X68277 dusp1 51_at_ D21261 tagin2 24_at_ M31724 ptp1b 6_ma1 6_ma1 1_at_ Z48431 mmp14 1_at_ U19261 traf1 1_at_ U19261 traf1 1_at_ U19261 traf1 1_at_ U19261 traf1 6_mat_ HT544 ecgf 0_at_ D10040 faci2 6_ma1 X03656 gcsf	-		-		7	0	2 1.8	1.8	5.5
7_at	E		16.1 47	47.1 11.	4	5 6.1	7.5	191	23.5
11_at_ D21261 tagin2 24_at_ M31724 ptp1b 6_rna1			16 15.	.4 0.	7	1.3	6 5.4	20	136
24_at_ M31724 ptp1b 6_rna1		10.5 15	15.9 12.	7.	4 7	3 8.6		0	1 2
6_rna1 X85116 epb72 1_at 248481				3.9	9.7		m	0.5	0 0
X85116 epb72	17	4.7 15	5.8 16	6.2 6.	7 8.1	1 4.1		3.5	73
1_at									
1at				2		1 13.8	8.0	6.5	12.7
HG544. ecgf at HT544 ecgf O_at_ D10040 faci2 6_rna1 X03656 gcsf			9	1	3 8.8	8 2.7	2	0	24
6_rna1		25.7 15.	.4 25.	2	8 12.7	7 6	5.8	9 5	α
0_at_ D10040 faci2 6_rna1				_	_	_			
6_rna1 X03656 gcsf 7_2t Y60417 gcm6	1	5.9 15.		.8 10.4	4 5.2	2 2.1	26.7	16.5	7
6_rna1		24./ 15	2 26.	2 13.	5	12.4	2.2	4.4	24.1
7 at Y50417	ating factor								
	19.	9.4 15.	2 37.6	9	1.2	0			- (
- 0,-		8.7 15	2			ά		5 0	ָרַ נְי

			HYPOTHETICAL MYELOID CELL LINE PROTFIN		-							
D29642_at_	D29642		8	9	1,1	10.2	,	-	Ċ		(L
X52541_at_	X52541	egrl	EGR1 Early growth response protein 1	000	15.1	200	2.7	1 0	4 6	4.0	ρ	y 0
-			WNT5A Wingless-type MMTV integration site		1:51		7	0.1	>	5	5	20
L20861_at_	L20861	wnt5a	5A, human homolog	11	ני		C	-				•
100071	2000		Variant urokinase plasminogen activator					1	5	+	+	0.4
A74039 at	X/4039	plaur	receptor (uPAR2) mRNA, partial cds	1.6	15	7.3	1.6	4.2	2.8	5	5.4	г -
IM13/92_dL	W13/92	aga	ADA Adenosine deaminase	13.5	14.9	108 1	0	-	2	26	6	000
M83667_rna1							;	2	2	o i	1.2	12.3
s_at_	M83667	cebbd	NF-IL6-beta protein mRNA	2.9	14.7	183	0	7	0	C	-	1
X05232_at_	X05232	mmp3	MMP3 Stromelysin	20 A	100	ς α	5 0	7:0	o c	0.0	7 0	ازر
X12451_at_	X12451	ctsl	CTSL Cathebsin L	0.01		2 0	0.0	7 1	3	5	5	
١,	D87953	£	RTP	10.0	1,4.	χ Q	10.0	Ç.	5.1	7	2.8	10.9
•	D42043	KIAAOORA	KIAAOO84 man and and and	1/.8	14.2	20.6	0	6.0	0.5	1.2	8.0	5
	MODOAA	4169604	NATIONAL BELIEF PARTIES COS	24.8	14.1	27.1	7.1	3.1	4.5	8.3	8.6	0
al .	1100673	11054036	INTEGRAL MEMBRANE PROTEIN E16	25.2	14.1	24.5	14.5	10	2.7	1.5	19	7 8
000072_al	2/9000	IIIOra	ILIOR Interleukin 10 receptor	9.5	14.1	9.1	10.6	7.	20	4.2	20) -
M54915_s_at		,										3
	M54915	pim1	PIM1 Pim-1 oncogene	11	13.7	37.2	2	2.	2	0		
			2',3'-cyclic-nucleotide 3'-phosphodiesterase			11:15	111	1	7.0	2.5	5	U.G
D13146_cds1			gene extracted from Human 2',3' cyclic.									
at	D13146	cub	nucleotide 3'-phosphodiesterase gene	15.9	13.4	25.3	6.2	4	101	r V	α	11
					-			1		2	2	71.7
U83461_at	U83461	copt2	Putative copper uptake protein (hCTR2) mRNA	3.6	13.4	19.1	0	101	10	Ľ	7	200
AB000115_at									J	7	ì	77.0
	ABUUUIIS	unknown	mRNA	8.6	13.1	24.9	8.4	26.9	28.7	7 %	<u>,</u>	27.6
710775	1010	<u>(</u>	AMPD3 Adenosine monophosphate deaminase		-					;	-	?]
012//3_s_d_ 012//3	012//5	ampd3	(isotorm E)	14.7	13.1	18.9	0.1	2.7	Ó	ď	1.0	
004110 at	004110	DIg3	l ob family	1.7	13.1	12.2	9	196	0	000	1 -	fu
003397_s_at				-					;			9
i	003397	41bb	Receptor protein 4-1BB mRNA	4.6	13.1	90.4	m	20 1	26.2	C	0	0
	4	;	INP10 Interferon (gamma) induced cell line;)		1	1		0.0
XUZ530_at	X02530	inp10	protein 10 from	12.5	13.1	442.2	137.9	290.4	501.4	5.4	205 9	451 4
Moos40_at	Mb8840	maoa	MAOA Monoamine oxidase A	11.2	13	117	000	1_	C		1	1 0
			ITGB3 Integrin, beta 3 (platelet glycoprotein			+		7	7	-	1.2	5
M35999_at	M35999	itgb3	IIIa, antigen CD61)	8.3	12.8	21.8	C	-		1 7		
)	;	5	5	7.7	<u>Ŧ</u>	5

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M37435_at_	M37435	mcsf	CSF1 Colony-stimulating factor 1 (M-CSF)	7	12.0	19	27.5		•		,	
U83171_at_	U83171	· opu	Macrophage derived chemokine precursor (MDC) mRNA	1 7	0 0 0	,)) L	17.1	3 0	4.1	0.0	
X06256_at_	X06256	itga5	ITGAS Integrin, alpha 5 (fibronectin receptor, alpha polynentide)	2	16.0	7.7	0.1		0.0	2.	m	0.5
104000	0		C1S Complement component 1, s	9.6	12.8	χ; (χ)	11.6	13.2	2.9	6.0	5.9	0.8
J04080_at_	204080	cls	subcomponent	4.2	12.6	61.6	5.6	8	31.4	3.7	6	α
M55067_at	M55067	ncf1	NCF1 47 kD autosomal chronic granulomatous disease protein	C	5	3	1					
Z11697_at_	Z11697	cd83	CD83 ANTIGEN PRECURSOR	187	126	7 47	1.0.1	78.5	22.1	4.4	8.6	17.2
1 37936 3‡	35075		MITOCHONDRIAL ELONGATION FACTOR TS	1	0.31	0.0	19.0	y U	- اه	4.1	10.4	7.2
U52682 at	1152682	irfd	I RECURSOR	6.1	12.5	19.6	9.0	5.5	4.0	0.6	2.6	5.1
1191616 at	191616	ikho	1 Kasas B assistant Regulatory Tactor 4	6.3	12.4	4.1	4.5	3.4	2.2	1.3	3.2	-
S66896 at	SERRE	Sec. 2	SCCA1 School (IKBe) mKNA	16.3	12.4	3.3	12.6	4.5	0	4.1	6.1	1.5
		2000	SERINE/THREONINE BROTEIN WINASE	78	12.3	47.6	0	0.2	3.3	0	0.2	1.5
X66363_at_	X66363	pctk1	PCTAIRE-1	11.0	0	22.2		7	,	,	 	
U20647_at_	U20647	znf151	ZNF151 Zinc finger protein 151 (nH7.67)	200	110	32.3	5 0	5	1.0	5	0	5.2
V00535_rna2	_		Interferon beta 1 gene extracted from Gene for	Ci	0.11	7.0	5	4.1	5	4.7	3.8	3.8
s_at_	V00535	ifnb1	human fibroblast interferon beta 1	0.8	11.8	187.4	68.4	33.2	165.0	,		
Doogood at	USBSBS	тарзк4	KIAA0213 gene, partial cds	10.8	11.7	7.2	α	1 14		2.5	> 0	7
M97936_at_	M97936	stat1	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1.41 PHA/RETA	,	:	1			1	2	0	4./
U15174_at_	U15174	nip3	Nip3 (NIP3) mRNA		71.4	16.9	13.4	/:/	11.4	48.3	40	28.5
X90858_at_	X90858	dn	Uridine phosphorylase	12.7	11.4	27.3	0.0	2.1	0.8	0.3	1.7	11.1
U44975 at	U44975	bcd1	DNA-binding protein CPBP (CPBP) mRNA,	1.01		10.9	4:4	× -	5	4.5	6:1	8.3
M27436_s_at			F3 Coagulation factor III (thrombonisetin	2.4	11.3	6.8	3.7	7.1	7.8	1.5	4.2	5.3
-	M27436	13	tissue factor)	7.	11.0	30 6				,	:	
LUSU69_at_	F08069	hspf4	DNAJ PROTEIN HOMOLOG 2	12.8		12.7	10.9	207	9.1	1.3	1.1	510
1	M37766	bcm1	CD48 CD48 antigen (B.cell membrane protein)	13.2	10.9	20.8	α	1.3	12	-		
<u> </u>	D14661	2 7 7	KIAA0105 gene	7.1	10.7	24.3	23.4	33.6	11.7	1 5	τ α	67.0
U03100_dt	003100	7-50	184-2 protein mRNA	29.4	10.7	8.2	11.4	5.7	5	6.4	200	; ; ; ;
											,)

+000/9/												
0/0/04_s_al	U76764	26pp	CD97 CD97 antigen (leucocyte antigen)	14.8	107	3.4	14.5	2.8	2.3	1 7	2	7 5
M64929_at_	M64929	ppp2r2a	PPP2R2A Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	(r	10	7	0		0	-		
U67171_at_	U67171		Selenoprotein W (selW) mRNA	2.5	10.6	5.6	0.8	333	0 4 rc	1 4	<u> </u>) o
D10923_at_	D10923	hm74	PROBABLE G PROTEIN-COUPLED RECEPTOR HM74	ιτ	0,	0	0) !	,		9
D50840_at	D50840	Scs	Ceramide glucosyltransferase	4.4	10.4	0.7	1.0	10.2	0.7	4.0	2.5	2.2
1410004_5_a	M16364	ckb	CKB Creatine kinase B ·	7.07	100	-	000	9	-			3
			ANPEP Alanyl (membrane) aminopeptidase	200	101	1	109.3	18.8	4.	2.5	2	4
M22324_at_	M22324	anpep	(aminopeptidase N, aminopeptidase M,	į		ı						
L08187_at_	L08187	ebi3	Cytokine receptor (EBI3) mRNA	17.4	10.4	2.7	6.0	1.9	0	2.2	3.1	7
U82979_at_	U82979	lir5	Immunoglobulin-like transcript-3 mRNA	112	101	17 17	2 7	5 4	7	5	7:7	12.5
X69910_at_	X69910	p63	P63 mRNA for transmembrane protein	101		7 0		1.0		7.7	4	1/.4
X52425_at_	X52425	il4r	IL4R Interleukin 4 recentor	0.0	1 5	4.07	4 0	2.3		3.9	6.4	29.3
			TOF11 Transcription factor 11 /L	7.0	0.7	2	2.9	3.1	4.4	<u>∞</u>	~	9.7
X77366_at_	X77366	nfe2l1	zipper type)	2.3	10	16.4	3.5	4.1	3.4	-	0	15.7
D79206_s_at_	D79206	sdc4	SDC4 Syndecan 4 (amphiglycan ryudoran)	0	C	5	,					
D38583_at_	D38583	s100a11	Calgizzarin	200	U. C	71.7	15.2	77.7	10.2	2.7	2.7	9
HG2981.					0.0		χ.		3.1	1.2	4.0	2.1
HT3125_s_at												_
	HT3125	cd44	Epican, Alt. Splice 1	13.1	0	α	•	-		7	(
L22342_at_	L22342	unknown	Nuclear phosphoprotein mRNA	8 6	0 7	-	7 .	1 -) r	7.7	2.3	1.
J04102 at	104102	atc)	ETS2 V-ets avian erythroblastosis virus E26				7	7.0	+	C.11	12.2	21.7
L08177 at	1 081 77	ehi2	CMKBD7 Champling 70 00	23.3	9.6	53.3	0.7	4.7	0	0	0.5	33
		3100	Chiral Cientokine (C.C.) receptor /	3.6	9.6	6.2	2.2	2.1	4.1	5.1	2	2.1
	U49835		CHIT1 Chitinase 1	1 7		0	-		,		-	
			COT Proto oncogene c cot (protein.			2	5	r.y	2.7	E.O	0	0.8
D1449/_at	D14497	cot	serine/threonine kinase)	4.1	9.5	27	0	0.6	4.	0.5		- 2
ואוספטסים מר	M02000	msm	MSN Moesin	7.3	9.5	3.7	2.4	5	=	0	 -	2 2

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			COKNIA Civilia depondent kinger									
U09579_at_	009579	cpne5	(p21, Cip1)	12	σ	Г	r.		-	0	,	(
D64142_at	D64142		Histone H1x	8	9.4	101	2 -	1 0	7 - 0	0.7	9 6	7.7
M86707 at	MR6707		GLYCYLPEPTIDE N.					-	j	t t	5	4.4
10101	10101	1	1 LINAUECANOTE RAINOFERASE	2.4	9.4	2.7	1.2	4.3	0.4	2.6	3.6	12.2
001024	001054	8111	Giutamate transporter	7.1	9.3	24.2	0.1	4.1	2.8	6.0	0.7	-
U30999 at	666080	cd166	U30999 Homo sapiens MV3 melanoma Homo	((4						
AF014958 at		201	Sapieris conta cione illetitu, mana sequence	9.6	9.3	6.3	3.4	0	0.1	3.7	3.5	2.8
	AF014958	ccr6	Chemokine receptor X (CKRX) mRNA	γ.	0	26.2	7		(,	,
U03398_at_	003398	41bbL	Receptor 4.1BB ligand mRNA	333	200	27.0		0.0	0.0	1.0	2.4	10
			MHC.encoded professome subunit gene 1 AMD7	25	1	7: /1	2	2.2	9.7	2.2	0.1	3.4
			E1 gene (proteasome subunit LMP7) extracted			-						
			from H.sapiens gene for major									
Z14982_rna1 at	714982	7000	histocompatibility complex encoded									
	702	, di 1111	processorile subunit LIMP/	3.6	9.5	4.6	4.2	8.7	8.6	5.1	5.9	13.0
			BONE MARROW STROMAL ANTIGEN 2 (BST.	-								
U28137_at_	D28137	bst2	2)	- CJ	9.1	12.9		σ	149	7 0	0	27.0
			GGTB2 Glycoprotein-4-beta-								3	9
- 1	029805	b4gait1	galactosyltransferase 2	13.4	6	12.9	6.1	4.7	m	0.7	C.	4
1413102/_dl	M3162/	1dax	X BOX BINDING PROTEIN:1	4.4	6	15.4	16.7	20.6	27.1	3.2	2 -	2
	00000		PML Probable transcription factor PML				-			11,	;	2
T	M/9462	шX	{alternative products}	3.1	6.8	6.2	2.7	6.7	6.0	7	ď	ď
,	0/466/		Tat interactive protein mRNA	3.5	6.8	3.4	17	102	26	2 0	9 0	0 0
	X01060	cd71	TFRC Transferrin receptor (p90, CD71)	26.3	8	13.7	0	200		, ,	0 0	7.70
713153_at_	713153		Kynurenine 3-monooxygenase	2.9	8.9	4.9	13	000		100	0.5	0 0
D26443 at	D26443	eaat1	FXCITATORY AMINO ACID TO ANAMORATE .	1			1					
1	M21186	S. Chro	CVDA CHIEF IN THE CONTRACTOR IER I	5.5	8.8	27.5	1.2	3.6	4.9	3.5	0.3	8.9
1	Meane	Cy50	CLDA Cytochrome D-245, alpha polypeptide	2.7	8.7	2	1.6	5.1	1.6	6.0	0.5	2.2
\top	Mococo	pgrnı	PGM1 Phosphoglucomutase 1	3.4	8.7	6.7	0.2	0.5	0	1.3	1.2	4.2
L22524_s_at_ L22524	L22524	7dmm	MATRILYSIN PRECURSOR	6	00	63.7	C	-	r.	Č	-	-
			Modulator recognition factor I (MRF-1) mRNA,					1		7	+	<u>, </u>
M62324_at_	M62324	mrf.1	3'end	4.8	8.6	10.2	7.9	6.1	14.3	α	3.4	6 9

Figure 1K

M87434_at_	M87434	oas2	69/71 KD	11.8	8.6	21.2	15.4	33.1	16.5	2.5	5.3	17.5
S54005_s_at_ S54005	S54005	thymosinb10		4.2	8.6	1.7	3	5.4	3.7	4 4	2,2	0
X01677_f_at_ X01677	X01677	g3pdh	GAPD Glyceraldehyde-3-phosphate dehydrogenase	5.2	8	0			a		7, -	2 -
	X07820	mmp10	MMP10 Matrix metalioproteinase 10 (stromelysin 2)	13.3	8.6	88.86	0 2		2 10	5 -	100	, v
U43185_s_at 	U43185	stat5a	STAT5A Signal transducer and activator of transcription 5A	7.6	α α	14.5	-	α ς	-	1 4	1 0	7
X17093_at_	X17093	hla-cda12	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F ALPHA CHAIN PRECURSOR	12.7	4 8	7 2	7 4	φ -	7 7	0.01	5 5	000
	003100	catenin-a1	CTNNA1 Catenin (cadherin-associated protein), alpha 1 (102kD)	2.9	8.3		4		2	2 - 2	1,6.4	0,7 C
U72649_at	U72649	btg2	BTG2 (BTG2) mRNA	3.1	8.3	4.7	1.5	60	9.0	3.2	0 0	1 4
U19557_s_at	U19557	scca2	Squamous cell carcinoma antigen 2 (SCCA2) mRNA	17.5	8.2	24.2	0	9.0	1.5		6	C
X92521_at_	X92521	mmp19	Clone rasi-1 matrix metalloproteinase RASI-1 mRNA	5.8	8.2	21	6.0	10.1	2.7	2.3	0.7	2.
Y00451_s_at_	, Y00451	alas1	ALAS1 Aminolevulinate, delta., synthase 1	17.8	82	14.6	3	, r	23.0	-		1
L07633_at_	L07633	pa28a	INTERFERON GAMMA UP-REGULATED 1-5111 PROTEIN PRECURSOR	- 4	α	12 1	7	3	6.53	7 6	14.6	
	L40377	cap2	Cytoplasmic antiproteinase 2 (CAP2) mRNA	7.4	Σ α	13.1	0 6	4 C	٥	2,7	5.4	20.1
	S81914	iex-1	IEX.1	7.9	8	10	11	0	s c	2 5 5	0.0	<u>.</u>
	M30894	torg	TCRG T cell receptor gamma chain	8.9	8	40.3	0	0.7	m	8	10	1 4
J	M93056	ē	LEUKOCYTE ELASTASE INHIBITOR	23.4	8	30.8	3.7	1.8	0.7	1.6	8.4	10
12/4/0 at	17/4/0	7.02	XIU4 mKNA	3.1	7.9	m	1.3	2.4	9.0	2.2	0.8	2.2
	M97935	stat1	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	4.1	7.9	10.5	2.5	г. С	100		17.0	36.7
U43522_at_	U43522	fak2	Protein tyrosine kinase PYK2 mRNA	5.2	7.9	16.3			5.8		129	25.0
	X91504		1FCOUP2 Transcription factor COUP 2 (a.k.a. ARP1)	2.4	7.9	6.6	0	1	0	12	C	3.7
MZ4009_at_	M24069	csda	DNA-BINDING PROTEIN A	14	7.8	12.1	0	0.8	0	0.3	0	0.1
U20158_at_	U20158	lcp2	76 kDa tyrosine phosphoprotein SLP-76 mRNA	3.7	7.8	8.6	80	12.6	3.4	m	2.3	m m

X60104_s_at_	X60104	egr4	EGR4 Early growth response 4	1 4	α /	,					-	(
HG2981. HT3127_s_at	HG2981. HT3127	444	Frican Att Colica 11		2	7.7	1	7	1.0		5	6.3
U49436 at	1149436	eif5	Electric Spinor 11	13.5		25.6	7	13.3	1:1	0.5	0.8	1.5
017	00000		(611)	2.6	7:7	16.1	1.2	5.5	0	1.4	2.2	5.7
HG2917. HT3061_f_at_	HG2917. HT3061	hla	Major Histocompatibility Complex, Class I, E (Gb:M21533)	5.7	7 6	σ	r.	r.	· ·	C	Ċ	(
M79463_s_at _	M79463	myl	PML Probable transcription factor PML (alternative products)	0	,	7.00		2		6.7	n Vi	9.7
U32645_at_	U32645	elf4	Myeloid elf-1 like factor (MEF) mRNA	0 0	0 7	13.3		4.2	4.1	7.1	5.9	11.1
_14076_at_	L14076			250	7 0	7.	0 -	0 -	4.1	0.6	2.5	7.2
			Thyroid receptor interactor (TRIP14) gene, 3'	ì	?	1	1.4	1.0	7	1.4	E:1	5.9
L40387_at_x01057_at	L40387	oasl	end of cds	4.6	7.5	43	105.3	185.2	124.5	1.7	0.4	13.6
221-81	(2010)	171	ILZKA Interieukin Z receptor, alpha	9.3	7.4	39.3	0	9.0	0.3	28	40	-
D61391_at_	D61391	prosap1	Phosphoribosypyrophosphate synthetase.	,	,						;	*
J22662_at_	U22662	Ixra	Nuclear ornhan recentor I XP slobs mDNA	7.7) S) (6.4	0	0.7	0	0	0	2.8
X70340_at_	X70340	tgfa	TGFA Transforming growth factor, alpha	0.10	2.	9.6	34.8	11.4	9.4	8.4	3.1	10.9
X51345_at_	X51345	innb	JUNB Jun B proto-paropaga	70,	, i	= ;	5	٥	0	3.3	4.4	8.6
D88422_at_	D88422	csta	CYSTATIN A	20.0	7.7	5.4	2.3	3.9	5.2		2	1.8
J41740_at_	U41740	golga4	Golgin:245 mRNA	14.0	7.	0.5		7	=	2.2	0.5	0.5
J69546_at	U69546		RNA binding protein Etr. 3 month	2.0	=	17.2	5.9	2.5	6.7	0.3	1.7	6.3
J05249_at_	J05249	rpa2	RPA2 Replication profeip A2 (32kD)	2.5	7	6.4		2.1	5.1	2.1	4.1	9.5
			Myleoid differentiation primary response	6.0	1	27.3	0.2	1.6	m		2.2	5.6
J70451_at_	U70451	myd88	protein MyD88 mRNA	0	7	0	ď	,	r	,	-	-
X82200_at_	X82200	staf50	Staf50 mRNA	101	1	12,1	0.0	7 . 7	1,1	0 .	2.4	7
D87116 at	087116	mankk3	DUAL SPECIFICITY MITOGEN.ACTIVATED			101	0.	1	10,	7.7	3.1	18.1
J04501 at	J04501	SVQ	GYS1 Glyconen synthese 1	13.5	6.9	18	12.2	2.1	2.9	5.6	1.6	7.3
M19650 s at		6/2	CNP 2' 3' Cyclic publicated 2'	8.6	6.9	4.1	0	0.8	0	1.1	0.3	2.2
- 1	M19650	cnp	phosphodiesterase	21.4	9	7 6	ις	α	a		-	6
X76648_at	X76648	glrx	GLRX Glutaredoxin (thioltransferase)	7	200	200			0 0	5	5	n N
			(200)	,	0	<u>.</u>	0.7	xò	2.2	~	7	0

						ļ	lnv	/er	1to	rs:	Nı	r Ha	.co	nei	n, <i>c</i>	16	11.							
,	7.7		6.4	,	2.3	1	5.6	0	19.3	0	7 7		ď	0	1.3	0		2.7	9	1 0	, i		5.2	23
,	6.7	7	2.3	,	0.0		m	2	2.6	6.0	0.7		7	α	0.7	0.1	0	0 -			0.2		0.3	
_	7 2		1	,	7.0		9.0	4	2.1	1.2	0		α		1;	_	0 0	7.7	0 -	-	-		0.2	0.6
,	2.6	-	5	,	2.0	2	0	14	4.2	1.6	219		α	α -	-	0	-	0					4.5	8.0
3 6	0.0	;	8.8	,	6.1		1.9	4.2		6.0	1.5		4 2	ι α	-	0	u	- α	α	0 0			0.8	3.6
0	0		3.9	o o	2.6	-	0.4	1.8	0.3	4.0	1 3		ς.	m		0	<u>u</u>	000	20 00	0 0			0.7	2.6
15.8	5.6		6.5	7	2 -		2.1	7.1	3.5	23.6	147.9		00	37	;	7.8	,	7.4	7	2 2 8			30.6	m
α	6.7	-	6.7	7	99		9.9	9.9	6.5	6.5	6.4		6.3	6.3		6.3	2	2 6	2 0	200			6.1	6.1
α	2.7		7.7	10.7	2.6		3.8	4.8	5.5	3.7	28.6		6.1	3.8		5.6	9	2 6	20 %	171	-		3.7	2
CORTICOSTEROID 11 BETA DEHYDROGENASE, ISOZYME 1	KIAA0082 gene, partial cds	ADAR Double stranded RNA adenosine	deaminase	MOP1 mRNA	PRKCD Protein kinase C, delta	PTPRA Protein tyrosine phosphatase, receptor	type, alpha polypeptide	Spermine synthase	Transmembrane protein	Metallothionein-I-A gene, complete coding sequence	Cyclooxygenase 2 (hCox 2) gene	Major Histocompatibility Complex. Class I. F.	(Gb:M20022)	Nrf2	DsRNA adenosine deaminase DRADA2b	(DRADA2b) mRNA	mRNA fragment encoding beta-tubulin. (from clone D-beta-1)	IL13 receptor alpha-1 chain	MDU1 Antigen identified by monoclonal antibodies 4F2, TRA1.10. TROP4, and T43	Interleukin 10 (1L10) gene	815A9 1 gene (mynein heavy viced heavy	from Homo sapiens chromosome 16 BAC clone	CIT98/5K-815A9 complete sequence	UBIQUITIN-CONJUGATING ENZYME E2-CDC34
hsd11			adar	hif1a	pkcd		lrp	sms	adam8	mtla	cox2		hla	nrf2		adarb1	tubulinB like	il13ra1	86po	110			rnyri11	cdc34
M76665	D43949	00,0	010439	U22431	D10495		M34668	249099	D26579	K01383	D28235	HG2915.	HT3059	S74017		U76421	V00599	Y10659	M21904	U16720		07210014	AL001340	L22005
M76665_at_	D43949_at_	000	U10439_at_	U22431_5_dl	D10495_at_			٦	D26579_at_	K01383_at_	D28235_s_at_ D28235	HG2915.	9_f_at_	S74017_at		U76421_at_	V00599_s_at_ V00599	Y10659_at_	M21904_at_	U16720_rna1 _s_at_		AF001548_rn	a1_a	L22005_at_

Figure 1N

In	162M	m	ς.

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Z35278_at_	Z35278	am12	PEBP2aC1 acute myeloid leukaemia mRNA	14.3	9	1 55	15.0	33	23.6	76	67	106
M87507_s_at							2	5		1	3:	0.51
000	M87507	casp1	IL1BC Interleukin 1, beta, convertase	1.7	9	5.9	1	4.4	2.7	0.1	3.3	19.7
U32849_at	U32849	nmi	Hou mRNA	5.2	9	16.1	10.4	10.5	24.4	27	123	23.9
D78156_at_	D78156	gap1m	RasGTPase activating protein, partial cds	7.2	5.9	3.6	0	0	0.8	0	C	0.0
D87434_at_	D87434		KIAA0247 gene	12.4		2	7	3.8	0	2.1	2.2	0
			S100A10 S100 calcium-binding protein A10	-								
			(annexin II ligand, calpactin I, light polypeptide									
M38591_at_	M38591	ca 1	(p11))	4.1	5.9	5.6	3.8	7.3	4.6	3	0.7	- 9
M73780_at_	M73780	itgb8	ITGB8 Integrin, beta 8	4.3	5.9	20.8		0.2	7.4	2.6	0.2	30
M91670_at_	M91670	psma2	Ubiquitin carrier protein (E2-EPF) mRNA	5.4	5.9	m	2.2	2.5	5.2	0.7		6.9
J	U11732	etv6	ETV6 Ets variant gene 6 (TEL oncogene)	4.4	5.9	6.4				ō	1.4	9
U42408_at_	U42408	lad1	Ladinin (LAD) mRNA	6.3	5.9	67.8	0.3	4.5	Δ	0	0	0
			GRANULOCYTE-MACROPHAGE COLONY.								2	
			STIMULATING FACTOR RECEPTOR ALPHA									
X17648_at_	X17648	gmcsfR	CHAIN PRECURSOR	9	5.9	12.9	0	1.9	0	0.5	6.0	8
HC3507	HC3507	_										
. 7600DL	_	-	iviajor Histocompatibility Complex, Class I									
HT3800_f_at_	_	hla	(Gb:X12432)	7	5.8	33	6.5	2.3	3.6	4	4	•
X15949_at		irf2	IRF2 Interferon regulatory factor 2	6.1	5.8	6.1			3	-	-	σ
X60592_at_	X60592	cd40	CD40 CD40 antigen	6.3	5.8	2			200	-	0	1.
HG987.	HG987.						3	2				1
HT987_at_	нт987	igfbp7	Mac25	2.3	5.7	000	4	4	2 7	,	C	,
U33821_at_	U33821	tax1bp1	Tax1-binding protein TXBP151 mRNA	2.4	5.7	10.3	0		- 2	1-	0	15.6
			IMMUNODEFICIENCY VIRUS TYPE I ENHANCER					1				2
"	X65644	hivep2	BINDING PROTEIN 2	9.1	5.7	12.3	3.8	6.3	4.7	2.2	0.5	7.4
D38551_at	D38551	unknown	KIAA0078 gene	7.3	5.6	3.9	28	4 4	2			ας
HG2167.	HG2167.									,		?
HT2237_at_	HT2237	pkht31	Protein Kinase Ht31, Camp Dependent	8.6	5.6	4.3	7.8	6.5	~	0	0	2
			INDUCED MYELOID LEUKEMIA CELL						1]		†
L08246_at	L08246	mcl1	DIFFERENTIATION PROTEIN MCL1	3.3	5.6	4.6	4.1	2.4	7.6	1		ď
L40393_at_	L40393	qunu	(clone S171) mRNA	1.5	5.6	9	9.0		C	00		200
			LYN V-yes-1 Yamaguchi sarcoma viral related	-								î
M16038_at_	M16038	lyn	oncogene homolog	7.9	5.6	9.1	11.6	6.7	ú	1.6	4.7	7.1
X58521_at_	X58521	Inup62	NUCLEAR PORE GLYCOPROTEIN P62	8.3	9.6	15	10.8	7.2	15.3	1.7	0.3	6.8

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X69886_s_at_	38869X	ž Ž	GK Glycerol kinase	4.8	5.6	18.3	0.4		2.5	0	4 6	27
X71874_cds1			Proteasome-like subunit MECL.1 gene extracted from H.sapiens genes for proteasome like subunit (MECL.1), chymotrypsin-like protease (CTRL.1) and protein serine kinase									
	X71874	lmp10	(PSK-H1) last exon	3.4	5.6	4.4	3.1	1.1	0	12	6.1	9.7
D32129_f_at_	D32129	hla-a	HLA-A MHC class I protein HLA-A (HLA-A28. B40, -Cw3)	8.5	5.5	7.4	5.7	, m	0 9	ر ب	,	,
U26424 at	1126424	krs.1	Stress responsive serine/threonine protein kinase Kre. 1 mBNA								 	
J59863_at_	U59863	itraf	TRAF-interacting protein I-TRAF mRNA	1.3	2.5	12.7	4.7	2 L	3.6	0 0	2.3	α ιτ α ο
Ī	X16396	MTHFD2	MTHFD NAD dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase	7.2	5.5	15.2	2.5	2.2	60	2.5		8 6
X519/0_at X79882_at	X61970 X70882	psc5	PROTEASOME ZETA CHAIN			8.8	5.6	6.4	2.7	1.1		6.1
005_al_	77 2002	d _A	CONTRICT	5.5	5.5	3.8	1.1	2.3	0.4	3.7	1.9	7.6
at	L10338	scnlb	SCN1B Sodium channel, voltage gated, type I, beta polypeptide	1.8	5.4	10	0	0	13	80	4	4
1906/_at_	L1906/	ntkb pb5	TRANSCRIPTION FACTOR P65	7.9	5.4	3.9	8.2	2.9	5.6	6	19	20
			HPRT1 Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan									
M31642_at_	M31642	hprt	syndrome)	5.2	5,4	6.2	2		۳ د	0	2	7 7
M58597_at_	M58597	cd15	FUT4 Fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	2.8		r.	3 7	0 0	200		1 0	
J83115_at_	U83115	aim1	Non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds	ά		0 0				0 -	2 1	1
HG4322.	HG4322.				;	2	1	1	3		0.0	χ.
HT4592_at_	HT4592	tubulinB	Tubulin, Beta	18.5	5.3	13.1	9.6	6	α v	T.	σ	-
U40369_rna1	035011	+0	Spermidine/spermine N1-acetyltransferase							,		
26 at	05050	391	(SOAT) gene	9.1	5.3	12.1	10.6	4.8	9.8	6.3	4.1	8.1
Т	030000 HG658		Manual gene, partial cds	1.9	5.2	4.5	1.7	9	5.1	1.3	1.6	6.4
at	HT658	hlа·с	(Gb:X58536)	7.3	5.2	2.3	6.2	3,5	5.9	2.5	2	-
M20566_at	M20566	il6r	IL6R Interleukin 6 receptor	2.4	5.2	3.1		5.3	10	α	1 -	100
						-	,	5	4.4	1	?	3

									In	ve	ntors	:		N	ir .	Ha	co	he	en	, et	al.											
	1046	1	120 6	120.0	0.	C		-	0	0,0	9 6	0.07	4:1	٦,	1 4	- u	0.0	٩	1	-	*		α		100	oi	0.8		1.7	10.7	13.2	0.8
r	σ	1-	77 5	200	5		5	0				0 0	2	2	100	0 0		1 0	0.8	0	5	o C	7.5	2 0	5 0	7.7	0.5			1.7	6.3	9.0
-	ά		1 9	2 -	;		1	7	? -	1.0	2 0		6:3	4	1 0	0 0	j -	?	-	7	-	4	1	10	7		1.2	-	-	1	3.1	2.2
	37.9	5,5	28.5	200	4	C		0	210	12	, 4	20	0.1	4	-	11.0	2 -		Σ.	7	-	0	0	c	α		3.7		0.3	27.3	6.1	1.4
	17.5		523	5.40	r		5	7	7 -	100	α -		1	00	ας	40	י לי	2 1		0		2.9	90	26	0		3.8		2.3	4.7	2.8	0
}	Ω		59.4		5	c	}	7		25.1	0	5.5	2	5		000		-	7 7		-	-	60	0.3	7		5		6.0	3.7	3.5	0.4
-	32 7	- 2	683	17.0	?	12 76	-	χ.	8 6	14.7	9	1-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0	1	7.3	3	7.6	i m) -	7:	4 4		4.3	8.1	8.5	σ		2		7.4	17.9	12.2	10.1
-	5.2	5.2	5.2	50	-			5.1	5.1	5	, r	יטיי	1	Ŋ	5	4 9	4 9	10		4.8		4.8	4.8	8 4	47		4.7		4.7	4.7	4.7	4.7
L	0	9	2			_ m		4	 00		3.6	2 4		2	9.5						-	0.8	4.3	8	6		2		2	8		6
	15.	3	3	4		_		∞	2	_	۳.			ού 	6	9	4	(١	12.		10	4	2	2				5.	4	1.	9
IGFBP4 Insulin-like growth factor binding	protein 4	Xq28 mRNA	Humig mRNA	Mitogen inducible gene mig-2	PAI2 Plasminogen activator inhibitor, type II	(arginine-serpin)	PTPN12 Protein tyrosine phosphatase, non-	receptor type 12	Platelet alpha SNAP mRNA	Unknown product	MUC1 Mucin 1, transmembrane	FTH1 Ferritin heavy chain	Sodium/potassium transporting ATPase beta.3	subunit mRNA	PGK1 Phosphoglycerate kinase 1	TRANSCRIPTION FACTOR RELB	LDHA Lactate dehydrogenase A	Profilin mRNA	DIAL COCOCOLIVITY MITOORY ACTER	PROTEIN KINASE KINASE 1	Platelet-derived growth factor (PDGFA) A chain	gene	MAP4 Microtubule associated protein 4	Sec7p-like protein mRNA, partial cds	Randomly sequenced mRNA		HLA-B null allele mRNA		HCK Hemopoletic cell kinase	IAP homolog B (MIHB) mRNA	Mch3 isoform alpha (Mch3) mRNA	IN 5.5 nucleotidase (CD73)
	igfbp4	cxorf6	mig			pai2		ptpg1	snapa	d1s1733e	muc1	fth1		atp1b3	pgk1	nfkb reIB	ldh1	pfn1		mapkk1		pdgfa	map4	sec7p-like	rac1		hla-b	<u>.</u>	IICK	ciap1	casp/	Clul
	M62403	U46023	X72755	224725		M31551		M93425	U39412	D28124	J05582	L20941		U51478	V00572	M83221	X02152	J03191		L11284		M19989	M64571	U59752	D25274		D49824	1012	182211	03/54/	U6/319	V22/40
M62403_s_at	į	U46023_at_	X72755_at_	Z24725_at_	M31551_s_at			M93425_at_	U39412_at_	D28124_at_	J05582_s_at_	L20941_at_		U51478_at_	V00572_at_	M83221_at_	X02152_at_	J03191_at_		L11284_at_	M19989_cds2	_at_	M64571_at_		D25274_at_		049824_s_at	ואיל דפנטדואו		03/54/_at_	VEE 740 et	197140_dL

_								• •			•				ma			••,	CI												
	6.8	1.9	-		ñ	5.9		3.7	2.4	2.2	0.9	3.5		14.1	í	5.2	8.0	0.4			19.6	0		1.4	12.4	5	2000	أذ		4.7	4.2
	10.3	2.9	-		4.1	2.7		11.2	2.4	4.8	0.3	3.3		0.1	7		7:7	0.4			1.6	1 7	1	0.5	4.6	2 -		7		0.6	1.4
	4.3	1.1	0	,	1.2	1.8			2.2	 	1.1	4	_	0	-	7,	7.	1.3	-		7			1	1.4	1.7	00	;		7	0.8
	5.8	0	,		0.3	5.9	-	ام);)	4.	0.8	5.9		4.5	c	0,0	3.6	1.7			17.7	2.4		2.4	3.7	4.6	5.3	;		8.1	14.3
	0.5	1.2	200		4.1	2		4.4 کاری	200	3.2	0.3	4		0.2		1 4	7	6.1			7	4.1		8	5.4	30.2	0.4	-		17.	<u>8</u>
	4	2.2	C			y. 9.	<u></u>	0.01	7.7	5.	2.2	1.4	-	17		10	7.7	2.5		,	1	6.1		3.4	8	5.5	6.0		(0.10	<u></u>
	4	4	33		200	0.0	<u></u>	2	4.0	1 0	7.5	9.6	0	20.5	27.1	1 4		4.3			1	5.3	;	4.6	8.6	7	17.4	-	(2) (2	4.7
-	4.7	4.7	4.6	-	0 0	0.4		7 4	0 6	1,	4.4	4.4		4.	4	4 4		4.0 در		- 0	-	4.3		ر ا ا	4.2	4.2	4.2			7 7	4.2
ļ.,	9.0	7	2.6		1/	+			2.7			8.3	٦		- 2	1 4						6									
,	١٩	2	- 7	,	0 4	2	v		100	2	0	×		ÿ		13				6.4	5	10.	C	vi c	9.4	2.9	5.1		u	o c	2.3
PML Probable transcription factor PML (alternative products)	Rah 13		Ret Transforming Gene	LPS-Induced TNF-Alpha Factor (117AF) mBNA	TGIF protein	GAPD Glyceraldehyde-3-phosphate	dehydrogenase	Homeobox gene	PGAM1 Phosphoglycerate mutase 1 (hrain)	ARH9 Aplysia ras-related homolog 9	SERUM PROTEIN MSESS	MDK Midkine (nellrite growth promoting (nellrite	(12)		Proto oncogene BCL3 gene	ICH-2 PROTEASE PRECURSOR	H2AZ H2AZ histone	GIU Chisterin (complement lyric inchistra	testosterone-repressed prostate message 2.	apolipoprotein J)	HLA.A MHC class I protein HLA.A (HLA.A28,.	B40, .Cw3)	Cytoplasmic dynein light chain 1 (hdic1) mbni	PSMA3 Proteasome component C3	CYBS Cytochromo h E		ILIA Interleukin I, alpha	SATB1 Special AT-rich sequence binding	protein 1 (blids to nuclear matrix/scaffold. associating DNA's)	ZNF173 Acid finger protein ZNF173	שינו די ל עוכים ווויפכי או סוכיוו לואו די ל
) A	rab13			litaf	hpe4		psma4	hlx1	pgam1	arh9			mdk		bc13	casp4	h2az			cli		hla-a	dlc1	hc3	cvh5	113	110		satbl	znf173	
X63131	X75593	HG2825.	HT2949	962420	X89750		D00763	M60721	J04173	L25081	M88338		M94250		U05681	U28014	M37583			M63379		M94880	U32944	D00760	W22976	Maggga	1120303			U09825	
X63131_s_at_X63131	X75593_at_	HG2825.	at	U77396_at_	X89750_at_	_	_at	ļ	at	_	M88338_at_			U05681_s_at	_	7	M3/583_at			M63379_at		M94880_t_at_	1			M28983 at	+		-	U09825_at	1

Figure 1R

					I	nv	en	to	rs:		N	lir I	Ha	coł	ıeı	1, 6	et e	al.											
0		10	0	2,0	î	3.2	0.4	4.5	(5		9.	14	7.	8	5	σ		4.	0	20.0		0	77	1	2 0	7.7	2.4	69
α	-	0.7	0	5 0	1	0	3.1	1.8	1.8	8		1		1	5.1		2 5	2 4	7	2 1	7.7		α	200		2.0	7!	4:1	23
5.	0	1.0	000	100		0	5.9	1.1	0.5	1.5		5	α C	1	1.8		1	27	7.7	7			1 1	ά	0	0 0	0.7	0.0	2
2 4			C	7		0	0	2.6	2.2	0	-	0.1	3	3.5	5.4		24.7	7	3	4 1				1	1	2 0	5 0	5	14.7
6.0		6.5	0	7.0		0.5	0.6	3.2	2.2	1.5		Ţ	00	2	1.7		13.2	0 0	7.3	1.2			1	0	2	?		2)	3.2
8.0	α	11.2	1 7			0	1.9	e	9	1.8	-	0.1	0		6.2		Ω̈	4 5		α.			0.3	122	2	7 -		1	2.8
2.4	2	3.8	6	900		11.2	2.8	4.7	2.4	6.5	-	5	10.2		10.5		9.3	5.4	;	13.4	-		m	67	0	1	0.0	<i>i</i>	14
4.2	2 4	4.2	4	4 1		4.1	4	3.9	3.9	3.9	0	0.0	3.9	-	33.00		3.8	38	3	3.7			3.7	3.7	3.7	27	,,,	· ·	3.7
1.9	3.7	7.2	4	2.4		3.3	2	6.1	5.1	2.8	L.	7	5.6		4.5		5.9	111		1.9			3.3	4.4	2.1	6 7	יי דו	7	2.4
Ubiquitin gene	TNNT2 gene exon 11 troponin	HISTONE H3.3	KIAA0162 gene	(clone cc44) senilin 1 (PS1; S182) mRNA	Heparan N-deacetylase/N-sulfotransferase-2	ביייים בייים בייים בייים בייים ביייים בייים ביים בייים ביים בייים בייים בייים בייים בייים בייים ביים ביים ביים ביים בייים בייים בייים ביים ביי	Terratricopeptide repeat protein (tpr2) mKNA	KIAAUUU5 gene	C4A Complement component 4A	RagA protein	Calcium ATPase isoform 3x/a mBNA		Pim-2 protooncogene homolog pim-2h mRNA	ATF4 CAMP dependent transcription factor ATF	4 (CREB2)		MHC class I molecule (MICB) gene	PolyA site DNA		Ras-Related C3 Botulinum Toxin Substrate		Nuclear Mitotic Apparatus Protein 1, Alt. Splice	Form 2	EDN1 Endothelin 1 (alternative products)	INTESTINAL MEMBRANE A4 PROTEIN	UBE1 Ubiquitin activating enzyme F1	Biliverdin-IXalpha reductase mRNA	Protein tyrosine phosphatase PTPCAAX1	(hPTPCAAX1) mRNA
	tnnt2	h3f3b	supt6h	ad3	(+000	illeste taro	2 101		c4a		atp2b3		pim2	;	att4		micb			ras-related			nmap1	edn1		alst	blvra		ptp4a1
049869	X98482	248950	D79984	L76517	1136601	1146571	04001	D13030	M59815	U41654	U57971		U77735		090209		U65416	224724	HG1102.	HT1102		HG2238.	HT2321	105008	109604	M58028	U34877		U48296
U49869_rna1 _at_	at	Z48950_at	at	L76517_at_	1136601 34	T	T	Ţ	Т	U41654_at_	U57971_s_at	Г	U77735_at_		090209_at_		7	at		HT1102_at_	HG2238.	HT2321_s_at HG2238	٦			_			U48296_at_

Figure 1S

				HIV	entors:	IN	ппа	co	nen, e	a ai.							
17.3	32.7	,	0	, e		2.9	1.7	2.5	8.4	, קר	2.7		S)	-	1.5	Ţ !	7 -
3.1	20.7	α c	0.0	4.0		1.6	0.1	6.	6.0	7.7	0.1		7.7	1.6		1 0	7.7
9	0.5	-	80	4.4		0.7	8.	<u>Σ</u>	0 1	0.0	500				6.7	1 6	200
2.6	30.8	r.	5.1	6:0			2.2	7	2) 0	9	- 10 - 12 - 12 - 12 - 12 - 12 - 12 - 12 - 12	-	7 7	7	α	- 0	
2.8	0	5.2	3.1	1.2			9 .	7.7	0 4		0.0	u u		5			5.5
0	9.0	ī.	5.2	0.3		4.7	2.0))) 	C.2 C.5	1 -	0.4	C		200	13.3	, ,	0.5
16.6	233.2	33	2.5	2.1			2. c	0.0	ر. د. د	0.01	3.2	0	-		1 00		2.3
3.7	3.7	3.6	3.6	3.6	(9 0	0,0	2 4	, w	0 0	3.5	4.6	,	7 7	3.4	000	33.1
2	12.5	5.7	2.2	2.4		7 0	0 -	110	0 8	2 6	2.6	2.8		27.4	3.6	0 -	1.9
Lysophospholipase homolog (HU.K5) mRNA	EBIT-IIgand chemokine	BETA-2-MICROGLOBULIN PRECURSOR	HNRPA2B1 Heterogeneous nuclear ribonucleoprotein A2/B1	DTR Diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)	Protein phosphatase:2A catalytic subunit alpha gene extracted from Human protein phosphatase 2A catalytic gubunit albeata	Annexin V (ANX5) gene 5'.intranslated region	Uridine diphosphoglucose pyrophosphorylase	HnRNP C2 protein mRNA	Translational initiation factor 2 beta subunit (elF-2-beta) mRNA	CSPG2 Chondroitin sulfate proteoglycan 2 (versican)	Lipid-activated protein kinase PRK1 mRNA	L43579 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 110298, mRNA sequence	ENO1 Enolase 1. (alpha)	NADH-CYTOCHROME B5 REDUCTASE	C5R1 Complement component 5 receptor 1 (C5a ligand)	CRFB4 Cytokine receptor family II. member 4	HSPA4 Heat shock 70kD protein 4
huk5 min3h/olo	III Dan/ elc	b2m	hnrpa2b1	dtr		annexinV	ugp2			cspg2	pak1		eno1	dia1	c5ar	il10rb	hspa4
U67963	001/100	100105	M29064	M60278	M60483	U01691	U27460	M16342	M29536	016306	N33053	L43579	M14328	M28713	M62505	71727	L12723
U67963_at	27770	J00105_s_at_	M29064_at_	M60278_at_	M60483_rna1 _s_at_	U01691_s_at 	U27460_at_	M16342_at_	M29536_at_	U16306_at_	U33053_at_	L43579_s_at_	#	M28713_at_	M62505_at_		L12723_at_

Figure 1T

						In	vent	ors	s:	· N	Vir	Ha	coh	en,	et al.									
60	200	0 6	0	0 -	1	5.1	C	عاد	623	5 6	7.7	1.1	7	1 0		1	0	9.5	27	, a		4.6	5	2.4
0	7	, r.	-	ο C	0.0	3.2	0	- C	0	, ,	5	2.1	, m	200		0	c	0	F	, ,		i i	2.7	1.3
6		90	-	100	7.0	2.3	90) -	174		1	2.6	α	0.4		0	0.7	8.0	10	2	1 1	7.7	1.1	0.2
-	0.5	0	-	5 -	1	5.9	0	20.0	114	-	2	0.7	2 7	4.4		4.6	0.7	4.7	0.4	0		7	0	0
-	- 2	2.5	- 4	2 0	21	1.9	-1	10.5		α 4		4.5	4	3.5		9.0	2,6	6.0	9.9	4.1	5		2.2	14.8
7 0	2.2		L C		-	4.7	С	9.2		1	,	2.4	-	2.5		0.3	4.0	0	6.0		ŗ	7.,7	1.5	7
3.7	3.4	1.7		17		10.3		2.7	35.9	20	1	3.1	4 0	6.8		91.6	2.4	20	9	3.7	,	2.0	12.3	4
83	333	3.3	3.3	0 0		3.2	3	3.2	3.2			3.1	3.1	3.1		3.1	3.1	3.1	3.1	3.1	,	1:5	ന്	3
2.3	2	3.9	, m	0 0		4	Ŋ	4.6	m	2.7		3.8	2	5.6		2.3	2.6	2.1	6.4	3.7		3	1.9	8.5
MIC2 Antigen identified by monoclonal antibodies 12E7, F21 and 013	Arginine-rich nuclear protein mRNA	Uridine nucleotide receptor (UNR) gene	Myelodysplasia/myeloid leukemia factor 2 (MLF2) mRNA	ALDOA Aldolase A	MACS Myristoylated alanine-rich C-kinase	Substidle	Triosephosphate Isomerase	Hbc647 mRNA sequence	K12 protein precursor mRNA	Nuclear chloride ion channel protein (NCC27)		Proteasome subunit p44.5	EIF4A2 Eukaryotic translation initiation factor 4A (eIF-4A) isoform 2	NP Nucleoside phosphorylase	SCYA1 gene (secreted protein I-309) extracted	Ironi Human secreted protein (1.309) gene	PEPTIDYL.PROLYL CIS.TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR	B12 protein mRNA	PGD Phosphogluconate dehydrogenase	ATP6E ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD	Galectin	PROTEIN TRANSPORT PROTEIN SEC61 BETA	SUBUNIT	FACTOR VIII INTRON 22 PROTEIN
66po			mlf2	aldoa	200	Hacs	ţ. To:		k12	ncc27		psmd11	eif4a2	. du	5061	1303		tnfaip1	pgd	atp6e	lgals9			dxs522e
M16279	M74002	U40223	U57342	X12447	010522	010322	HT2375	U68494	U77643	093205		AB003102	D30655	K02574	M57506	000 / 014	M80254	M80783	030255	X76228	249107		125085	M34677
M16279_at_	M74002_at_	U40223_at	U57342_at_	X12447_at_	010522 at	U10322 at		U68494_at_	U77643_at_	U93205_at_	AB003102_at	ı		K02574_at_	M57506_rna1	-ar-		M80783_at_	U30255_at_	X76228_at_	Z49107_s_at		ı	M34677_at_

Title. Assponse of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

			TYROSINE-PROTEIN KINASE RECEPTOR ECK					-		l	-	
M59371_at_	M59371	eck	PRECURSOR	1.3	m	5.3	2.4	2.2	5.5	1.1	1.4	2.3
M84332_at_	M84332	arf1	ARF1 ADP-ribosylation factor 1	2.1	3	2.9	2.3	5.2	-	1	3.2	0
U16799_s_at									+	?	1	
	016799	atp1b1	Na, K-ATPase beta-1 subunit mRNA	7.1	Ċ.	œ	7	ō	<u> </u>	000	٣	ď
U56402_s_at			Chromatin structural protein homolog		-	-	;	1	5	111	7	3
t	U56402	spt5h	(SUPT5H) mRNA	2.9	m	2	5,5	5.2	m	1.1	0	7
U90313_at_	U90313		Glutathione-S-transferase homolog mRNA	4.1	m	3.7		60	0	8	3.0	4 6
			Sin3 associated polypeptide p18 (SAP18)	-							2	?
- 1	U96915	sin3	mRNA	3.3	m	5.4	12	6.5	7.4	1 2	4	7.2
X17042_at_	X17042	prg	PRG1 Proteoglycan 1, secretory granule	6.1	m	3.4	4.2	1.6	4 4	29	2.3	1 6
	X65873	kif5b	KINESIN HEAVY CHAIN	2.8	m	2.2	80	25	0 7	0	-	α
X81198_at_	X81198	arcn1	COATOMER DELTA SUBUNIT	1.9	m	2.6	2.4	m	2.5	0.7	60	1 4
Z19554 s.at	219554	vin Ei	VIM Vimentin	с	~	-	2 0	7 0	,	-		,
	706501	177			,	2		;	7.7	1	0.0	7.6
AB004884 at	170077	c04/	integrin associated protein mKNA,	4.7	m	3.9	5.5	4.1		1.4	1.4	5.6
5	AB004884	pkua	PKU-alpha, partial cds	^	0	ď	,	'n	7 7	0	0	0
D63134_at_	D63134		ETS-like 30 kDa protein	α		71.5	1 -	200		2 0) u	
D87673 at	D87673	hsf4	Heat shock transcription factor A	000	0.7	77.7	7	7 0	5 6	5 6	0.1	16.4
HG4683.				o t		7.	4.1	5.7	ر ا	5	Э).
HT5108_s_at HG4683	HG4683.		Tumor Necrosis Factor Receptor 2 Associated									
1	HT5108	traf2	Protein Trap3	3.2	2.9	1.5	e	1.8	0	0.5	2.5	2.7
L435/6_at	L43576		(clone EST02946) mRNA	2.1	2.9	17.1	1.4	4.8	5.7	0	=	6.5
M31932_at_	M31932	fcgr2a	FCGR2A Fc fragment of IgG, low affinity IIa, receptor for (CD32)	9.5	000	C.	0	0,	<u></u>	-	-	
M96995_s_at						i				+	†	ţ.
	M96995	grb2	GRB2 Growth factor receptor-bound protein 2	5.3	2.9	3.6	2.2	3.1	0		1.2	2
U07139 at	107139		CAB3b mRNA for calcium channel beta3	r		Ĺ		,		 		
X05908 at	X05908	anxal	ANX1 Annexin (linocortin l)	7 0		5		7.0	4.0	5	0	0.2
				3.6	6.3	4.0	v.	0.0	5.2	7.8	4.0	3.6
X07619_s_at_X07619	X07619	cyp450db1	Cytochrome P450 db1 variant b	8.8	2.9	8.2	0	7.3	2.4	4.2	0.2	13
												[

Title: sponse of Dendritic Cells to a... Inventors: Nir Hacohen, *et al.*

				1	Inven	nors:	Nir i	Taco	nen,	C	t at.									
<u></u>	0 7	;	4.5	2.9	1 2	8.1	α ς	5 5		0	σ			m	0	J.		12	13.1	
-	4 4		П	1.6	1.7	-	7.0			1.3	0	1		4.2	7	7	4.2	7 1	10	
0	23		1.4	2.6	1.6	1.3	7 0	0	1 (2.3	0.0	19		9.0	C C	2	<u>درا</u>	0	ά	2
8.9	4.2		2.2	0	0	2.2	α		5 -	5	4.2	1	1))	'n			0 0		6
4.0	13		2.2	-	1.3	7.1	1	2	,	7	2.2	28		7.5	4 5	2	<u>5</u>	4 0	200	
0.3	7.3		4.1	9.0		1.5	7 4	-	, ,	5	1.3	22		1	6	i c	6.3	C	c	1
12.5	7.5		4.8	3.1	2.6	21.5	en en	11 4		30.0	11.1	4.9		۸:۷	4	:	1 1	19.1	9.7	0.00
2.9			2.8	2.8	2.8	2.8	8	α ς		2.8	2.8	2.7	,	/->	27	,	/·.'y	2.7	27	7 0
2.3	6.4		æ	11.4	9.1	6.4	21.8		0	0	5.4	4.2	,	7.7	2.6	:	0.11	5.6	4.4	
GUANYLATE CYCLASE SOLUBLE, ALPHA.3 CHAIN	EWSR1 Ewing sarcoma breakpoint region 1	Small Nuclear Ribonucleoprotein, Polypeptide	C, Alt. Splice 2	Nuclear Factor NF 116	VDR Vitamin D (1,25- dihydroxyvitamin D3) receptor	STAT3 Signal transducer and activator of transcription 3 (acute-phase response factor)	DAF Decay accelerating factor for complement (CD55, Cromer blood group system)	PAM Peptidylglycine alpha amidating monooxygenase	HEN	Port Scriet, chair 1 (and joined CDS)	KSIN Kestin (Keed Steinberg cell expressed intermediate filament associated protein)	Proteasome subunit HsC7.1	FK506-Binding Protein Alt Solice 2	2 22 10 10 10 10 10 10 10 10 10 10 10 10 10	Transcriptional Coactivator Pc4	Thyroid receptor interactor (TRIP7) mRNA, 3		Inhibitor of apoptosis protein 1 mRNA	Osteoclast stimulating factor mRNA	PGF Placental growth factor, vascular endothelial growth factor, related protein
guc1a3	ews			nfil6	vdr	stat3	daf	pam	nefh		rsn	psmb2			TCPC4	trin7		ciap2	ostf1	Døf
X66534	X66899	HG1322.	HT5143	HG3494. HT3688	J03258	L29277	M31516	M37721	x15306		X64838	D26599	HG1139. HT4910	HG4297.	HT4567	40357		,	U63717	X54936
1	at	HG1322. HT5143_s_at HG1322	. 0.000	HG3494. HT3688_at_	J03258_at_	L29277_at_	M31516_s_at _	M37721_at_	X15306_rna1 at		X64838_at_	D26599_at_	HG1139. HT4910 at	HG4297.	HT4567_at	140357 at	U45878_s_at		U63717_at_	X54936 at

Figure 1W

litle: Esponse of Dendritic Cells to a...
Inventors: Nir Hacohen, et al.

				ln	vento	ors	:	Nir	Ha	co	he	n, <i>et</i>	al.							
1.6	6.2	C	ς α	5	13.8	0	3.1	3.6	4	5.5		σ		2.8	0		7	, 'c	25.0	1.1
1.8	1	1 7	=	1.7	1.2	0.1	1.4	ō	2.4	0	0.5	-		1.6	10.7	9		α 4	0	0.3
6.0	1.4	1.7	-	1.5	9.0	0.7	0	66	6.0	1.4	60			4.2	~	C	0		13	6.5
0.2	0	0.5	2	0.5	8.2	21.6	9:1	10.2	4.5	1.8	0 3			7.8	10.3	7	C	1-1	2.4	3.4
6.0	0	-	Ľ.	2.3	5.6	11.3	2.3	6.3	8.7	2.1	1.4	4 2		3.6	16.9	3.5	1	4	4	0.1
2.2	0.4	1.7	6	0.2	6.0	6.4	4.2	0	4.9	4.4	0 5	2 2		4.1	38.4	0	0	=	2.8	1.4
7.6	12.2	7.2	2.5	5.7	13.7	2.2	4.8	4	5.5	12.8	0	9.9		4.7	8	0	2 9		2.5	1.8
2.7	2.7	2.7	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6		2.5	2.5	2.5		2.5	2.5	2.5
3.3	0.7	37.7	80	5	4.4	0	3.4	6.0	1.7	5.5	0.2	3.6		2	2.9	0	1.9	20.5	1.9	2.6
ARHG Ras homolog gene family, member G (rho G)	SERYL-TRNA SYNTHETASE	DNA-BINDING PROTEIN A	Single-Stranded Dna-Binding Protein Mssp-1	ANX7 Annexin VII (synexin)	FACL1 Long chain fatty acid acyl-coA ligase	ERF.2 mRNA	TOP1 DNA topoisomerase i	Cytochrome P450 (CYP2A13) gene	YMP mRNA	Grb2-related adaptor protein (Grap) mRNA	Elongation factor 1 beta	REL V.rel avian reticuloendotheliosis viral oncogene homolog		Fas-binding protein (DAXX) mRNA, partial cds	Monocyte Chemotactic Protein 1	Bactericidal Bpi'Gene	PP2A B56-beta mRNA	NATURAL KILLER CELLS PROTEIN 4 PRECURSOR	Scaffold protein Pbp1 mRNA	HSPA6 Heat shock 70kD protein 6 (HSP70B")
rhoG		csda		anxa7	facl1	erf2	top1		emp3	grb2-rel	eef1b2	nfkb crel		daxx	mcp1		ppp2r5b	nk4	pbp1	hspa6
X61587	X91257	X95325	НG2639. Н T 2735	J04543	L09229	U07802	007806	U22028	U52101	U52518	X60489	X75042		AF006041	HG4069. HT4339	HG4336. HT4606	L42374	M59807	U83463	X51757
	X91257_at_	X95325_s_at_	±.	J04543_at	البد		U07806_s_at 	_r_at_	٦		X60489_at_	X75042_at_	AF006041_at		s_at	HG4336. HT4606_at_	L42374_s_at_ L42374		U83463_at	X51757_at

1	D00762	psma3	PROTEASOME COMPONENT C8	2.8	2.4	4.2	82	0	5.2	00	1	6
7	D26600	psmb4	PROTEASOME BETA CHAIN PRECURSOR	3.4	2.4				10	6.3	7.7	4:4
D87446_at	D87446		KIAA0257 gene, partial cds	5.2	24	7	100	7 0	-	5 0	9 6	-
	12072		SIAT4A Sialyltransferase 4A (beta-			5		2	-	7	7	ÿ
	139/2		galactosidase alpha-2,3-sialytransferase)	3.1	2.4	1.4	1.1	1.9	2.3	0.4	0.7	4
3 s at	74707	Suli	KPL3 Ribosomal protein L3	3.7	2.4	4.5	2.3	2.7	2.1	1.7	2.6	2.2
,	M55998	collagen-a1	Alpha: I collagen type I gene 3' end	Q Q	Ċ	C			,	 ,		
M63180_at N	M63180	tars	TARS Threonyl-tRNA synthetase	0.0	4:00	20.00	1.0	9.0	16.4	٥١	0	0
			ID2 Inhibitor of DNA binding 2, dominant	7	7.7	9.0	5.1	Σ.	10	0.5	6.0	9
M96843_atN	M96843	id2b	negative helix-loop-helix protein	14.6	2.4	1.6	6	C.	0	2.4	,	O.
ŀ	U28386		RCH1 RAG (recombination activating gene)	α ,	C	- u				1 6	7 7	0 0
J28963_atU	U28963		Gps2 (GPS2) mRNA		4:00	10.4	0.7	7 (χ. Σ.	2.7	2.7	80
				1,75	2:4	5.5	<u>ا</u>	2.5	1.9	4.0	0	1.7
			ERBB2 V.erb.b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma	-		•						
낡	X03363	erbb2	derived oncogene homolog)	2.6	2.4	ď	C	7	Ċ	C		
J.	Y07909	emp1	B4B	6.1	2.4	200	2 4	1 2	0 0	5 -	7 0	5 -
Y08409_atY0	08409	thrsp	Spot14 gene	4.6	24	4 5	100	2 2	-	r c	0	
- 1	249835	grp58	PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR	0	, ,		1 0	0.7	1.0			Σ
AF001294_at						0.2	20	3.2	2.9	8.0	0.9	4.1
	AF001294	ldi	IPL (IPL) MRNA	2.6	2.3	9	4.5	2	α	0	ď	,
	04208/		KIAA0118 gene, partial cds	7.1		10.9		19		30	2.0	γ α
U00032_atD	U50532	HML2	Macrophage lectin 2	0	2.3	0	c	7	de	10	3 0	
L00352_at	L00352	Idir	LOW-DENSITY LIPOPROTEIN RECEPTOR PRECIIESOR	-						ŝ	5	3
Τ				21.4	2.3	9.5	5.5	2.8	6.0	1.9	7.7	4.6
	L10343	pi3	PI3 Protease inhibitor 3, skin-derived (SKALP)	4.1	2	22.9	<u>2</u>	1 7	ά	Č	2	
7	M23254	capn2	CAPN2 Calpain, large polypeptide L2	22	0 0	4.4	0 0	, u	, ,	j [5	<u>.</u> ن
U47634_atU	U47634	b-tub4	TUBB Beta-tubulin	8 8	2 2	00	100	200	2.7		7.0	0 0
U78798 at 10	1178798	traff	TNF receptor associated factor 6 (TRAF6)			1	0.1	6.3		-	6.0	9.0
Т	X16706	foel2	FOS BEI ATED ANTICEN 2	4.4	2.3	5.1	0.2	2.5	0.5	0.2	0.5	4.6
7	20.01	10312	LOS-NELATED ANTIGEN Z	8	2.3	30.2	5.3	m	2.1	2.7	0	6.0

X84709 at	X84709	fadd	Mediator of receptor-induced toxicity	1.7	2.3	2.5	2	2.1	0	0.3	-	3.4
	X94754	mare	Yeast methionyl-tRNA synthetase homologue	1.5	2.3	4.5	-0	0.7	6	0	9.0	2.2
T	014812		KIAA0026 gene	1.7	2.2	5.2	3.5	c.i E.	6.3	0.7	1.4	2.7
	L06132	vdac1	VDAC1 Voltage-dependent anion channel 1	4.4	2.2	3.2	1.7	2.5	0	1.3	9.0	3.4
M27533_s_at	M27533	cd28lg	lg rearranged B7 protein mRNA VC1-region	2.6	2.2	36.8	4.0	3.8	5.5		4.7	19.8
x60003 s at	хбооз		CAMP.RESPONSE ELEMENT BINDING PROTEIN	1.8	2.2	3.3	0.7	1.7	0.4	2.2	0.2	0.7
X70811 at	X70811	adrb3	ADRB3 Adrenergic, beta 3. receptor	2.7	2.2	2.3	0.4	1.1	3.1	1.5	9.0	2.8
HG3417. HT3600_s_at HG3417. HT3600	HG3417. HT3600		Gtp Cyclohydrolase I, Alt. Splice 1	4.9	2.1	12.8	د؛ د:	12.1	3.2	0.8	9.0	7.5
M11717_rna1	M11717	hsnala	Heat shock protein (hsp 70) gene	2.8	2.1	m	9.6	3.5	2.7	5.1	2.3	1
M85169 at	M85169	d17s811e	Homologue of yeast sec7 mRNA		2.1	3.7	4.4	0.8	1.6	4.6		2.3
1114969 at	U14969	rpl28	Ribosomal protein L28 mRNA	1.6	2.1	1.5	2.1	2.5	2.7	0.7	0.5	=
			MEF2A gene (myocyte specific enhancer factor 2A, C9 form) extracted from Human myocyte									
U49020_cds2	1149020	mef2a	specific enhancer factor 2A (MEF2A) gene, first coding	1.7	2.1	2.5	2.8	1.7	0.7	2.4	0.8	3.5
1159070 21	1158970	tom34	Putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA	2.9	2.1	7.4	0	0	7.6	5.6	2.7	7.7
X07743 at	X07743	plek	PLECKSTRIN	9.7	2.1	5.7	13.9	10.7	2.7	3.6	1.6	5.6
X80230 at	X80230	cdc2 4	mRNA (clone C.2k) mRNA for serine/threonine protein kinase	1.6	2.1	9	6.0	0.7	0	1.3	0.8	5.9
X89985 at	X89985	bcl7b	BCL7 B cell lymphoma protein 7B	3.2	2.1	3.2	5.7	6.5	4.3	1.9	0.3	0.9
725884 at	725884	clcn1	CIC-1 muscle chloride channel protein	3.2	2.1	1.9	0	1.4	2.7	1.6	0.1	0.5
Z47727 at	247727	rbp7	RNA polymerase II subunit	2.7	2.1	3.3	1.2	4.8	1.9	0.4	9.0	1.8
D14826 s at	014826	crem	CREM CAMP responsive element modulator	3.4	~	6.3	13.7	7.8	50.6	5.1	1.6	7.4
D31887 at			KIAA0062 gene, partial cds	3.2	2	45.2	0.4	9.0	6.8	1.2	0	0.1
	D86961		KIAA0206 gene, partial cds	15.1	5	9.9	19.5	4.8	-1	1.2	2.4	3.7
1 32866 at	132866	enr1	Effector cell protease receptor 1 (EPR-1) gene, partial cds	2.4	<u>c1</u>	1.5	0.4	<u>c1</u>	1.2	0.5	9.0	1.9
L32000_a1_	Lococo	· ii										

M10901_at_	M10901	gcr	GRL Glucocorticoid receptor	1 9	6	3.0	4.2	4.71	1 2	1	-	-
U73824_at_	U73824	dap5	P97 mRNA	4.3	1 (-1	5 0		3.4	3.77	1 (α - C	įα
			Epidermoid carcinoma mRNA for ubiquiting					i i				?
D83004_at_	D83004		bendless gene product	m	1.9	ю (С)	0.7	2.4	0.1		1	2
M10277_s_at	M10277	actb	ACTB Actin. beta	2 1	0	,	, ,	-	0		-	
M27749_r_at											1	-
ļ	M27749		Immunoglobulin-related 14.1 protein mRNA	5.6	9.	4.2	Ö	0	5.6	0.5	Ċ	0.7
U88629_at_	U88629	ell2	RNA polymerase II elongation factor ELL2	2	1.9	8.1	0		1.5	9.0	0	-
X53416_at_	X53416	аррх	FLN1 Filamin 1 (actin-binding protein 280)	1.6	1.9	2.6	1.3	1.2	0	9.0	0	
X59770_at_	X59770	11172	INTERLEUKIN 1 RECEPTOR, TYPE II PRECURSOR	0.5	9:1	1.2	9	5.3	4.0	2.3	7	1
X80910_at_	X80910	ppp1cb	PPP1CB Protein phosphatase 1, catalytic subunit, beta isoform	2.9	6	27	40	-	- 9	c	, C	1 1
X87838_at_	X87838	ctnnb1	CTINNB1 Catenin (cadherin-associated protein), beta 1 (88kD)	6 4	-	4	α	C Tr		α	5 -	2
Y08265_s_at_			DAN26 protein, partial		1 6		17		-		2 6	
L38951_at_	L38951		Importin beta subunit mRNA	1.9	18	17	~	0.5	2.5	19	σ	
U28015_at_	U28015	casp5	TY protease	2.6	8	16.2	3.4	C	23.2	200	٥١٥	1
U44799_s_at	U44799		U1-snRNP binding protein homolog mRNA	2.2	18	3.6			4 0	-	6	
			Mitochondrial NADH dehydrogenase									
			precursor (NDUFS8) nuclear mRNA encoding									
U65579_at_	U65579	ndufs8	mitochondrial protein	0	1.8	0	0	0	0	1.5	0	C
U71364_at_	U71364	cap3	Cytoplasmic antiproteinase 3 (CAP3) mRNA	3.7	1.8	28.4	0	1.5	-	0	3.5	8 6
U03644_at_	003644		Recepin mRNA	1.6	1.7	3.4	1.9	4.1	9	6.0	2.3	8.3
U22897_at_	U22897	ndp52	Nuclear domain 10 protein (ndp52) mRNA	3.4	1.7	8.3	6.5	3.4	8.6		1.6	6.2
J04617_s_at J04617	J04617	efla	EEF1A1 Translation elongation factor 1-alpha-1	1.8	1.6	1.7	80	23	8	-	α σ	[]
M23114_at_		atp2a2	ATP2A2 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	3.4	1.6	1.6	-		C	-		3.0
S82297_at_	S82297	b2m	BETA: 2-MICROGLOBULIN PRECURSOR	9.5	1.6	3.1	6.3	4.4	3.4	1.3	0	1.4

Figure 1AA

Figure 1BB

S75168_rna1			Matk≂megakaryocyte∙associated tyrosine kinase [human, Genomic, 2617 nt 13									
at	875168	ctk	segments]	0.3	1 2	0	0	0 7	C	1 7	-	
U50196_at_	U50196	adk	ADK Adenosine kinase	0	1.2	1.8	0.2	1.1	0	0.7	0.1	10
J03592_at_	103592	ant3	ANT3 Adenine nucleotide translocator 3 (liver)	0.5	1.1	C	0 3	о С		-	-	α
M11119_at_	M11119	PL1	Endogenous retrovirus envelope region mRNA (PL1)	C	=			20 -		4		9
			ERCC1 Excision repair cross complementing					3	1	7	7.0	7
			rodent repair deficiency, complementation									
,			group 1 (includes overlapping antisense									
M13194_at_	M13194	ercc1	sednence)	0	1.1	0	0	0.7	0	c	C	0
U80040_at_	U80040	aco2	ACO2 Aconitase 2, mitochondrial	0.7		0	0 7	0 7	c	· -	200	
X06956_at	X06956		TUBULIN ALPHA-4 CHAIN	1.1		0	m	14	c	; c	ά	0
1	_		RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE						,	,	22.5	9
X59543_at	X59543	rrm1	M1 CHAIN	1.1	1.1	0	0.5	C	Ċ	0		
X67247_rna1							2	,		<u>;</u>		
at	X67247	rps8	RpS8 gene for ribosomal protein S8	0.5	1.1	9.0	0.5		0.5	C	1 1	7
D14662_at_	D14662	aop2	KIAA0106 gene		-	C	1	70		000	: -	3
D25538_at_	D25538	adcy7	KIAA0037 gene	O		C	Ĉ	200	0	7 (1 4	
D26308_at_	D26308	blvrb	NADPH-flavin reductase	C		c	0	ο α	5	? -	2 0	
D79990_at_	D79990		KIAA0168 gene	0.7	1	0	000	0 0	5 0	1.1	> -	
L13939_s_at_	L13939	ap1b1	Beta adaptin protein mRNA	-	-				-	2	1 1	9
M23197_at_	M23197	cd33	CD33 CD33 antigen (differentiation antigen)	0	1		0 4	, ,	5 0	5 0	0.0	5 6
D82348 at	D82348		5-aminoimidazole-4-carboxamide-1-beta-D.								0	
D87433 at	D87433	Viss0246	KIAAAAA KAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	5	V	5	8.0	1	o l	O	0.7	0
100 P	201	Niaauz40	NIAMUZ40 gene, partial cds	0	0.9	0	0	0.3	0	0	9.0	0
M22632_at_	M22632	got2	GOT2 Glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	0.1	6.0	0	0		C	c	C	
M58285_at	M58285	hem1	Membrane associated protein (HEM:1) mRNA	C	C	- C		, r		,		
M93221_at_	M93221	mmr	M6PR Mannose receptor	0	000	0 6	σ	ο α	5 0	0.7	2) 0	5
				5	ر د.د	<u>ن</u>	<u>0</u> .0	<u>0</u> .0	5	7.7		5

				In	ivent	ors	: N	lir H	acohen,	et ai								
4.0	0	1 2	-	6.0	0.6	0	C	40		0	0	0.5	0	0	0	6.0	0.5	0
9.0	0	0	6	-	0	9.0	1.7	0.7		0	0.5	C	0.4	0 7	0	9.0	0.4	0.3
3.2	0.7	800	80	0.7	C	0	- 2	0		C	0.3	0.3	0	6 0	0	0.4	80	2.1
0	0	0	2.1	1.6	0	0	0	5.0		o C	0	0	0.4	c	0	CA	0	0
0.8	0	9.0	2.2	2	-	0	6.0	0.5		-	6.0	17		9.0	1.1	8.0	-	0
0.1	0	0	3.6	3.8	2.6	0.4	0	4.0		4	1.5	0.5	0	9.0	3.3	1.7	9.0	0.5
0	0	0	0	2.1	-0	0	0	0.7		0	0	0	0	0	0	0.7	0.2	0
6.0	6.0	8.0	8.0	8:0	0.8	8.0	0.7	0.7		0.7	0.7	0.7	0.7	9.0	9.0	9.0	9.0	0.5
0.2	6.0	0	0	1.9	8.0	0	0	0.2		-0	0	111	0	0	6.0	0.4	0	0
Silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA	Retinal protein (HRG4) mRNA	PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE	High mobility group protein (HMG·I(Y)) gene exons 1-8	LMNA Lamin A	60S RIBOSOMAL PROTEIN L10A (CSA-19).	FBP1 Fructose-bisphosphatase 1	Tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds	Allograft inflammatory factor 1 (AIF 1) mRNA	L44L gene (L44 like ribosomal protein) extracted from Human Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like	ribosomal protein (L44L) and FTP3 (FTP3) genes	KH type splicing regulatory protein KSRP mRNA	Gene encoding prepro form of corticotropin releasing factor	RPS26 Ribosomal protein S26	Transforming growth factor-beta induced gene product (BIGH3) mRNA	LST1 mRNA, cLST1/E splice variant	RPL17 Ribosomal protein L17	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR	TGFBR2 Transforming growth factor, beta receptor II (70-80kD)
ncor2	hrg4		hmgiy	cmd1a		fbp1		aif1		agmx1		crh	rps26	віснз	b144	rp123	hla-dma	hnpcc6
U37146	U40998	D31766	L17131	M13452	012404	U21931	U12595	019713		U78027	U94832	V00571	X69654	M77349	U00921	X55954	X62744	050683
U37146_at_	U40998_at_		L17131_rna1 _at_	M13452_s_at	U12404_at_	U21931_at_	U12595_at_	U19713_s_at =		U78027_rna3 _at_		V00571_rna1 _at_	9654_at	M77349_at_		X55954_at_	X62744_at_	D50683_at_

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			PPP3CA Protein phosphatase 3 (formerly 2B).						-	-	H	ſ
			catalytic subunit, alpha isoform (calcineurin A									
		calna	alpha){alternative products}	Н	0.5	0	=	1	0.3	0.6	1.9	0
M28825_at_	M28825	cdla	CD1A CD1a antigen (thymocyte antigen)	0	0.5	0.1	0	1.4	0	8.0	1.5	0
M61827_rna1	700131	2442	case (SMO) ellelastical	C	u	u C	'n	0	6.0	-	u C	
-	WOTOT.	2253	Ceurosiaiiii (CD43) gene	5 0	0.0	200	? ·	1 0	2.0	1.0	? .	1 0
U51587_at_	U5158/		Golgi complex autoantigen golgin-97 mRNA	0	0.5		0	0	0	8.0	1:2	0.5
J04430_s_at_	J04430	acp5	ACP5 Acid phosphatase 5, tartrate resistant	0	0.4	1.2	0.5	9.0	0	6.0	9.0	3.8
			PTGS1 Prostaglandin-endoperoxide synthase 1							-		
			(prostaglandin G/H synthase and					-				
M59979_at_	M59979	cox1	cyclooxygenase)	0	0.4	0	0.7	9.0	0	0	0	0
			UBIQUITIN CARBOXYL TERMINAL HYDROLASE							-		
U47927_at_	U47927	isot	1	0	0.4	0	1.4	0.7	0	1.4	0	ō
			Naip gene (neuronal apoptosis inhibitory									
			protein) extracted from Human basic									
			transcription factor 2 p44 (btf2p44) gene,									
			partial cds, neuronal apoptosis inhibitory									
U80017_rna2			protein (naip) and survival motor neuron									
at	U80017	gtf2h2	protein (smn) genes	0	4.0	0	0.7	0.2	0	0.4	0.7	9.0
Z28407_at_	228407	rp18	RPL8 Ribosomal protein L8	1.2	0.4	0.8	2.1	0.4	2.7	1.5	9.0	1.3
M11313_s_at	M11313	mCe.	A2M Alcharyamannaniin	- 0	0		,	<u>u</u>	-	, c	0	<u> </u>
	0101111	95111	Acid Cipila C. Hiaci Ogloballii	7.7	5.5	7	7	2:5	2	5		2
U24266_at_	U24266	aldh4	Pyrroline-5-carboxylate dehydrogenase (P5CDh) mRNA, long form	0	0.3	0.2	ō	0.3	0	0.1		0
			Chromosome 16p11.2 BAC Clone CIT987SK.						_	-		
	U46025		234F9 complete sequence	0	0.3	0	0.3	0.2	0		0.3	0
X55733_at_	X55733		EUKARYOTIC INITIATION FACTOR 4B	0.2	0.3	0	0.3	0.3	0	0.1	8.0	6.0
١.	297074		Rab9 effector p40	0.2	0.3	0	1.6	9.0	0	2	1.5	0.5
D87466_at_	D87466		KIAA0276 gene, partial cds	0	0.2	0	1.	0.5	1.2	0.4	0.2	0
U09578_at_	N09578	3pk	MAPKAP kinase (3pK) mRNA	0	0.2	0	1.1	0.4	0	0	0	0
	0	!	ATP5D ATP synthase, H+ transporting,			-		,				<u> </u>
at	X63422	atbod	mitochondrial F1 complex, delta subunit	0	0.2	0	1.4	0.7	0	9.0	0	0
X78817_at_	X78817	RhoGAP4	KIAA0131 gene, partial cds	0	0.1	0	9.0	1.1	0	0	0.1	0

Figure 1EE

0	0.5	8.0	0		<u>্</u> য		ा		- ग	-	7-7	ות	ଠା	0	ाट	_	0	10	T	m			ा	া	া	0	₹†	r	ा	w.	m
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0.3	9.0	1.1	0	1	0.1		4.0		2.5	8.0		7.	1.2	1.2	0.7		0	0		0.3			6.0	0	0.3	0	9.0			0.7	0.3
0	0	1.5	0	α -	9		5		2	1.4	L		0.3	0	0		0	0		0.7			0.4	7	0.8	0	0		1.7	0	0.4
0	0	0	0	7 7		-	5	C	5	0	,		5	0	0		0	0	-	5		-	6.7	5	0.0	5	0		0	0	0
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0	0	0.4	0	- c			7.0	c	5	0.4	-	5 6	2	0	0		0	0	,	5			0.5	5 0	5 0	5	ō	() C	0	1.4
0	0	0	0	C	-		1	0	2	0	C	5 0	5 0	0	0		0	0	-	5			5 0	5 0	5 0	5	0		5	5	0
0	0	0	0		,		5		>	0		0	5 0	Ы	0		0	0		7			5 0		5 0	5 1	0		5 0	5	0
0	0		0	_						1																					
										0.4				O	U		0	0								ار	٦	(7	0
DENN mRNA	KIAAA179 mana martin 240	CHANGE BEING, DATHAL CUS	State	Cancellous bone osteoblast mRNA for GS3955		Tyrosine Kinase Svk		Cpg-Enriched Dna, Clone S19		Zinc Finger Protein Hzf4	LBR Lamin B receptor	Frizzled gene product mRNA	Phosphomevalonate kinase monin	A DODA .	ADURA3 Adenosine receptor A3	FCERZ FC tragment of IgE, fow affinity II,	receptor for (CU23A)	LYL-1 protein gene	GC-RICH SEQUENCE DNA-BINDING FACTOR	TCF3 Transcription factor 2 /FOA	immunoglobylin enhancer binding factors	F12/F47)	VCL Vinculin	Br140 mRNA	PLCB2 Phospholipase C. heta 2	Chromosome 17c21 mbn/ alana i 1113	Chan City o MID -1 II TO STATE OF THE CONTROLL OF THE CONTROL O	mRNA	tivated protein kinase (Pak1)	OUT OUTD EXCEPTION ANIMASE (LANT) BEINE	DOLLOUIT pyropilospilatase
denn denn	ppzc-line kiaa0179	C+3C	3190			syk		Cpg-Enriched			lþ.	fzd2	pmvk		adoras	2422	cuz3	INI I	tcf9			e2a	vcl	br140	plcb2			ciita		+ -	lage
AB002356	D80001	DREEAD	210000	D87119	HC3730		HG3995-	HT4265	HG4126.	H14396	L25931	L37882	L77213	05224	L///30	MISOSO	MADESO	IN 22030	M29204			M31523	M33308	M91585	M95678	U18009		U18259	U24152	1131930	2000
AB002356_s_ at	D80001 at	.1~	15.000	D87119_at_	HG3730.	18-15-100	HG3995.	HT4265_at_	HG4126.	H14390_at_	L25931_s_at_	L37882_at_	L77213 at	177730 -+	L///30_d(_	M15050 24	Т	1N/22030_41	M29204_at			M31523 at	M33308_at	M91585_at	M95678_at	U18009 at		U18259_at	U24152 at	1131930 at	-,5-000

Figure 1FF

Inventors:	Nir Hacohen, et al.	

	1000		Putative holocytochrome c-type synthetase	(-	-		-		
U36/8/_at	U36/8/	nccs	mKivA	5	2	5	5	5	5	7. T	7.5	7
U41767_s_at	U41767	adam15	Metargidin precursor mRNA	0	0	0.5	1.5	0	0	0	0	0.3
U51269_at_	U51269	arvcf	Armadillo repeat protein mRNA	0.1	O	0	0	0	0	1	0.8	0.1
U51336 at	U51336	itrpk1	Inositol 1,3,4-trisphosphate 5/6-kinase mRNA	0	-0	-0	0.5	0	0	0	1.1	0.2
U53446 at	U53446	dab2	Mitogen-responsive phosphoprotein (DOC.2) mRNA	0	0	0	0	0	0	0	0.2	0
U62739 at	U62739	bcat2	Branched-chain amino acid aminotransferase (ECA40) mRNA	0	-0	.4.0	0	0	0.6	0.5	0	0
	1163825	DIPA	Hepatitis delta antigen interacting protein A	0	-	0	6.0	17	0	0	4.0	0
Τ	U68142		RaIGDS-like 2 (RGL2) mRNA, partial cds	0	0	0	-	0	0.8	0.4	0	0
U70439_s_at	U70439	ssp29	PHAPI2b protein	-0	- 0	ō	0.7	0.7	0	0	6.0	0.4
1178525 at	U78525		Eukaryotic translation initiation factor (eIF3) mRNA	0	0	0	6.1	0	0	0.1	0.5	0
U79285 at	U79285		GLYCYLPEPTIDE N. TETRADECANOYLTRANSFERASE	0	0	0	9.3	0	3.5	2.2	2.7	
U79288_at	U79288		Clone 23682 mRNA sequence	0	0	0	9.0	0	5.1	0	0	0.8
U93049_at	U93049	slap-130	SLP-76 associated protein mRNA	0	0	0	0.4	0.1	0	0	0.2	0.5
			FES Feline sarcoma (Snyder Theilen) viral (v. fes)/Fujinami avian sarcoma (PRCII) viral (v.									
X52192_at_	X52192	fes	fps) oncogene homolog	0	0	0	0	4.0	0	0.2	0	0
X69978_at_	82669X	ercc5	ERCC5 DNA excision repair protein ERCC5	6.0	0	0	1.4	0	0	0	1.2	0.3
X79204_at_	X79204		SCA1 Ataxin 1	0	0	0	0	9.0	0	0.3	6.0	0
X90824_s_at_ X90824	X90824	usf2	USF2a & USF2b, clone P2	0	0	0	6.0	0.3	ō	0	0.5	1.1
X97074_at_	X97074	claps2	CLATHRIN COAT ASSEMBLY PROTEIN AP17	0	-0	0	0.1	6	0	0.1	0.3	0
Y13247_at_	Y13247		Fb19 mRNA	0	0	1.4	0	1.7	0	0	0	0
Z34897_at_	234897	hrh1	HRH1 Histamine receptor H1	0	0	0	0	0.3	0	0	9.0	0.1
Z50749_at_	Z50749	ppp1r7	Sds22-like mRNA	0	0	0	0.3	9.0	0	0.1	0.1	0

Inventors:	Nir Hacohen, et al.

arryin	GBA	gene symbol	gene Name	leco	heco	teco	fpr8	hpr8	tpr8	ican	mcan	tcan
1413755	227011	L T	G1P2 Interferon, alpha-inducible protein (clone									
18/13/02 at	M13/55	cigsi	IFI-15K)	214.1	545.6	57.4	253	662	100.2	302.7	208.8	34.3
V00594_at	V00594	mt2a	Metallothionein isoform 2	1683.1	1698.4	143.4	371.1	414.5	ı	333	261	74.2
M21121_at_	M21121	rantes	SCYA5 Small inducible cytokine A5 (RANTES)	728.7	661.7	83.4	717	396.6	1153	1136	87.4	43.7
			ISG-54K gene (interferon stimulated gene)									ò
M14660_at_	M14660	g10p2	encoding a 54 kDA protein, exon 2	5.9	25	27.9	109	312.4	206	~	Ľ	33.4
			INP10 Interferon (gamma) induced cell line;							1	5	3
X02530_at_	X02530	inp10	protein 10 from	12.5	13.1	442.2	137.9	290.4	501.4	ις. 4	205 9	45; 4
M24594_at_	M24594	g10p1	IFI56 Interferon induced protein 56	19.8	71.6	77.5	1	266	141 1	186	248 6	89.6
1	1	:	TNF-related apoptosis inducing ligand TRAIL				ı				2	
U3/518_at_	U37518	trail	mRNA	14.7	34.2	134.3	171.9	230.1	590.2	5.7	109.1	318.2
U59286_at_	U59286	itac	Beta-R1 mRNA, partial cds	34.9	27.6	237.9	201.6	207.8	340.8	88	74.4	389 7
100000	2000		INTERFERON ALPHA INDUCED 11.5 KD									
Ab/325_at_	76/375	1112/	PROTEIN	136.8	143.4	618.8	265.8	192.2	498.1	20	212.1	604.2
L40387_at_	L40387	oasl	I hyroid receptor interactor (TRIP14) gene, 3' end of cds	4.6	7.5	43	105.3	185.2	124 5	1 7	C	12
			I Wooding State of the State of									
M33882_at	M33882	mx1	of murine (interferon-inducible protein p78)	61.1	166.8	84 7	06	1522	σ σ	7	307.3	
L19779_at_	L19779	h2a	Histone H2A.2 mRNA	53.2	154	83.4	40.2	122.8	65.8	7.9	10.8	33.4
V00594_s_at_	V00594	mt2a	Metallothionein isoform 2	167 1	337 3	-	0	0 000	6	3	5	7
			TUMOR NECROSIS FACTOR: INDITION F	: [5: /55	2	0.4.0	166.0	0.4.0	4.60	27.70	4.
M31165_at_	M31165	tnfaip6	PROTEIN TSG-6 PRECURSOR	172.2	163.5	624.1	60 6	1002	101	7 1	ú	ά
			6-16 gene (interferon-inducible peptide									2
U22970_rna1			precursor) extracted from Human interferon.									
_s_at	U22970	g1p3	inducible peptide (6-16) gene	115.3	68.2	5.8	70.6	97.1	13.7	13.1	7	rt.
J	X07834	sod2	SOD2 Superoxide dismutase 2, mitochondrial	57.7	104.1	240.9	34.7	92.1	91.6	66	1/2	116.5
M34455_at	M34455	ido	IDO Indole 2,3 dioxygenase	273.7	27.5	219.8	279.5	89.2	97.8	-	3.4	106
			SOD-2 gene for manganese superoxide									
X65965_s_at_ X65965	X65965	sod2	dismutase	233.7	149.2	204	143.7	86.3	86.3	10.6	35.9	109.3
U52513_at_	U52513	ifit4	RIG-G mRNA	25.1	39.3	96.2	92.1	84.6	86	13.2	39.1	94.7
X99886_s_at_ X99886	3886X	mcp2	MCP-2 gene	519	7.	26.3	0.00	200	47.0	0	000	5
				,	;	2.5	1	0.4.0	7	ţ	73.0	79.5

164.9 446 19.3 372.7 82 10.5 46 30.1 164.9 446 19.3 372.7 82 10.5 46 30.1 408.5 379.2 1267.5 70.5 76.5 269.4 146 43 73.8 125 11.4 52.8 73.8 8.5 7.4 9.6 87 158.7 41.1 65.3 73.5 22.9 7.6 5.9 42.6 130 46 38.8 72.5 49.2 51.4 43.1 58.1 87.3 93.6 73.7 66.9 27.4 10.4 27.4 40.2 66.9 32.5 56.1 59.5 25.2 12.8 11 40.2 66.9 32.5 56.1 59.5 25.2 12.8 11 40.2 66.9 32.5 56.1 59.5 25.2 12.8 11 43.8 28.9 21.9 189.3 58.8 17.7 44 9.6 34.3 42.2 56.1 53.3 47.7 11.6 31.7 38.4 28.4 59.4 50.6 58.8 1.5 9.9 4.6 38.4<	M30818		тх2	MX2 Myxovirus (influenza) resistance 2, homolog of murine	21	A 47	3 04	0 0	000	0	0		3	
13 84.2 13.1 15.3 81.7 30.3 55.9 20.8 7.5 408.5 379.2 1267.5 76.5 269.4 14.6 43 111 73.8 125 11.4 52.8 73.8 8.5 7.4 9.6 6.3 87 158.7 41.1 65.3 73.5 22.9 7.6 5.9 9.6 42.6 130 46 38.8 72.5 49.2 51.4 43.1 47.5 58.1 87.3 93.2 23.3 69.6 83.5 26.5 11 56.3 761.9 728.2 93.6 73.7 66.9 27.4 10.4 27.4 14.9 40.2 66.9 32.5 56.1 59.5 25.2 12.8 18 20.2 144.1 226.5 116.7 73.8 58.6 48.5 27.2 14.9 96.6 39.3 34.3 42.2 56.1 53.3 47.7 11.6 31.7 41.3 17.8 82.5 14.6 <	M69203 mip1b to mouse Mip-1b)		SCYA4 Sn to mouse	SCYA4 Small inducible cytokine A4 (homologous to mouse Mip-1b)	164.9	44 6	19.3	40.3	82.3	10.4	19.8	39.4	43.2	
408.5 379.2 1267.5 70.5 76.5 269.4 146 43 111 73.8 125 11.4 52.8 73.8 8.5 7.4 9.6 6.3 42.6 138 41.1 65.3 73.5 22.9 7.6 5.9 9.6 42.6 130 46 38.8 72.5 49.2 51.4 43.1 47.5 58.1 87.3 93.2 23.3 66.9 27.4 10.4 27.4 14.9 761.9 728.2 93.6 73.7 66.9 27.4 10.4 27.4 14.9 40.2 66.9 32.5 56.1 59.5 25.2 12.8 18 20.2 16.7 30 48.7 41.5 58.8 117.7 4.2 20.5 80.4 16.7 30 48.7 75.1 11.6 31.7 41.3 43.3 42.3 52.3 53.3 4.4 96	X57351_s_at_X57351 ifitm2 RPS3 Ribo		RPS3 Ribo	RPS3 Ribosomal protein S3 / wrong name	13	84.2	13.1	, r	21 7	30.3	t u	7.00	1 1	
73.8 125 11.4 52.8 73.8 8.5 7.4 9.6 6.3 42.6 130 46 38 72.5 49.2 51.4 43.1 47.5 58.1 58.3 56.9 56.3 58.2 56.9 56.3 58.3 56.9 56.3 56.3 56.9 56.3 56.9 56.3 56.9 56.3 56.9 56.3 56.9 56.3 56.9 56.3 56.9 56.3 56.9 56.3 56.9 56.3 56.9 56.3 56.9 56.	X04602_s_at_X04602		IL6 Interleu	kin 6 (B cell stimulatory factor 2)	408 5	379.2	1267 5	70 5	1	200		0.07		
87 158.7 41.1 65.3 73.5 22.9 7.6 5.9 6.9 42.6 130 46 38.8 72.5 49.2 51.4 43.1 47.5 58.1 87.3 98.2 23.3 69.6 83.5 26.5 11 56.3 761.9 728.2 93.6 73.7 66.9 27.4 10.4 27.4 14.9 40.2 66.9 27.4 10.4 27.4 14.9 40.2 66.9 27.4 10.4 27.4 14.9 40.2 66.9 27.4 10.4 27.4 14.9 40.2 56.1 59.5 25.2 12.8 18.0 20.2 144.1 225.5 115.7 73.8 58.6 48.5 27.2 81.1 43.2 43.3 42.3 48.3 76.1 53.3 43.7 11.6 31.7 41.3 38.4 28.4 99.4 34.6 50.8	M23178 mip1a ALPHA PRECURSOR		MACROPHA ALPHA PRE	SE INFLAMMATORY PROTEIN 1. SURSOR	73.8	125	11.4	200		μ. α π. α	14.0	24 0		11
42.6 130 46 38.8 72.5 49.2 51.4 43.1 47.5 58.1 87.3 98.2 23.3 69.6 83.5 26.5 11 56.3 761.9 728.2 93.6 73.7 66.9 27.4 10.4 27.4 14.9 40.2 66.9 32.5 56.1 59.5 25.2 12.8 18.9 20.2 144.1 225.5 115.7 73.8 58.6 48.5 27.2 81.1 43.2 43.8 28.9 21.9 189.3 58.3 23.3 4.4 96.6 39.3 34.3 42.3 76.1 53.3 47.7 11.6 31.7 41.3 17.8 8.2 14.6 62 53 23.9 1.2 12.2 7.7 3.2 5.2 68.3 59.4 52.3 53.9 1.6 77.5 128.6 81.9 42.2 68.3 59.4 50.9	a20		TNFAIP1 Tur protein A20	nor necrosis factor alpha inducible	87	158.7	41.1	65.3	73.5	9 20	1 4		5.0	ivem
58.1 87.3 98.2 23.3 69.6 83.5 26.5 11 56.3 761.9 728.2 93.6 73.7 66.9 27.4 10.4 27.4 14.9 40.2 66.9 32.5 56.1 59.5 25.2 12.8 18 20.2 16.7 30 48.7 41.5 58.8 117.7 4.2 20.5 80.4 144.1 225.5 115.7 73.8 58.6 48.5 27.2 81.1 43.2 34.3 28.9 21.9 189.3 58.3 23.3 4.4 96 39.3 34.3 42.3 48.3 76.1 53.3 47.7 11.6 31.7 41.3 3.2 5.2 68.3 59.4 52.3 53.9 1.2 7.5 128.6 81.9 42.2 5.7 70.3 51.6 6.5 9.9 4.6 2.9 38.4 28.4 99.4 50.4	131584 ccr7 (MKBB7 Ccr7		Interferon re	gulatory factor 7 (humirf7) mRNA	42.6	130	46	38.8	72.5	49.2	51.4	43.1	47.5	
761.9 728.2 93.6 73.7 66.9 27.4 10.4 27.4 14.9 40.2 66.9 32.5 56.1 59.5 25.2 12.8 18.20.2 16.7 30 48.7 41.5 58.8 117.7 4.2 20.5 80.4 144.1 225.5 115.7 73.8 58.6 48.5 27.2 81.1 43.2 43.8 28.9 21.9 189.3 58.3 23.3 4.4 9.6 39.3 34.3 42.3 48.3 76.1 53.3 47.7 11.6 31.7 41.3 17.8 8.2 14.6 62 53 23.9 1.2 12.2 7.7 3.2 5.2 68.3 59.4 52.3 58.6 1.6 77.5 128.6 81.9 42.2 68.3 59.4 50.6 68 1.5 26.4 75.9 9 0 0.1 41.4 60.4			CIVING V CUE	mokine (C.C.) receptor 7	58.1	87.3	38.2	23.3	9.69	83.5	26.5	=	56.3	
40.2 66.9 32.5 56.1 59.5 25.2 12.8 18 20.2 16.7 30 48.7 41.5 58.8 117.7 4.2 20.5 80.4 144.1 225.5 115.7 73.8 58.6 48.5 27.2 81.1 43.2 43.8 28.9 21.9 189.3 58.3 23.3 4.4 96 39.3 34.3 42.3 48.3 76.1 53.3 47.7 11.6 31.7 41.3 17.8 8.2 14.6 62 53 23.9 1.2 12.2 7.7 3.2 5.2 68.3 59.4 52.3 58.6 1.6 77.5 128.6 81.9 42.2 5.7 70.3 51.6 6.5 9.9 4.6 2.9 38.4 28.4 99.4 34.6 50 68 1.5 26.4 75.9 0 0.1 41.4 60.4 49.8 97.9 0 0 0	mt1h		Metallothionei		761.9	728.2	93.6	73.7	6.99	27.4	10 4	27.4	2.0	- 1
16.7 30 48.7 41.5 58.8 117.7 4.2 20.5 80.4 144.1 225.5 115.7 73.8 58.6 48.5 27.2 81.1 43.2 43.8 28.9 21.9 189.3 58.3 23.3 4.4 96 39.3 34.3 42.3 48.3 76.1 53.3 47.7 11.6 31.7 41.3 17.8 8.2 14.6 62 53 23.9 1.2 12.2 7.7 3.2 5.2 68.3 59.4 52.3 58.6 1.6 77.5 128.6 81.9 42.2 5.7 70.3 51.6 6.5 9.9 4.6 2.9 38.4 28.4 99.4 34.6 50 68 1.5 26.4 75.9 0 0.1 41.4 60.4 49.8 97.9 0 0 0 0 0 40.5 48.5 192.3 0 0 0 0	A33632 Wars IRYPTOPHAN		IRYPTOPHAN	'L-TRNA SYNTHETASE	40.2	6.99	32.5	56.1	59.5	25.2	12.8	18	20.2	••••
144.1 225.5 115.7 73.8 58.6 48.5 27.2 81.1 43.2 43.8 28.9 21.9 189.3 58.3 23.3 4.4 96 39.3 34.3 42.3 48.3 76.1 53.3 47.7 11.6 31.7 41.3 17.8 8.2 14.6 62 53 23.9 1.2 12.2 7.7 3.2 5.2 68.3 59.4 52.3 58.6 1.6 77.5 128.6 81.9 42.2 5.7 70.3 51.6 6.5 9.9 4.6 2.9 38.4 28.4 99.4 34.6 50 68 1.5 26.4 75.9 0 0.1 41.4 60.4 49.8 97.9 0 0 0 0 0 40.5 48.5 192.3 0 0 0 0			OIAS (2'-5') olig	goadenylate synthetase	16.7	30	48.7	41.5	ı	117.7	4 2	20.5	80.4	raco
43.8 28.9 21.9 189.3 58.3 23.3 4.4 9.6 39.3 34.3 42.3 48.3 76.1 53.3 47.7 11.6 31.7 41.3 17.8 8.2 14.6 62 53 23.9 1.2 12.2 7.7 3.2 5.2 68.3 59.4 52.3 58.6 1.6 77.5 128.6 81.9 42.2 5.7 70.3 51.6 6.5 9.9 4.6 2.9 38.4 28.4 99.4 34.6 50 68 1.5 26.4 75.9 0 0.1 41.4 60.4 49.8 97.9 0 0 0 0 0 40.5 48.5 192.3 0 0 0 0	tinia	0.00	INF lumor neci	osis factor	144.1	225.5	115.7	73.8		48.5	27.2	81.1	43.2	
34.3 42.3 48.3 76.1 53.3 47.7 11.6 31.7 41.3 17.8 8.2 14.6 62 53 23.9 1.2 12.2 7.7 3.2 5.2 68.3 59.4 52.3 58.6 1.6 77.5 128.6 81.9 42.2 5.7 70.3 51.6 6.5 9.9 4.6 2.9 38.4 28.4 99.4 34.6 50 68 1.5 26.4 75.9 0 0.1 41.4 60.4 49.8 97.9 0 0 0 0 0 40.5 48.5 192.3 0 0 0			rilorbolin i mk	VA, partial cds	43.8	28.9	21.9	189.3	58.3	23.3	4.4	9.6	39.3	-, -
17.8 8.2 14.6 62 53 23.9 1.2 12.2 3.2 5.2 68.3 59.4 52.3 58.6 1.6 77.5 81.9 42.2 5.7 70.3 51.6 6.5 9.9 4.6 38.4 28.4 99.4 34.6 50 68 1.5 26.4 0 0.1 41.4 60.4 49.8 97.9 0 0 0 0 40.5 48.5 192.3 0 0	X57522 tap1 TAP1 Transport		TAP1 Transport	er 1, ABC (ATP binding cassette)	34.3	42.3	48.3	76.1	53.3	47.7	11.6	31.7	41.3	
32 5.2 68.3 59.4 52.3 58.6 1.6 77.5 38.4 28.4 99.4 34.6 50 68 1.5 26.4 0.1 41.4 60.4 49.8 97.9 0 0 0 40.5 48.5 192.3 0 0 0	alasī		ALAS1 Aminolev	rulinate, delta-, synthase 1	17.8	00	14.6	62	2,7	0 00	-		1	
81.9 42.2 5.7 70.3 51.6 6.5 9.9 4.6 38.4 28.4 99.4 34.6 50 68 1.5 26.4 0 0.1 41.4 60.4 49.8 97.9 0 0	X/Z/55 mig Humig mRNA		Humig mRNA		3.2	5.2	68.3	59.4	523	585	110	77 5	1.00 €	
38.4 28.4 99.4 34.6 50 68 1.5 26.4 75. 0 0.1 41.4 60.4 49.8 97.9 0 0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	J04130 mip1b to mouse Mip-1b)		SCYA4 Small it of mouse Mip-	nducible cytokine A4 (homologous 1b)	810	42.2	7	20.2	512	200		? .	0.021	
0 0.1 41.4 60.4 49.8 97.9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	GBP1 Guanyiate M55542 gbp1 inducible, 67kD		GBP1 Guanyl inducible, 67	ate binding protein 1, interferon. KD	38.4	280	00	200				4.0	6.7	
d 0.1 0 0 40.5 48 5 1923 0	M62402 igfbp6 6		IGFBP6 Insul 6	in-like growth factor binding protein			1) \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	8	00 0	0	70.7	6.67	
0.1 0 0 40.5 48.5 192.3	IFNA gene (in	IFNA gene (in	IFNA gene (in Human leuko	terferon alpha-d) extracted from			7.1	4.00	δ.	y. y.	>	-	4.0	
	J00210 ifna13 gene	a d	gene	a plia	0.1	0	ō	40.5		90 3	C			

Figure 2B

_			Location Constant									
D28915_at_	D28915	mtap44	protein p44	α	29.6	л 2	101	. 70	0	0	166	Ç
J04164_at_	J04164	ifi17	RPS3 Ribosomal protein S3 /wrong name	25.8	57.2	27.75	37.7	75.6	70.0	1.5.0	0.00	0 10
L19871_at_	L19871	atf3	ATF3 Activating transcription factor 3	10.6	10.1	, , 0	5 6	2.0	5.0	2 1	20.5	33.1
						5	7.07	20	12.4	0.4	0.7	λ υ
L05072_s_at_ L05072	L05072	irf1	IRF1 Interferon regulatory factor 1	48.2	24 5	63	63.7	0 80	200	6	2	<u> </u>
U29680_at_	U29680	bcl2a1	Bcl·2 related (Bfl·1) mRNA	1053	070	7 879	10.5	200.2	117 5	1	0	0.00
D14661_at_	D14661		KIAA0105 gene	7 7 1	10.7	2/0/0	25.7	20.7	11/3	7 0	0.0	1/9.1
V00535_rna2	_		Interferon beta 1 gene extracted from Gene for			2	1.53	2.5	†	-	0.1	ò
_s_at_	_	ifnb1	human fibroblast interferon beta 1	0.8	1	187.4	68.4	33.0	1651	,		C
M87434_at_	M87434	oas2	69/71 KD	118	ν α	010	- L	22.5	16.51	7 5 6	2 0	7 7
M92357_at_	M92357	tnfaip2	B94 PROTEIN	29.6	39.7		20.5	3.15 2.15 2.15 2.15 2.15 2.15 2.15 2.15 2	277	3,0	2.0	7 00
J05037_at_	J05037	sps	L-SERINE DEHYDRATASE	c		0		21:0	1 2 2 1	7 -	2	707
HG1612. HT1612 at	HG1612. HT1612	macmarcks	Macmarcks	2	, 6		:	2 6	9 9	3 7	3 3	t i
M22976 at	270CCM		OVD O +	13.6	200	444.7	11.3	30.2	16.9	3.4	11.8	15.6
11/22370 91	M22370	cyno	CTB5 Cytochrome b-5	2.9	4.2	2	5.5	30.2	4.6	1.7	2.1	5.6
M58603_at_	M58603	nfkbp50	NFKB1 Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	26.1	30.4	29.9	15.	30 1	10.7	C	7	10.4
			Exon 1b; used only in type 2 transcripts from					1:33		2	,	t l
X94563_xpt2			H.sapiens dbi/acbp gene exon 1 &									
_r_at	X94563		2./ntype=DNA /annot=exon	14.2	m	m	4.6	29	80	80	0.5	1.1
M55067 at	M55067	ncf]	NCF1 47 kD autosomal chronic granulomatous disease protein	7	100	,	3	6	5			!
X60592_at_	X60592	cd40	CD40 CD40 antigen		2 2	24.6	13.1	27.6	1.77	4.0	20 C	11.5
M87503 at	M87503	isgf3	TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT	<u> </u>	5 2	0		5 6	2			
) 	PTX3 Pentaxin-related gene ranidly induced by		201		n.	C:/7	0.2	0.1	Σ.1 Σ.1	0.0
M31166_at_	M31166	ptx3	IL-1 beta	82.7	88.0	807.3	21	27.0	1000	r.	0	20.0
AB000115_at	AB000115	unknown	E S	a o	1.01	2	Ö	1 6	2 6			27.0
U72882 s at			Interferon induced lengths apparatoin (15035)	5	17.51	24.3		r.0.1	7.07	ن 1	7.0	ر ا ا
	U72882	ifi35	mRNA, partial cds	23.2	58.9	39.5	22	26.7	21.2	20.3	29.3	52.5
U33017_at_	U33017	slam	Signaling lymphocytic activation molecule (SLAM) mRNA	320.7	343.9	685.7	4	25.00	~	1,0	24.2	2.4
							2)	7	-	F.F.	5

L22343_at	L22343	ifi175	Nuclear phosphoprotein mRNA	0.5	2.1	7	4.5	25.4	36.7	0.1	2.6	11.9
D90070_s_at_	020060	pmaip1	LRP1 ATL derived PMA-responsive (APR) peptide	1.3	31	125.8	16.9	24.1	249.1	0	0.4	11.1
S76638_at_	876638	nfkb p52	NFKB2 Nuclear factor of kappa light polypeptide gene enhancer in B·cells 2 (p49/p100)	23.7	32.2	27	14	24.1	5.6	1.1	2.8	15
U66838_at_	U66838		Cyclin A1 mRNA	2.3	22.1	53.5	12.3	23.5	65.7	1.1	1.9	23.6
t	Y00081	il6	1L6 Interleukin 6 (B cell stimulatory factor 2)	144.3	71.8	1281.1	39.5	22.4	95.7	0.5	15.8	39.3
U80073_at_	U80073	tap	Tip associating protein (TAP) mRNA	2.3	1.5	6.1	19.7	21.8	31.1	0	2.6	7.6
			PRG2 Proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major									
at	Z26248	prg2	basic protein)	0	1.2	1.1	2.3	21.3	9.7	0	0	0
╗	690807	hspf4	DNAJ PROTEIN HOMOLOG 2	12.8	11.1	12.7	10.9	20.7	9.7	1.7	3.9	8.8
	M31627	xbp1	X BOX BINDING PROTEIN.1	4.4	6	15.4	16.7	20.6	27.1	3.2	3.1	4.6
J04056_at_	J04056	cbr1	CBR Carbonyl reductase	0.1	3.9	9.0	3.7	20.5	7.4	4.2	7.3	
U19523_at	U19523		GCH1 GTP cyclohydrolase 1 (dopa-responsive dystonia) (alternative products)	18.8	20.8	139 7	τ. α	20.5	, C	0	200	137.8
U03397_s_at								2	2	;	1	0.701
	U03397	41bb	Receptor protein 4.1BB mRNA	4.6	13.1	90.4	m	20.1	26.2	C1	2.3	13.8
			PDE4B Phosphodiesterase 4B, cAMP-specific									
		-	(dunce (Drosophila)-homolog phosphodiesterase									
L209/1_at_	L209/1	dpde4	E4)	23.9	38.2	124.8	12.1	19.8	43.2	0.5	1.5	20.1
			Mitogen induced nuclear orphan receptor									
U12767_at_	U12767	minor	(MINOR) mRNA	49.2	39.4	17.1	37.8	19.7	13.7	24.6	17.3	15.7
ı	D64110	btg3	Tob family	1.7	13.1	12.2	1.6	19.6	9.1	2.6	1.1	9.9
at	879639	ext1	EXT1 Exostoses (multiple) 1	4.9	18.3	47	8.1	19.4	6.8	3.5	6.0	5.3
	HG2724-										Ī	
HT2820_at	HT2820		Oncogene TIs/Chop, Fusion Activated	0	0	20	18.8	19.3	9.68	0	0.6	101.1
M16364_s_at										1		
1	M16364	ckb	CKB Creatine kinase B	50.5	10.4	11.1	109.5	18.8	7.4	5.5	7	4
	X77584	txn	TXN Thioredoxin	22.4	39.5	5.2	16.8	18.4	7.9	3.8	8	2.5
-1	U09278	fap	Fibroblast activation protein mRNA	0	0	0	14.8	17.9	67.4	0	0	0
M62403_s_at	M62403	igfbo4	IGFBP4 Insulin-like growth factor-binding protein	15.0	r,	32.7	α τ	175	37.0	α	6	3 801
		. 12.0.		7:51	7.5	36.7	0.10	7	5/.5	0.0	2.1	0.40

Figure 2D

1170451 34	1170451	00	Myleoid differentiation primary response protein								-	
0.0401 at	0,0401	100511	INJUGO TIRINA	2.2	7	2.8	6.3	17.2	7.1	1.6	2.4	7.1
U30303_d1	U38383	SIUUAII	Calgizzarin	9	9.6	3.7	5.8	17	3.1	-		0
U/2661_at_	U72661	ninj1	Ninjurin1 mRNA	43.8	31.1	48.8	22	1	74	201		20 2
HG4069- HT4339_s_at	HG4069.							-				3
		mcp1	Monocyte Chemotactic Protein 1	2.9	2.5	2.8	38.4	16.9	10.3	7	10.7	9.5
X57579_s_at_ X57579	X57579	activinba	Activin beta-A subunit (exon 2)	166.9	233.7	47.2	20 CC	α 91	0		0.01	6
M62831_at_	M62831	etr101	Transcription factor ETR101 mRNA	4.6	20.4	4.3	6	16.6	1101	1 0	20.0	0.4.0
			PPP2R2A Protein phosphatase 2 (formerly 2A).							5	2	7:1
M64929 at	M64929	ppp2r2a	regulatory subunit B (PR 52), alpha isoform	8	10.6	5.7	9.5	15.7	8.4	H	9	7.7
V82200 24	0003004	nem45	HEM45 mKNA	34.6	43.7	191	27.2	15.5	73.3	8.8	43.4	1161
A02200 at	702200	Stalou	Starbu mKNA	10	7	13.1	7.8	15.4	16.7	2.1	3.1	18.1
D28364_at_	D28364		Annexin II, 5'UTR (sequence from the 5'cap to the start codon)	α	0	-	2 7 7				,	
U82979_at_	U82979	lir5	Immunoplobulin-like transcript. 3 mBNA	100	1 0	1	7.47	77.7	7 0	1.4		7
U00672 at	U00672	il10ra	It 10R Interleukin 10 recentor	21.7	1	14.0	٠,٠	15.1			4.3	17.4
			DIM SPECIFICITY PROTEIN PLOSPINATASE	3.6	14.1	2.7	10.6	15	9.5	4.2	5.9	5.1
L11329_at_	L11329	dusp2	PAC-1	52.1	177.6	16.1	16.2	17 7	,	7		C
D31885_at_	D31885		KIAA0069 gene, partial cds	1.9	3.4	0	0 9	14.5	7 -	0 -	1.0	۲.۶
VE2206+ VE2206	20000	-						-		;		1
755596 24	DEECOC	HILTER	ILIKN Interleukin I receptor antagonist	65.5	26.4	6.9	28.7	14.4	4.6	4.3	7.7	4
1104636 rps 1	050000	(prsc1	Cysteine protease	0	6.0	1.2	2.5	14.3	3.8	0.1	0.1	6.4
at	U04636	cox2	Cvclooxvgenase-2 (hCox-2) gene		000	0						Γ
M29696_at_	M29696	il7r	ILZR Interleukin Z recentor	217	120.0	0000	15.3	13.8	47.7	2	4.7	54.9
X98253 at	X98253		7NF183 mapa	101.7	30.0			13./	15	6	11.5	23.2
U66711 rna1			100 BC110	5		9.0	9.9	13.7	34.5	0.5	0	0
_s_at_	U66711	ly6e	Ly-6-related protein (9804) gene	α	24.7	,	7	000	Ċ	,	1	-
U60800_at_	U60800	sema4d	Semaphorin (CD100) mRNA	13	17.6	37.4	7 0	12.0	r o	1 0	1	4 7
					2	;	?	200	i i	0.0	14:0	20.5
M37766 at	M37766	bcm1	CD48 CD48 antigen (B-cell membrane protein)	13.2	10.9	20.8	8.2	13.4	13.1		6.4	2000
USUSSS at	USUBBS	tctell	CW-1 mRNA	23.1	17.9	33.6	16.9	13.3	15.1	5.1	13.5	300
									-		· ·	2]

U65416_rna1									-			
_s_at	U65416	micb	MHC class I molecule (MICB) gene	2.9	3.8	9.3	Ŋ	13.2	24.7	1.4	2.5	9.5
X06256_at_	X06256	itga5	ITGAS Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	6.2	12.8	3.8	11.6	13.2	2.9	0.9	2.9	0.8
Y00787_s_at_	Y00787	8!!	INTERLEUKIN-8 PRECURSOR	89.1	234.5	40.9	8.6	13.1	8.4	8.2	10.8	10.5
U19261_at_	U19261	traf1	Epstein-Barr virus induced protein mRNA	25.7	15.4	25.2	00	12.7	9	5.8	9.5	1
M13690_s_at	M13690	c1nh	C1NH Complement component 1 inhibitor (angioedema, hereditary)	16.9	34.1	209.8	13.8	12.6	86.2	9.9	30.1	358.9
U20158_at_	U20158	lcp2	76 kDa tyrosine phosphoprotein SLP-76 mRNA	3.7	7.8	8.6	8	12.6	3.4	m	2.3	3.3
X04500_at_	X04500	ii1b	IL1B Interleukin 1, beta	199.3	598.3	184.4	9.1	12.6	20.2	24		487
HG3417. HT3600_s_at	HG3417. HT3600		Gtp Cyclohydrolase I. Alt Splice I	0 4	ć	0,0	,		, ,	, c	0	, ,
Z49107_s_at_ Z49107	249107	igals9	Galectin		3	2 6	17.1	1 2	7 6	5 6	, r	5 4
D86962_at_	D86962	grb10	KIAA0207 gene	2.2	1.7	37.1	19.5	12		1 -	13	6
	U02020	pbef	Pre-B cell enhancing factor (PBEF) mRNA	26.9	26.4	37.4	6.9	11.9	14.5	2.5	1.4	8.5
	X78992	erf2	ERF.2 mRNA	0	6.0	1.5	20.6	11.9	24.9	0.2	0	0.1
IJ	U22662	ixra	Nuclear orphan receptor LXR-alpha mRNA	1.5	7.3	9.6	34.8	11.4	4.6	8.4	3.1	10.9
U07802_at_	U07802	erf2	ERF-2 mRNA	0	2.6	<u>.;</u>	.1	11.3	21.6	0.7	0.1	0
D79206_s_at_	D79206	sdc4	SDC4 Syndecan 4 (amphigiycan, ryudocan)	6.3	6.6	21.1	5.7	13.2	10.2	()	2.7	9
M24283_at_	M24283	icam1	ICAM1 Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	70.6	32.4	20.7	787	11	3.4	9.5	9	9.3
U15932_at_	U15932	gdsnp	Protein tyrosine phosphatase mRNA	57	76.5	44.5	9.6	11.1	8.8	2.2	4	13.4
HG3884.	HG3884.	3			-							
H14154 at	H14154	npx42	Homeotic Protein Hpx-42				4.3	11	2.8	0	0	0
X9/324_at_	X97324		Adipophilin	0	0.6	2.8	2	10.8	5.7	0	0	9.9
U09937_rna1			Urokinase-type plasminogen activator receptor gene extracted from Human urokinase-type									
_s_at_	009937	plaur	plasminogen receptor	17	26.9	14.5	12.5	10.7	2.4	m	3.5	3.7
X07743_at_	X07743	plek	PLECKSTRIN	9.7	2.1	5.7	13.9	10.7	2.7	3.6	1.6	5.6
U32849_at_	U32849	nmi	Hou mRNA	5.2	9	16.1	10.4	10.5	1,1,7	7.7	12.3	ŀ
								1		1		ı

						ī	nv	en	or	s:	Nir	· Hac	ohe	1, e	t al.									
9	2.3	1.6	10.3	9.8	17.2	22.6	7.8	1.5	72.9	7.2	0	1.2		0 0	31.0	8 4	7.2	0.5	11 4		19.1	5.2	4.2	12.7
1.3	13.4	8.0	12.8	1.6	1.5	4.7	1.6	9	2	0.5	0	2.5			23.6	3.7	10.4	1.2	e.	1	Z4.8	1.8	1.7	6.5
F	32	0.3	6.0	=	0.2	D	1.5	0.3	1.4	-1	0	4.0			6 1	4 3	4.1	-	80		40.1	1.9	5.9	8.0
20.1	14.1	15.8	10.4	2	24.9	12	2.7	23.2	43	8.1	55.7	1.7	C	10.4	2	4.7	9	3.8	10.4		77.7	8.3	5.2	13.8
10.5	10.4	10.2	10.2	10.2	10.2	10.1	10	10	10	10	6.6	8,6		9 6	96	9.5	9.5	9.4	6	(5.3	9.3	9.5	9.1
9.2	4.1	5.6	4.5	5.3	m	2.9	14.5	3.4	8.2	6.3	10.2	6.8			12.9		19.6	3.2	3.7			5.5	23.	5.1
2.7	8.4	8.0	16.1	6.1	52.2	19.1	24.5	16.2	26.5	10.4	0	2.6		0.4		1	8.6	0.7	5.3	,	24.3	4.9	4.2	27.9
3.2	27.5	2.7	4.2	5.8	80	13.4	14.1	1.8	3	0.5	0	10.5	0		20.6	19.6	12.6	4	4.5	000	4.02	1.9	2.4	15.6
4.6	29.8	0.5	1.2	6.1	1	3.6	25.2	5.6	0.8	0.5	0	2	-		30.6	23.9	18.7	2.7	2.8	0	0.61	7.1	2.8	8.4
Hbc647 mRNA sequence	Actin bundling protein mRNA	CLC Charot Leyden crystal protein	SSA1 Sjogren syndrome antigen A1 (52kD. Iribonucleoprotein autoantigen SS.A/Ro)	IRF2 Interferon regulatory factor 2	APT1 Apoptosis (APO-1) antigen 1	Putative copper uptake protein (hCTR2) mRNA	INTEGRAL MEMBRANE PROTEIN E16	TY protease	RPS3 Ribosomal protein S3	HISTIDYL.TRNA SYNTHETASE	Zinc finger transcription factor hEZF (EZF) mRNA	PROBABLE G PROTEIN.COUPLED RECEPTOR HM74	Calmodulin Ivna	Msgl·related gene 1 (mrg1) mRNA	LMP2 gene extracted from H.sapiens genes TAP1, TAP2, LMP2, LMP7 and DOB	MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN MAD3	CD83 ANTIGEN PRECURSOR	Mitochondrial 16S rRNA gene (partial)	FUT4 Fucosyltransferase 4 (alpha (1.3) fucosyltransferase, myeloid-specific)	Interferon inducible RNA dependent protein	14 2 2 CONTENT TAIL	14-3-3 PROTEIN TAU	PROTEASOME COMPONENT C8	Epb72 gene exon 1
	snl	clc	ro52	irf2	fas	copt2	d16s469e	casp5			ezf	hm74	calmod	mrg1	tap2	ikba	cd83		cd15	r.	21	tau	psma3	epb72
U68494	U03057	L01664	M62800	X15949	X63717	U83461	M80244	U28015	X57351	211518	U70663	D10923	HG1862. HT1897	U65093	X66401	M69043	Z11697	65/0/2	M58597	8790511	010000	V20408	D00762	X85116
_at		L01664_at_	M62800_at_	X15949_at_	X63717_at_		-	-at_	X57351_at_	Z11518_s_at_	U70663_at_	D10923_at_	HG1862. HT1897 at	U65093 at	X66401_cds1_at_	M69043_at_	Z11697_at_	Z70759_at_	M58597_at_	U50648_s_at	7- 000	A56468_at_	D00762_at_	X85116_ma1 _s_at_

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5.6 8.9 31.4 3.7 6.4 18.9
9 8.9 14.3 0.8
9 8.9 14.3
9 14.9
4.2 4.7 0 51.9
2.3 4.
ZNF173 Acid finger protein ZNF173 SODIUM. ATD CHLÖRIDE. DEPENDENT BETAINE TRANSPORTER ADAR Double-stranded RNA adenosine
8 2 4
U09825 znf173 U27699 slc6a12 U10439 adar Z48481 mmp14 U52101 emp3
8 6 8 8 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

							111	vemo	иъ.		INI	1 1	1a	CO	110	11,	et c	ш.								
28.5	88	41.5	10.9		10.4			0.6	18			1.6	1.8	1.6	8.9	5.4		5.3	5.9	-	-	18		1.7	0.7	7.1
40	6	2.1	2.8		4.3		0	1.6	6.0			0.7	0.1	0.5	0.3	8.9		4.2	4.9	u .	?	Ō		Ó	c	4.7
48.3		9.2	-	-	1.7		2.7	0.3				1.3	0	2	1.7	2		1.5	2.1	0		0.6		0.4	7 0	1.6
11.4	200	13.7	5.1		7.8	_	2.6	7.9	- m			4.6	24 5	8.6	15.3	8.1		7.8	7.7	,	,	2.8		2.8	80	
7.7	7	7.5	7.5		7.4	-	7.4	7.4	7.3			7.3	7.3	7.3	7.2	7.2		7.1	7.1	1	+	7	T	7	89	
13.4	,	101	10.6		3.7		5.7	6.2	2.4			3.8	5.4	4	10.8	6.5		3.7	4.7	u C	-	4.7		4.8	98	11.6
16.9	127 1	61.3	8.8		0.4		0 00	0	5.3	<u></u>		5.6	2.4	12.7	15	10.8		8.9	4.5		7	4.3		1.4	0.3	9.1
11.4	17.3	18.4	14.4		2.2		2.3	1.8	3.7	-		5.9	0	15.9	5.6	15.2		11.3	5.5	~		6.0		8.0	5.1	5.6
7.4	28.9	5.7	10.8		0		1.5	6.0	1.6			4.1	9.0	10.5	8.3	8.7		2.4	1.3	٥ تا		6.3		0.3	0.2	7.9
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1.ALPHA/BETA	Phospholipid scramplase mRNA	Reticulocalbin	CTSL Cathepsin L	MNDA Myeloid cell nuclear differentiation	antigen	TCEB1L Transcription elongation factor B (SIII),	polypeptide 1-like	JUP Junction plakoglobin	Centractin, Alpha	S100A10 S100 calcium binding protein A10	(annexin II ligand, calpactin I, light polypeptide	(p11))	Desert hedgehog (hDHH) mRNA, partial cds	Alpha-tubulin mRNA	NUCLEAR PORE GLYCOPROTEIN P62	PROTEASOME IOTA CHAIN	DNA-binding protein CPBP (CPBP) mRNA,	partial cds	TRAF-interacting protein I-TRAF mRNA	Tronomyosin Tm30nm Cytoskeletal		Ras-Related Protein Rap1b		Histone H4 gene, clone FO108	TINUR	LYN V.yes.1 Yamaguchi sarcoma viral related oncogene homolog
stat1	plscr1	rcn1	ctsl		mnda		skpla	db3				cal11	dhh	dusp1	nup62	psma6		bcd1	itraf	tm30nm		rap1b			nurr1	lyn
M97936	AF008445	D42073	X12451		M81750		247087	268228	НG4606. НТ5011			M38591	U59748	X68277	X58521	X59417		U44975	U59863	HG3514. HT3708	HG3521.	HT3715		M16707	S77154	M16038
M97936_at_	AF008445_at	D42073_at_	X12451_at_		M81750_at_		Z47087_at_	s_at_	HG4606. HT5011_at_			_,[at	1_at_	X59417_at_		U44975_at_	U59863_at_		Γ	HT3715_at_	M16707_rna1	_s_at_	S77154_s_at_	M16038_at_

Figure 21

			DMI Drobable transcentistics to the DMI									
M79462_at_	M79462	myl	Find Froducts (ranscription factor PML) {alternative products}	.3	ď	0	7 7	7	c u	,	0	0
			Brain expressed HHCPA78 homolog [human, HL-			;				5.		0.0
 S73591 at	S73591		60 acute promyelocytic leukemia cells, mRNA, 2704 nt1	C			,		((
				0.7	1.0	5	2.1	ò	3.2	0.3	0.4	0.8
X14684_s_at_ X14684	X14684	ssp	SSB Sjogren syndrome antigen B (autoantigen La)	2.7	0	ď	α	7	1,0	1		,
D84276_at_	D84276	cd38	CD38 CD38 antigen (p45)	32.4	70.7 X 0.7	1683	0.0	00.	20.00	4.0	4.0	2,2
M12174_at_	M12174	arh6	ARH6 Aplysia ras related homolog 6	-	000		1 0	2 4	5 -	100	04.0	1351
U16811_s_at	, ,				1.5	7.0	5	2	7	0.0		
100107	016811	Dakı	Bak protein mRNA	0.9	3.7	1.9	3.9	9.9	3.7	2.8	1.5	1.7
HGZ167. HT2237_at_	HGZ16/- HT2237	pkht31	Protein Kinase Ht31, Camp-Dependent	80	5.6	4 د	α,	υ υ	,	-	<u>u</u>	,
X89985_at_	X89985	bci7b	BCL7 B cell lymphoma protein 7B	32	2 1		7		100	10		7 0
Z48950_at	248950	h3f3b	HISTONE H3.3	7.2	4.2	i a	2	2 15		1	2 0	0 0
X61970_at_	X61970	bsc5	PROTEASOME ZETA CHAIN	4.3	5.5	88	2.6	6.4	27	-	i a	ار
4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		(IMMUNODEFICIENCY VIRUS TYPE I ENHANCER.							:		5
Ab5644_at	X65644	nivep2	BINDING PROTEIN 2	9.1	2.7	12.3	3.8	6.3	4.7	2.2	0.5	5.4
M/2885_rna1		0	G0S2 gene extracted from Human G0S2 gene, 5'		-		-		-	-	-	
_s_at	M/2885	G0S2	flank and cds	126.1	38	44.9	10.8	6.2	5.3	10.4	11.3	18.7
L22342_at_	L22342	unknown	Nuclear phosphoprotein mRNA	3.8	9.7	11.4	4.1	6.1	-	11.5	12.2	21.7
M62324_at_	M62324	mrf.1	Modulator recognition factor I (MRF·1) mRNA, 3' end	4 8	9 8		7	1 9		-	,	
U01691_s_at				2	0.0	10.2	ñ.	Ö	14.3	ρ.Τ	3.4	9.7
	U01691	annexinV	Annexin V (ANX5) gene, 5'-untranslated region	<u></u>	3.6	4.3	6.2	œ	0	α		,
D10040_at_	D10040	fac12	FACL1 Long chain fatty acid acyl coA ligase	24.7	15.2	26.2	13.5	5.9	12.4	2.2	4	24.1
U96915_at_	U96915	sin3	Sin3 associated polypeptide p18 (SAP18) mRNA	e e	m	5.4	12	σ 	7 4	-	- 2	7.3
X96719_at_	X96719	aicl	AICL (activation induced C-type lectin)	0	1.7		4	5.0	5	1 5	10	γα
S59049_at_	S59049	ier1	RGS1 Regulator of G-protein signalling 1	4.5	25.9	15.9	2.2	5.8	9 1	99	10.5	300
0	0		ACTIN, AORTIC SMOOTH MUSCLE (ALPHA.	<u> </u>			-	T		;	+	;
X13839_at	X13839	acta2	ACTIN 2)	0.1	0.7	1.2	7.5	53 00	5.6	0	5.4	3.4
X54304_at_	X54304	mlcb	Myosin regulatory light chain mRNA	3.6	5.9	1.3	6.4	5.8	4.8	1.6		m
K01396 at	K01396	aat	PI Protease inhibitor 1 (anti-elastase), alpha-1-antitrvosin	6 1	, u	,						
	1 1 2 1	, ,	The state of the s	47.3	55.4	75.5	4./	5.7	2.9	6.0	4.7	m

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1 20773 at	1 20773		mRNA in the region near the btk gene involved in	(·				-	
			(clone hEHK1-L) EHK1 receptor tyrosine kinase	6.9	ν <u>.</u>	7.7	3.2	2.7	2.9	<u>~</u>	9.0	2.6
L37360_s_at_		efna3	ligand (EFL-2) mRNA	0.5	2.2	1.6	0	5.7	0	-	3.4	o
U03105_at_	U03105	b4·2	B4-2 protein mRNA	29.4	10.7	8.2	11.4	5.7	, rc	6.4	26	7
J04111_at_	J04111	jun	C.jun proto oncogene (JUN), clone hCJ.1	2.2	4.2	2.4	19.1	5.6	13.4	1.6	0.5	14
M86400_at_	M86400	ywhaz	YWHAZ Tyrosine 3-monooxygenase/tryptophan 5 monooxygenase activation protein, zeta polypeptide	9.9	80	2	y Y	u u	α	-	-	
U18937_at_	U18937		Histidyl-tRNA synthetase homolog (HO3) mRNA	1.7	1.6		<u> </u>	77	4	α (1 0	1 -
X05908_at_	X05908	anxal	ANX1 Annexin I (lipocortin I)	5.2	2.9	6.4	7.5	5.6	5.2	28	0 4	36
L40379_at_	L40379	trip10	Thyroid receptor interactor (TRIP10) mRNA, 3: end of cds	34.8	37.1	33	5.3	5.5	7.6	22.2	0 00	13.5
M23254_at_	M23254	capn2	CAPN2 Calpain, large polypeptide L2	2.2	2.3	4.4	2.4	5.5	2.3	0.7	3.1	4.6
X96506_s_at_ X96506	X96506	nc2a	NC2 alpha subunit	1.8	1.4	0.8	4.8	5.5	2.4	9.0	0	11
D00760_at_	D00760	hc3	PSMA3 Proteasome component C3	9.4	4.2	8.6	8	5.4	3.7	1.4	4.6	12.4
냁		thymosinb10	THYMOSIN BETA-10	4.2	8.6	1.7	ю	5.4	3.7	4.4	3.2	0.6
U22398_at_	U22398	Dws	Cdk-inhibitor p57KIP2 (KIP2) mRNA	0	1.7	0.1	5.1	5.4	11.7	0.7	-	2.2
U68063_at_	U68063	srfs10	Putative splice factor transformer2-beta mRNA	1.4	1.8	0	1.8	5.4	2.9	1.2	9.0	0.5
X56841_at_	X56841	hla·e	HLA-E MHC class I antigen HLA-E	0.7		5.7	5.8	5.4	11.3	-	1 9	oc o
AF014958_at	AF014958	ccr6	Chemokine receptor X (CKRX) mRNA	3.6	9.2	36.3	3.7	5.3	9.9	5.1	4.3	0
	HG2917. HT3061	hla	Major Histocompatibility Complex, Class I, E (Gb:M21533)	5.7	7.6	0	r.	r.	~	, c	0 0	, ,
M97935_s_at	M97935	stat1	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1.ALPHA/BETA	4 1	7 0	10.5) L	2 2	2 0	17.0	7 7
X94232_at_	X94232	MAPRE2	Novel T-cell activation protein	0.4	1.2	1		5.3	3.2	0.6	5.71	200
D28124_at_	D28124	d1s1733e	Unknown product	7.1	5	14.7	25.1	5.2	12	2.6	E	3.3

Figure 2K

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HG544.	HG544.								ľ			
HT544_at_	HT544	ecgf	Endothelial Cell Growth Factor 1	5.9	15 3	4.8	10.4	5.2	2.1	26.7	16.5	
J00105_s_at_	J00105	b2m	BETA.2.MICROGLOBULIN PRECURSOR	5.7	3.6	ď	п	2	u u	-	0	
U56402_s_at	1156402	c 0.457	Chromatin structural protein homolog (SUPT5H)					3.5			0	-
X85133 at	X85133	rhhoe	BDO 1 ONLY	2.9	8	2	5.5	5.2	3	1.1	0.1	7.6
771 200 0+	771200	odan,	אוועווא איועווא אייייייייייייייייייייייי	0.8	2.5	4.8	4.2	5.2	30.4	0.7	0	1.3
12/1309 at	2/1309	derensing	Skin-antimicrobial peptide 1 (SAP1)	19	0.5	7.7	12		6.4	1.2	5.3	0.3
M21180_at_	M21186	cyba	CYBA Cytochrome b-245, alpha polypeptide	2.7	8 7	2	1.6	5.1	1 6	60	0.5	000
MO3/10E at	1402425	1	PTPN12 Protein tyrosine phosphatase, non-									
18133423 at	193423	ptpg1		8.4	5.1	33	2.5	5.1	2.3	1.3	2.4	-
5/8085_at_	2/8082	pdcd2	PDCD2 Programmed cell death 2	1.5		9.0	1.6	2	33	c	C	0
X/4104_at_	X/4104	ssr2	SSR2 Signal sequence receptor, beta	0.8	2	0	5 1	7	17	-	0	? -
Z14978_at	214978		ALPHA-CENTRACTIN	0.5	0	C		7	7 Y	? .	5	7 0
					3	7		;	5	>	2	
D42040_s_at_	D42040	ring3	RING3 PROTEIN	1.3	1.7	1.8	7.3	2	7	1 4	2.1	27
HG2639.											+	
HT2735_s_at HG2639	HG2639.										_	
-	HT2735		Single-Stranded Dna-Binding Protein Mssp-1	83	2.6	2.5	σ	ľ	0			0
	X63679	tram	TRAMP protein	2.6	40	σ-	7 7) L	2 0	, ,	1 0	5 0
,	X89750	hpe4	TGIF protein	5.7	4 6	9 9	000	2	0 4	1 0	2:1	7 0
D30755_at_	D30755	NAF1	VIM Vimentin	563	000	10.0	100		2	0.1	7 7	2)
HG987.	HG987-			?	7.07	13.0	13.3	D. 4	ر ا	14.1	5.3	<u>.</u>
HT987_at_	нт987	igfbp7	Mac25	2.3	5 7	α C	α	0	,	,		
X57985_rna2	1		GL105 gene (histone H2B) extracted from			i			,,,	7.1	5	7.7
at	X5/985		H.sapiens genes for histones H2B.1 and H2A	0.8	0.8	10.9	2 1	4	499	-	-	0
X78687_at_	X78687	nen	G9 gene encoding sialidase	0.4	0.7	0	3.2	4	27	0	100	0,0
Y10032_at_	Y10032	sgk	Putative serine/threonine protein kinase	0	0	1.6	2.5	4	5.4	α	3	200
100011			SLC6A8 gene (creatine transporter) extracted									
at	U36341	slc6a8	Ifon Human Aq28 cosmid, creatine transporter (SLC6A8) gene, and CDM gene, partial cds						ı	(
U40369_rna1			Spermidine/spermine N1-aretyltransferase	7	1	1	17.7	φ.	\; \;	0.0	5	2.1
at	U40369	sat	(SSAT) gene	9.1	5.3	12.1	10.6	4	σ	<u>ب</u>		ά
				-	7.1	1)	<u>;</u>	;	5	7.5	=

Figure 2L

000	1000		Nuclear chloride ion channel protein (NCC27)		,	,						
U93205_at_	093205	nccz/	MKNA	2.7	3.2	12.2	5	4.8	1.6	0.4	3.6	c1 C1
100000	10000	L A	GGTB2 Glycoprotein-4-beta		(,			,		
U29805_at	029805	D4gait1	galactosytransterase Z	13.4	6	12.9	6.1	4.7	3	0.7	3.5	4.5
M10901_at_	M10901	gcr	GRL Glucocorticoid receptor	1.9	2	3.9	4.2	4.7	11.5	1.2	1.5	1.4
U03851_at_	U03851	capza2	Capping protein alpha mRNA, partial cds	0.4	1.5	0	3.9	4.7	4.9	1.1	0.5	1.2
U37547_at_	U37547 ⁻	ciap1	IAP homolog B (MIHB) mRNA	4 8	4 7	179	3.7	4 7	27.3	1.1	1.7	10.7
			NATURAL KILLER CELLS PROTEIN 4							T		Γ
M59807_at_	M59807	nk4	PRECURSOR	20.5	2.5	10.6	11.1	4.6	11.4	5.6	4.8	16.3
M63438_s_at			GLUL Glutamate-ammonia ligase (glutamine								r	
	M63438		synthase)	1.6	0.2	0.2	2.6	4.6	137.4	0	0	1.2
X05855 s_at_X05855	X05855		EEF1G Translation elongation factor 1 gamma	4.0	2.2	0.3	4	4 6			C	C
			BTG1 B-cell translocation gene 1, anti-					2				
X61123_at_	X61123	btg1	proliferative	30.4	26.8	14.4	ω .1.	4.6	4	3.6	7.4	9.7
AB006782_at					-					-		Ţ
_	AB006782	gal9	Galectin-9 isoform	1.7	3.5	1.1	6.9	4.5	3.6	4.5	9.3	-
D14874_at_	D14874	adm	ADM Adrenomedullin	18	20.1	46.2	3.4	4.5	10.4	2.5	5.2	16.1
					-							
D29642_at_	D29642		HYPOTHETICAL MYELOID CELL LINE PROTEIN 3	9.6	15.1	10.3	2.2	4.5	3.4	0.4	3.8	9.5
	HG4297.									-		
HT4567_at_	HT4567	TCPC4	Transcriptional Coactivator Pc4	5.6	2.7	4.8	6.4	4.5	6.3	2.5	4.3	9.5
U57971_s_at							-					_
	U57971	atp2b3	Calcium ATPase isoform 3x/a mRNA	2	3.9	1.9	1.5	4.5	1.6	0		6.0
X92106_at_	X92106	blmh	Bleomycin hydrolase		1.4	0	1.6	4.5	5.5	0.3	1.4	0
			2',3'-cyclic-nucleotide 3'-phosphodiesterase gene						-			
D13146_cds1			extracted from Human 2',3'-cyclic-nucleotide 3'-									
at	D13146	cnp	phosphodiesterase gene	15.9	13.4	25.3	6.2	4.4	10.1	5.6	3.8	11.2
D38551_at_	D38551	unknown	KIAA0078 gene	7.3	5.6	3.9	2.8	4.4	3.5	0	9.0	2.8
			INTERFERON GAMMA UP REGULATED 1.5111									
L07633_at_	L07633	pa28a	PROTEIN PRECURSOR	5.1	8.1	13.1	S	4.4	9.9	2.3	4.3	20.1
M82882 at	M82882	a Lija	ETS.BELATED TRANSCRIPTION FACTOR ELE 1	,	7 0	Ö	,	,	-	-	,	
1	S82297	b2m	BETA-2-MICROGI OBLILIN PRECLIRSOR	0.5		۰ 1	7.6	t V	7 7	7 7	210	
ı	000001	2000	A consisted and a constant of the constant of	?!	2 0	7.0	? !		1	21	5	1
004209_at_	004409	тарл	Associated microtibrillar protein mKNA	=	2	4.8	1.7	4.4	6.5	Ö	0	5.9

			GAPD Glyceraldehyde-3-phosphate					-	-			
D00/63_at_	000/63	psma4	dehydrogenase	6.1	4.5	m	10.5	4	Œ	7	11.0	2
D78132_s_at_		rheb2	Ras homologue enriched in brain (RHEB) gene, Ras-related GTP binding protein gene	0	000	o	,		,	,		
L76200_at_	L76200	guk1	Guanylate kinase (GUK1) mRNA	T	8.4		3.3	4.3	3.5	1	5 O	3.1
HG2915. HT3059_f_at_	HG2915. HT3059	hla	Major Histocompatibility Complex, Class I, E (Gb:M20022)	9	7	α	O U	C	0	-	,	
M19645_at	M19645	grp78	78 KD GLUCOSE REGULATED PROTEIN PRECURSOR	4.2		C	δ, α	2 6	ο α		0,0	0.0
M79463_s_at 	M79463	myl	PML Probable transcription factor PML {alternative products}	5.8	7.6	13.3	2		0 1	2 2	, o	1 -
- 1	S68271	crem	CREM CAMP responsive element modulator		6.0	2 4	126	6 4	α α α	-		000
U28488_s_at 	U28488	c3ar1	Putative G protein-coupled receptor (AZ3B) mRNA	9.0	m		2		7 6	1 0	0 0	0) (
X74039_at_	X74039	plaur	Variant urokinase plasminogen activator receptor (uPAR2) mRNA, partial cds	1.6	15	7.3	1.6		28	5. 5.	4	3.6
X75042_at_	X75042	nfkb crei	REL V.rel avian reticuloendotheliosis viral oncogene homolog	3	26	9	,		u u		,	
D30655_at_	D30655	eif4a2	EIF4A2 Eukaryotic translation initiation factor 4A (eIF-4A) isoform 2	,	5 6		7 -	7 7	0 0	9 0	0 0	4.0
M94880_f_at_ M94880	M94880	hla-a	HLA-A MHC class I protein HLA-A (HLA-A28, B40 . Cw3)	1 0	7	1 (0 1	1	, ri	× ×	<u> </u>	2.1
U03644_at_	U03644		Recepin mRNA	10.9	1.3	3.4	7.0	1.1	2.4	- I	1.7	5.9
U50327_s_at	U50327		Protein kinase C substrate 80K·H gene (PRKCSH)	2.6	6:0		2.1	4	6.0	<u> </u>	2.3	ю с
U60519_at_	U60519	casp10	Apoptotic cysteine protease Mch4 (Mch4) mRNA		9.0	6.7	3.1	4	7 1	c	0	, r
003403 at	U834b3	1dad	Scaffold protein Pbp1 mRNA	1.9	2.5	2.5	2.8	4.1	2.4	7	800	100
X77366_at_	X77366	nfe211	ICF11 Transcription factor 11 (basic leucine zipper type)	2.3	c	16.0	۵,	-	,		-	
M63838_s_at	M63838	ifi16	Interferon gamma induced protein (IFI 16) gene	-				+	4.0	5 -	2 0	15.7
M76766_at_	M76766	etf2b	GTF2B General transcription factor IIB	5 6	1.	> .	0:7	Ŧ (Ŧ	7.0	7.5	7.8
1		1	בי בי מבויבומו נומווזכווחנותו ומרוחו וום	7	1.1	5.1	8	3.9	2.5	0.7	2.3	2

									5.		1 411	11	acoi	nen,	Cı												
	2.8	χ.	0.8	c	0 -	7.0	14.5	0.5	,		:	8.2	,	7.	1.1	u	99.9	1.2	(8.7	9.0	1.6	,	4.4	2	-	1.8
	0.5	7	-	C			3	0.7	-	2.1		5.9	-	-	0	6	Ď,	9.0	,	1.0	0	8.0	,	7 .	2.1		1.2
6	7)-	-10	1.3	-	-	1 .	<u>.</u>	0.1	0	200		m	7 0		7	7 00	, , , ,	1.4	-	4.6	0	1.1	,		5.7	2.5	1.4
		7.0	6.1	3.7	7	2 6	7.67	10.5	10	10		9.4	α		6.1	<u>ب</u> ب		2.1	1	0 0	2.3	6.8	-	1 C	ر ان	5.9	
0	2.0		3.5	α π	α		ρ n	3.8	3 7	37	,	3.7	3.7		7,	2 7		3./	0	0 0	ر. 0.	3.6	C C) C	3.5	3.5	3.5
6	0.2	2.3	4 0	ى	7			2.3	7.	2.1	-	4.2	13.3	2 -	y	بر در		3.5				4.8	<u>u</u>	2	٥	62	
-	J C	7	+	7	7.3	2 4	0	1/5.8	6	0.5	;	δ.14	Ω.	-	1	62.2	-	0.1	, t	ì	5	0.2	0	, 0	0.0	2 3	8.9
0 0	7.2	3.0	7.0	4.7	rc	7 6	\ -,	2	0	1.4	2	21.8	4.6	L C		48.6		7	0		0.1	m	-α	200	۲:3	5.2	3.1
	4 X		<u>,</u>	Ŋ	8.2	, c	? .	7.7	0	1.2	1 00	7.07	3.6		3	54.1	, c		Ċ.	1 7	5:7	9.0	26	1	21	7.3	5.6
		+	+		m	_	\perp	+				1			+			+		-	+	_		-	\downarrow		H
RAF1 V-raf-1 murine leukemia viral oncogene homolog 1	JUNB Jun B proto-oncogene	SMT3B protein		HLA-B null allele mRNA	Sodium/potassium-transporting ATPase beta-3 subunit mRNA	Bci-2 binding component 3 (bbc3) mRNA, partial cds	PTX3 gene promotor region	Pre-mPNA enlicing factor CD-20 CHITE	(sequence from the 5'cap to the start codon)	Mr 110,000 antigen	PIM1 Pim-1 oncogene	CED1 Complement of the F	(C5a ligand)	LIPA Lipase A, lysosomal acid, cholesterol esterase		IAP homolog C (MIHC) mRNA	VIM Vimentin		Fas-binding protein (DAXX) mRNA, partial cds	KIAA0138 gene	CRM1 protein	CINET PLOTEIL	Rer1 protein	Serine/threonine protein kinase	Major Histocompatibility Compley Class 1	(Gb:X58536)	NP Nucleoside phosphorylase
raf1	quni	smt3h2		hla∙b	atp1b3						pim1		c5ar	lipa		ciap2	vix		daxx		crm1	11115	pex10	dyrk1a		hla∙c	du
X03484	X51345	X99585		D49824	U51478	U82987	X97748		D28423	D64154	M16750		M62505	U04285		U37546	Z19554		AF006041	D50928	Y08614		AJ001421	D86550	HG658.	HT658	K02574
X03484_at_		X99585_at_		D49824_s_at_	U51478_at_	U82987_at_	X97748 s at			D64154_at	M16/5U_S_at		M62505_at	U04285_s_at	U37546 s at		Z19554_s_at_	AF006041_at	_	_at		21 at		0_at_	HG658.		K025/4_at_

_													•••		••••		-,												
32.5		1 0	23.5	9.8	C	1 0	110	Īα		C	6.0	1.4	196	2	1	11	2.2	17	9		C	110	0 0		4		3.4	19	2.2
11.8	2		13.7	٥٠	0	1.2	2 6	ν α		,		4.4	42	a -	2	8.9	4.8	0.8	23		C	000		J	6 0		3.7	8.6	7
27.3	1.0	i L	U. C	3.5	7	; -	1 (*	7		a	0.1	2.5	7 6	-		ıO	1.3	9.0	2		0	2	- L		0.8		2.5	ω. 33	2
11.5	27		0 00	50.7	r.	ν α	200	30		100	75.5	3.6	23.4	26	2	8.9	4.3	1.8	14.7		00	200	4 6	?	2.9		6.9	4.5	25
3.5	ب			0.0	4	3.4	3.4	3.4		77	2	3.3		32	;	3.2	3.2	3.2	3.2		32	3.2	30		3.2	-	3.1	3.1	7
5.6	0	-	11.4		3.4	2	4.5			2	3.5	5.6	15.8	m	,	9.4	4.3	3.4	2.8		3.7	13.2			3.9		5.7	7.1	25
21	m	1 1	10/	2.0		κ α	4.1	2			,	0.5	22.1	4.7		13.1	4.4	1.1	14		0	23.7	c		2.6		7.4	27.1	1
19.5	2.1	1 2	2101	24:0	0	17	12.4	2		_	-	4.0	6.1	3.9	-	5.3	4.4	2.2	3.7		0.5	1.2	12		2.4		5.5	14.1	E
9	28	7 0%	ά α	3	8.0	3.4	6.3	4.3		0.3		1	14.3	6.1		18.5	3.7	6.0	2.4		0	4.6	6.0		2.3	ï	α. Σ. Ω	24.8	1.3
Mac-2 binding protein mRNA	Heat shock protein (hsp 70) gene	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 2	ADENOSINE AZA RECEPTOR	mRNA fragment encoding beta tubulin, (from	clone D-beta·1)	Nuclear domain 10 protein (ndp52) mRNA	IRF4 Interferon regulatory factor 4	P97 mRNA	Carboxy Mathyltraneforace Acceptant	Splice 1	PAGA Proliferation-associated gene A (natural		PEBP2aC1 acute myeloid leukaemia mRNA	KIAA0005 gene	(:	n, Beta	PGAM1 Phosphoglycerate mutase 1 (brain)	Integrin-linked kinase (ILK) mRNA	Protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA	IFNA gene (interferon alpha·h2) extracted from	Human gene for leukocyte (alpha) interferon H	BETA-DEFENSIN 1 PRECURSOR	HSPB1 Heat shock 27kD protein 1	PROBABLE PROTEIN DISULFIDE ISOMERASE ER	60 PRECURSOR	HLA-A MHC class I protein HLA-A (HLA-A28,		Nichovot gene, partial cus	EIF2A Eukaryotic translation initiation factor 2A
тас2ър	hspala	GBP2	adora2a			ndp52	irf4	dap5				paga	ami2		0	tubuling	pgamı	¥	ptp4a1		ifna14	defensinb1	hsp27	ļ	grp58		KIAAOORA	100000	
L13210	M11717	M55543	X68486		J00314	U22897	U52682	U73824	HG1400.	HT1400		X67951	235278	D13630	HG4322.	104173	3041/3	040282	U48296		V00533	X92744	223090		249835	032129	D42043	102645	JU2645
L13210_at_	-at_		Ι.				7	U73824_at_	HG1400- HT1400 s at					at	HG4322.		3041/3_d(U40282_at_	U48296_at_		f at		Z23090_at_		249835_s_at_ 249835	D32129 f at D32129	D42043 at	T	JUZ045_at_

M2006A 24	MOODEA	1405014	HNRPA2B1 Heterogeneous nuclear	C	C	C	C L	ŗ	-	C	,	
M36341 at	M36341	1111 20201	AREA ADP. ribosylation factor 4	17	о - п	2.7		7.0	1.0	0.0	0.4	200
700071	700071	7.00.7	Piet and industrial racial		7.7		2.3	7.0	2.0	1.7	1.0	0 1
04880/_at_	04880/	ausp4	Dual specific protein phosphatase mKNA	9.6	29.6	4./	2.4	3.1	9.8	9.7	5.6	21.7
			KAI1 Kangai 1 (suppression of tumorigenicity 6,				_					
			prostate; CD82 antigen (R2 leukocyte antigen,								_	
			antigen detected by monoclonal and antibody				•					
U77948_at_	U77948	bap135	[IA4])	Ó	0.5	0	1.5	3.1	2.7	0	0.7	9.0
			GNB1 Guanine nucleotide binding protein (G				-	-		_	_	
X04526_at_	X04526	gnb1	protein), beta polypeptide 1	1.8	m	0.8	3.8	3.1	3.5	6.0	1.4	2.6
X52425_at	X52425	il4r	11.4R Interleukin 4 receptor	8.6	10	10	2.9	3.1	4.4	1.8	2	9.7
D14695_at_	D14695		APOA2 Apolipoprotein A·II	3.7	2.1	0.1	4.4	3	8.3	0.4	9.0	4.8
			PTGER2 Prostaglandin E receptor 2 (subtype							-		
L28175_at_	L28175	ptger4	EP2), 53kD	0.9	0	1.1	2.3	m	17.4	0	0.5	1.2
U23070_at_	U23070		Putative transmembrane protein (nma) mRNA	0.8	1.2	4.8	2.2	3	6.2	0.2	0.1	1.
	,	;										
U32944_at_	U32944	dlc1	Cytoplasmic dynein light chain 1 (hdlc1) mRNA	2.9	4.3	5.6	3.4	m	2.4	-	0.2	1.4
X81198_at_	X81198	arcn1	COATOMER DELTA SUBUNIT	1.9	ന	2.6	2.4	m	2.5	0.7	6.0	1.4
Y08682_rna1								-	-		_	
		cpt1b	Carnitine palmitoyltransferase I type I	0.3	1.8	6.0	9.9	m	6.1	8.8	4.5	7.1
at	D63506	unc18·c	Unc-18homologue	2.2	1.7	2.5	3.7	2.9	2.5	1.2	0.1	-
	L19067	nfkb p65	TRANSCRIPTION FACTOR P65	7.9	5.4	3.9	8.2	2.9	5.6	6	1.6	2.9
U47634_at_	U47634	b-tub4	TUBB Beta-tubulin	3.8	2.3	2.2	2.8	5.9	4.3	1.1	6.0	9.0
D26599_at_	D26599	psmb2	Proteasome subunit HsC7-I	4.2	2.7	4.9	2.2	2.8	2	1.6	4	4
D87078_at_	D87078		KIAA0235 gene, partial cds	0	9.0	0	3.3	2.8	5.3	6.0	0	0.1
HG3076.										-		
HT3238_s_at HG3076-	HG3076.		Heterogeneous Nuclear Ribonucleoprotein K, Alt.					_				
	HT3238		Splice 1	1.4	1.1	4.8	8.9	2.8	17.3	1.9	2.1	4.5
HG3954.											-	
HT4224_s_at			Landsteiner-Wiener Blood Group Glycoprotein									
		icam4	(Lw) (Gb:L27671)	2.4	4.8	1.2	m	2.8	m	1.5	0.2	6.0
S74017_at_	S74017	nrf2	Nrf2	3.8	6.3	3.7	e	2.8	1.8	3.1	2.8	1.9
U67319_at_	U67319	casp7	Mch3 isoform alpha (Mch3) mRNA	1.9	4.7	12.2	3.5	2.8	6.1	3.1	6.3	13.2
U76764_s_at									-		-	
1	U76764	cd97	CD97 CD97 antigen (leucocyte antigen)	14.8	10.7	3.4	14.5	2.8	2.3	1.7	2.3	7.5

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	1.3	0.6	1	3 0.5 0 2.8	2 0 0.8		1:1	1 7 2 6 2 2	0.0	2.0	0.1	3.2 3.2 9.3	0.8 2.8 14		1.3 0.8 4.2			1.5 1 0.	0.7 0.7	2 0.3 5	0.0	1
000	<u>ا</u> :	0	-	2.8	2.7 5.2			27 21		<u></u>		.7 18.7	.7 26.2		2.7 3.1		4	3.	0. P. I	.6 19	3.2	
,	_			1.6	2.7	0	1	23.0			1	9	2.7 2.		3	-		ا ۵	7.5	9.6	1.5	
и С	J 1	-	1.4	7.8	4	0		4.5	2	6 200	7:/27	2.7	2.1		D.			1.1	50	1.5	2.4	
120	, , ,			1:4	0.3	æ	20 -	2.4	5.3	1			0.1		8	<u>и</u>		2.0	*	0	1.5	
C	2 6		4.4	5.1	1.5	80	α ο	3.7	6.0	α,		1.3	0	•	1.8	٦		> -	t	0	1.1	
Clone 23652 mRNA sequence	HNRPK Heterogeneous nuclear ribonucleoprotein K	P85 beta subunit of phosphatidyl-inositol-3.	MACH-alpha, 2 protein		Cadherin FIB2, partial cds	Cytoskeleton associated protein (CG22) mRNA	Heat Shock Protein. 70 Kda (Gh-Y00371)	RPL3 Ribosomal protein L3	Immunoglobulin related 14.1 protein mRNA	IL12A Natural killer cell stimulatory factor (IL12A)	UBE2A Ubiquitin conjugating enzyme E2A (RAD6	22VD3 cmooth mingle mosting control of the control	ZZADA SITIOUTII ITIUSCIE PROTEIN (SMZZ) MKNA	NNA Polymerase II largest subunit gene extracted from H.sapiens gene for RNA pol II largest subunit even 1	a goal subuilly, exoll 1	SRF Serum response factor (c.fos serum response element-binding transcription factor)	LGALS1 Ubiquinol-cytochrome c reductase core	ODC1 Ornithine decarboxylase 1	GLCLC Glutamate-cysteine ligase (gamma-	glutarriyicysteine synthetase), catalytic (72.8kD)	Butyrophilin (BTF1) mRNA	
	hnrpk	pik3r2	casp8				hsp70	sui1	flambda1	il12a	radba	sm22	31116.6	rool2	100	srf	lgals1	odc1	<u> </u>	מונונ		
U90911	72727X	X80907	X98172		AB000896	D49738	нG2855. HT2995	L26247	M2/749	M65291	M74524	M95787		X74874		J03161	J04456	M33764	MODESE		U90543	
U90911_at_	X72727_at_	X80907_at	Γ	ä		at	at		M2//49_at_	M65291_at_	M74524 at	Τ	1	X74874_rna1		J03161_at	J04456_at		M90656	1		

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HG4582	HG4582.				-	-				r		
HT4987_at	HT4987		Glucocorticoid Receptor, Beta	7	1.6	1.5	2.8	2.5	-	1.3	1.2	0.2
M91670_at_	M91670	psma2	Ubiquitin carrier protein (E2-EPF) mRNA	5.4	5.9	m	2.2		5.2	0.7	3.1	6.9
U14969_at_	U14969	rpl28	Ribosomal protein L28 mRNA	1.6	2.1	1.5	2.1	2.5	2.7	0.7	0.5	
U41740_at_	U41740	golga4	Golgin-245 mRNA	3.3	7.1	17.2	5.9		6.7	0.3	1.7	6.3
U77846_rna1					-							
_s_at_	U77846		Elastin gene, partial cds and partial 3'UTR	2.9	1.3	3.6	m	2.5	3.1	1.7	0.1	1.3
Y08409_at_	Y08409	thrsp	Spot14 gene	4.6	2.4	4.5	2.9	2.5	9.1	0	4.0	18
1 08246 at	108246	mcl1	INDUCED MYELOID LEUKEMIA CELL DIEFERENTIATION PROTEIN MCI 1		u u		-	C	7 0	-	-	0
1132519 at	1132519		GAP SH3 hinding protein mRNA	200	0 -	1,0	7 0	1.7		1 0	0.0	0 5
720670	073067	27,14,5	Mit College Process College	7 0	1	7.0	7.0	4.7	7.7	0.4	2.5	4.1
2296/8_at_	8/9677	mitt	Mit- mKNA	9.0	1.5	5.9	7.1	2.4	9.4	0.5	6.0	_
D28118_at_	D28118	db1	081	1.7	1.7	1.5	5.6	2.3	4.9	1.9	1.1	1.9
HG3597.	нG3597.		Major Histocompatibility Complex, Class I									
HT3800_f_at	HT3800	hla	(Gb:X12432)	7	5.8	3.3	6.5	2.3	3.6	4	4.3	1.6
J00207_rna2	0		IFNA gene (interferon alpha-a) extracted from									
at	702001	IIIna2	Human leukocyte interteron (leif) alpha a gene	4.0	0.5	6.0	2.1	2.3	14.3	0	0.7	-
J04617_s_at J04617	J04617	efla	EEF1A1 Translation elongation factor 1-alpha-1	1.8	1.6	1.7	1.8	2.3	3.8	1.3	0.8	1.1
M63835 at	M63835	fcgr1	HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I 'A FORM' PRECURSOR	C	2		~	,	0	,	9	2 2
U07806_s_at								2		+	5	1.0.4
1	007806	top1	TOP1 DNA topoisomerase I	3.4	5.6	8.4	4.2	2.3	1.9	Ö	1.4	3.1
i i		·	CYTOCHROME C OXIDASE POLYPEPTIDE VIA.				-					
X15341_at	A15341	coxbai	LIVER PRECURSOR	0.5	1.4	0	1.6	2.3	4.2	1	9.0	1.1
X69910_at_	X69910	p63	P63 mRNA for transmembrane protein	5.8	10.1	26.4	4.1	2.3	9.7	3.9	6.4	29.3
AF001294_at				_		-					-	
I	AF001294	ldi	IPL (IPL) mRNA	5.6	2.3	9	4.5	2.2	2.8	2.9	3.9	3.1
D31884_at_	D31884		KIAA0063 gene	3.5	1.3	3.4	5.9	2.2	6.9	2.4	=	1.6
D38128_at_	D38128	ptgir	PTGIR Prostaglandin 12 (prostacyclin) receptor (IP)	29.8	34.8	71.9	7.9	2.2	16.2	=	2.1	65.6

111 Response of Dendrine Cens to a... Inventors: Nir Hacohen, et al. 16.9 0.8 2.3 8.0 2.3 2.7 6.0 0.4 0.8 5.9 0.2 25.2 3.6 5.6 0.3 9.0 9.0 1.4 0.7 0.8 0.1 0.7 0.1 0.1 5.6 4 8.0 0.7 1.4 0.9 0.9 2.3 0.1 0.7 0.8 9.7 13.5 2.9 2.3 5.5 4.6 2.9 1.9 67 2.1 2.4 2.6 6.2 1.7 2.5 1.6 2.2 12 12 2.2 2.2 2.2 2.1 2.1 2.2 2.1 2.1 1.2 12.2 9.8 10.1 3.8 2.4 6.5 3.6 8.9 ω . 6.3 4.3 4.1 2.1 4.5 0.2 24 8 37.2 7.8 222 18 2.1 4.8 5.3 2.1 0.0 2.8 0.8 0 6.9 13.7 0.9 6.7 0.8 0.8 2.9 8.1 1.3 1.5 1.3 13.5 15.9 10.7 2.5 1.9 4.5 11 TAP2 Transporter 2, ABC (ATP binding cassette) ZFP36 Zinc finger protein homologous to Zfp.36 Small Nuclear Ribonucleoprotein, Polypeptide C, protein 51) CD86 CD86 antigen (CD28 antigen ligand 2, B7. 2 antigen)
Androgen regulated homeobox protein (Nr.X.3.1)
mRNA CLN3 Ceroid-lipofuscinosis, neuronal 3, juvenile exons 1-8 Thymosin beta-4 mRNA TYROSINE-PROTEIN KINASE RECEPTOR ECK LMNA Lamin A BCL6 B cell lymphoma protein 6 (zinc finger High mobility group protein (HMG·I(Y)) gene ZNF2 Zinc finger protein 2 (A1-5) DUAL SPECIFICITY MITOGEN ACTIVATED PROTEIN KINASE 81 (Batten, Spielmeyer vogt disease) JNK ACTIVATING KINASE 1 C4A Complement component 4A JUNB Jun B proto oncogene PIM1 Pim-1 oncogene Alpha-CP1 mRNA PRECURSOR MOP1 mRNA Alt. Splice 2 EB1 mRNA in mouse mapkk3 cmdla hmgiy ptmb4 nkx3a hif1a 98po pim1 jnkk1 tap2 junb pcl6 c4a bts ttb

M54915

U20734 U22431 U24166

U20734_s_at U22431_s_at

D87116

D87116_at

M54915_s_at

X78925

(78925_at_

U32680

U24166_at_ U32680_at_ L36870_at_

136870

M13452_s_at

M13452 U00115 U04343 **U80669**

U80669_at_ Z29505_at_

U04343_at_

J00115_at

HT5143_s_at | HG1322. ____HT5143_

_17131_rna1

L17131 M17733

M17733_at

M74447 M92843

M92843_s_at

M74447_at_

M59815

M59371_at_ M59815_at_

M59371

Inveors:	Nir Hacohen, et al.

D00017_at_	D00017	anx2l4	ANX2 Annexin II (lipocortin II)	1.2	3.2	ō	1 2	0	60	,	40	0
D10522_at_	D10522	macs	MACS Myristoylated alanine-rich Ckinase substrate							7	'n	0
D25274_at_	D25274	racl	Randomly sequenced mRNA	100	3.2	10.3	4.7	5	2.9	2.3	3.5	5.1
L41887_rna1			Splicing factor, arginine/serine-rich 7 (SFRS7)			0	010	y.	0 5.3))	7.7	8:/
at	L41887	sfrs7	gene	0.8	0	0	2.2	σ	7.3	4.4	4	
M/354/at	M/354/	d55346	POLYPOSIS LOCUS PROTEIN 1	0	6.0	0		0	10.6	- 2	1 5	
U62962_at_	062962	eif3s6	Int-6 mRNA	0.3	0.7	80	-	0		2 0	? -	-
U89505_at_	U89505	rbm4. lark	Hlark mRNA	1.3		4.2	i a	10	7	1 5	-	5
V00536_rna1	7,00536	j	IFNG gene extracted from Human immune		-		<u>-</u>		+	1	-	4.0
X75755 rna1	00000	20	Interferon (IFIN-gamma) gene	9.4	1.2	124.2	46.7	1.9	25.7	6.0	1.4	27.8
_s_at_	X75755	sfrs2	PR264 gene	1.5	c	0.7	1	0	,	Č		1
X93920_at_	X93920	9dsnp	Protein tyrosine phosphatase (tissue type: foreskin)	2.2		107			2 6	1 0	2) (
Y00285_s_at_	Y00285	igf2r	IGF2R Insulin-like growth factor 2 receptor	α ο	1 4	-			1 1	2	5 -	S C
D38491_at_	D38491		HYPOTHETICAL MYFLOID CFLLLINE PROTEIN 2	6					2		7	ν. Σ
			ApM2 mRNA for GS2374 (unknown product		5	7:1	-	χ.	7	0.4	0	89.
	D45370		specific to adipose tissue)		0.6	0	0	α	7	-		
049400_at	D49400		Fetus brain mRNA for vacuolar ATPase	9.0	0.5	0	23	α	σ-	† - 1 -	7.7	7 0 4
WZ6/U8_S_at	907.3CM								-	+		7.5
M94856 at	M94856	fahns	FIMA Prothymosin alpha	0.1	1.2	0.5	1.8	1.8	1.9	4.0	0.8	1.3
Т	X06614	rara	Recentor of retinoic acid	1.6		6.0	3	1.8	1.8	1.2	1.4	2
			HLA CLASS I HISTOCOMPATIBILITY ANTIGEN F	0.0	5	5		1.8	0	0	6.0	1.3
X17093_at	X17093	hla-cda12	ALPHA CHAIN PRECURSOR	12.7	8.4	5.5	r.	α	7	210	12.4	C
D90209_at_	D90209	atf4	ATF4 CAMP-dependent transcription factor ATF. 4 (CREB2)	4	000				2		1.71	7.0
HG417.	HG417.				9	2	7.0	+	5.4	20	5.1	8.4
s_at_	HT417		Cathepsin B	ď	-	-	·	,				
M57710_at_	M57710	galbp	LGALS3 Lectin, galactoside binding, soluble, 3 (galectin 3) (NOTE: redefinition of symbol)	0 2	0 40	-	0 7	1 ,	0 0	1.5	7.7	0.0
				<u>.</u>	-	7	1.1	1./	1.0	<u>0</u>	7.7	2.5

M23197_at	M23197	cd33	CD33 CD33 antigen (differentiation antigen)	0	1	0	0.5	1	c	60	0	C
U18062_at_	U18062		TFIID subunit TAFII55 (TAFII55) mRNA	0.5	2.1	2.2	12.2	9	13	0.4	m	4.2
X17042_at_	X17042	prg	PRG1 Proteoglycan 1, secretory granule	6.1	m	3.4	4.2	1.6	4.4	2.9	3.3	1.5
Z30425_at_	230425		Orphan nuclear hormone receptor	1.4	9.0	1.4	4	1.6	2.7	0.4	0.7	3.5
AF012024_s_ at_	AF012024	icap.1b	Integrin cytoplasmic domain associated protein (Icap.1a) mRNA	1.3	1.0	C	200	- L	α.	-	, c	
D50863_at_	D50863	tesk1	TESK1	0	2.6	0		12	2.4	2.4	0	25
U90913_at	Ú90913	unknown	Clone 23665 mRNA sequence	0	1.4	0	0	1.5	0	1 6	0.5	0.4
U94592_at_	U94592	ucp2	Uncoupling protein homolog (UCPH) mRNA	0	0.7	0	0.5	1.5	0	0.1	0.2	0
			Liver mRNA fragment DNA binding protein UPI					-	-			
X04347_s_at_ X04347	X04347		homologue (C-terminus)	1.6	1.3	9.0	2.3	1.5	11.2	0	2.8	0.1
M35128_at_	M35128	chrm1	Muscarinic acetylcholine receptor gene	0.7	-	2	1.4	1.4	3.2	ō	0.8	2.1
U86602_at_	U86602		Nucleolar protein p40 mRNA	6.0	0.7	0	1.1	1.4	0	0.2	0	0
D13640_at_	D13640	pp2c-like	PUTATIVE PROTEIN PHOSPHATASE 2C	0	0	0	0	1.3	0	0	9.0	0.5
D79990_at_	026620		KIAA0168 gene	0.7	-	0.3	2.2	1.3	0	1.3	Ξ	0.8
L11066_at	111066	hspa9	MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR	-	0	c	1 7	-	-	0	7	5
			Clone CIITA-8 MHC class II transactivator CIITA						,			;
U18259_at_	U18259	ciita	mRNA	0	0	0	0	1.3	0	1.7	0	0
M31516_s_at		***********	DAF Decay accelerating factor for complement									
1	M31516	daf	(CD55, Cromer blood group system)	21.8	2.8	3.3	4.7	1.1	8.2	0.7	0.7	0.8
U68105_s_at	0.00							-				
Y78817 at	V78817	PhoCADA	PABPL1 Poly(A)-binding protein-like 1	80	60	80			0	0	8.0	0.5
- 100 /		200	GOTO Cutomic avalgantia trans	5	7:5		<u>ه</u>	7	5	5	5	0
M22632_at_	M22632	got2	work didding coxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	0.1	6.0	C	C		C		C	C
J03592_at_	103592	ant3	ANT3 Adenine nucleotide translocator 3 (liver)	0.5	F	0	0.3	6.0	0	-	-	C
			Ras GTPase-activating-like protein (IQGAP1)									
L33075_at_	L33075	iqgap1	mRNA	0.1	0.7	0	9.0	6.0	0	1.3	0.1	0
	0	:	INPPL1 Inositol polyphosphate phosphatase-like								-	
L36818_at_	L36818	Inppl1	protein 1 (51C protein)	0	0	0	0.7	6.0	0	0.7	6.0	0.3
U05572_s_at	1 L 2	Ġ					-		-			
	7/5500	manzb1	MAN'B Mannosidase alpha B (lysosomal)	0.5	1.7	0.7	0.4	0.9	0	0.6	0.4	0.4

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0	2.4	1.1	0	0.8				10	0.4		0.4	0	0.5	200	77	C			2.3	0		0	0	0
	1.4	6.0	0				1 4	0	9.0		0.6	ō		ά	9	0			0	0		0	0.1	0.5
1.2	0.3	-		1.5			0	12	8.0	-	3.2	0.7	2.5	-	?	0			0	1.4		9.0	1.2	9.0
0	0	0	0	0			-	0	0		0	0	0		7	0			0	0	\vdash	0	0	0
6:0	6.0	6.0	8.0	8.0			8	0.8	0.8		0.8	0.8	0.7	7 0	,;,	0.7	-		0.7	0.7	-	0.7	0.7	9.0
	1	2.1	0	0.4			80	0.8	3.5		0.1	0	8.0	. 0	3	0.2	<u> </u>		0	0.3		1.4	1.4	0
	4.7	2.5	0	0			0.5	0.3	0	,	0	1.8	0	0	2	0			0	0		0	0	0
0.7	3.7	0	-	0		_	1.2	6.0	0.6	- (6.0	-	0.4	0	11.5	0			1.1	6.0		0.2	0.7	1
- 0	5	o,	0	0			9	0	9.		0.2	0.7	-	C	,	- 0			0	_	_	0	0	0
		Ö					0		-	(٥	Ó	0.1							0.1				
Tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds	Biliverdin-IXalpha reductase mRNA	ALPHA-CENTRACTIN	NADPH-flavin reductase	KIAA0179 gene, partial cds	ITGAM Integrin, alpha M (complement	CD11b (n170) macrophage antigen alpha	polypeptide)	M6PR Mannose receptor	SSBP Single-stranded DNA-binding protein	Silencing mediator of retinoid and thyroid	HOLLIONE ACTION (SIME) MRINA	Translation initiation factor elF-4gamma (partial)	ORF, Xq terminal portion	DNA-DIRECTED RNA POLYMERASE II 23 KD POLYPEPTIDE		Tyrosine Kinase Syk	ERCC1 Excision repair cross-complementing	rodent repair deficiency, complementation group	1 (includes overlapping antisense sequence)	Clone 23693 mRNA sequence	ATP5D ATP synthase, H+ transporting,	mitochondrial F1 complex, delta subunit	RETINOBLASTOMA BINDING PROTEIN P48	KIAA0037 gene
	blvra		blvrb	kiaa0179			cd11b	mmr	ssbp	2000	IICOIZ			polr2e		syk			ercc1		1 U	atpod	rbp48	adcy/
U12595	U34877	X82206	D26308	D80001			J03925		M94556	1137146	03/140	234918	D16469	D38251		HG3730. HT4000			M13194	U79254	77,400	X63422	X/4262	025538
U12595_at_	U34877_at_	Ţ	П	D80001_at_			J03925_at_	M93221_at_	M94556_at_	1137116 at	03/140_8(Z34918_at_	D16469_at	D38251_s_at_	HC3730.	HT4000_s_at HG3730			M13194_at_	U79254_at_	7	Ţ		U25538_at_

												114	COII	C11,	U	ш											
	C	0.7		0.1	0	0	(0 0	0					•		ग	0	0.4	٥	% %	0	0.9		(اد		-
	-	3.2		7.0	0.9	0.1	-	0.0	9 6	2 4	5	ā		1	5	5	0	0	0.0	87	0	0.7		(5 7))	~
	0	0.7	-	2.0	0.3	0.1	Ċ	0.0	1 0		7	0		-	5	5		-1	5	5	5	2.3		C	ρ Ο	5	
	Ó	0	-	5 0	5	0		5 0				C	+		5 0	5 0	5	5 0	5 0	2.1	5	0		Č	5 0	5	
	9.0	9.0	9 0	0 0	0.0	0.0		2 0	0 0			0		C	0 0	5 0	4.0	4.0	2 0	200	0.6	0.5		0	7 0	7.0	0
	0.7	2.1				0.3		100				0.5		-			0.6	7.0	5 0	5	5 0	5			10		~
	0	0		5 0	5 0	5	C	0				0	\vdash			5 6	5 -	, 0	000	0 0	5 .					5	c
	0.4	1.3		5 0	5 0	7	6	0 -	0	α	-	0		9	000	1 4	<u> </u>	0.0	300	5 0	2 ,	4:4		7	1 0	>	0.3
	0	1.2	~ 0) c		5	2	-	C		-	0		o				10	2 0) c	5 0	o o		4		,	0
						1					L		_				2			<u></u>					<u>'</u>		
PTGS1 Prostaglandin endoperoxide synthase 1 (prostaglandin G/H synthase and	(cyclooxygenase)	Pyridoxal kinase mRNA	SNRP70 U1 snRNP 70K protein	SCA1 Ataxin 1	Sds22-like mRNA		A2M Alpha-2-macroglobulin	ESD Esterase D/formylglutathione hydrolase	Membrane associated protein (HEM:1) mRNA	PCCA Propionyl-coA carboxvlase alpha chain	LIMKI gene (LIM-kinasel) extracted from	LIM-kinase1 (LIMK1) gene		(furin, membrane associated receptor protein)	MAPKAP kinase (3pK) mRNA	Transcriptional activator hSNF2b	Dynamitin mRNA	KIAA0246 gene, partial cds	Brk mRNA for tyrosine kinase	Stac	KIAA0223 gene, partial cds			Transcription Factor liia	ADORA3 Adenosine receptor A3	Chromosome 16p11.2 BAC Clone CIT987SK.	234F9 complete sequence
_	COXI		rnpulz		ppplr7		a2m	esd	hem1	bcca		limk1		fur	3pk			kiaa0246		stac				TFliia	adora3		
000	6/66GM	088000	X04654	X79204	250749		M11313	M13450	M58285	879219		U62293		X17094	U09578	U29175	U50733	D87433	X78549	D86640	D86976		HG4312.	HT4582	L77730	1	U46025
0000	100606 at	Uosouo_at_	اليد	_	Z50749_at	M11313_s_at		M13450_at_	M58285_at_	S79219_s_at_	U62293 rna1	_s_at									D86976_at	HG4312.	HT4582_s_at HG4312	٦	L77730_atl		U46025_at_

			Naip gene (neuronal apoptosis inhibitory		-		-	-	-	ŀ	-	ſ
			protein) extracted from Human basic									
U80017 rna2			transcription factor 2 p44 (bitzp44) gene, partial cds, neuronal apoptosis inhibitory protein protein and emission and emission meters.									
_at	U80017	gtf2h2	(riarp) and survival motor heuron protein (smn) genes		4 0	C	0	0		-	7	Ç
			H-IDH gamma gene (NAD(H) specific isocitrate				5	1		-	<u></u>	0.0
 Z68129 cds1			dehydrogenase gamma-subunit precursor)						•			
_at	268129	idh3g	TRAP delta gene	C	C			0	-		C	
0000	00000		High density lipoprotein binding protein (HBP)		1		1	7.7			0.0	5
กไ	M64098	dallah	mRNA	0.2	0.1	0	0.3	0.1	-0	0	9	
_4	011/91	cak	CCNH Cyclin H	0.7	2	0	6	0	c	000	α	100
D38521_at_	D38521		KIAA0077 gene, partial cds	0.2	0	0	0.3	C	0	100	200	
D80000_at_	080000		KIAA0178 gene, partial cds	1.1	0	0	0.1	0	c	0 0	90.0	7 0
HG22/4- HT2370 at	HG22/4. HT2370		Rna Polymerase II 14 5 Kda Subucit		-	 		-	-			
			INTEDECEDON ALPHA OPETA PROTECTOR ALPHA	5	5	5	5	0	0	~	<u>∞</u>	6.0
J03171_at_	103171	ifnar1	CHAIN PRECURSOR	C		٦,		-	à	0	-	(
			HMGCL 3-hydroxymethyl-3-methylglutaryl		-	-		7	5	0.0	1:5	7.0
			Coenzyme A lyase									
L07033_at_	L07033	hmgcl	(hydroxymethylglutaricaciduria)	0	-	2.3	- C	C	c	α	-	0
0.00			GNA11 Guanine nucleotide binding protein (G			-		-	,	2	-	7
M69013 at	M69013	gna11	protein), alpha 11 (Gq class)	0	0	0	0	C	C	Č	<u></u>	
M8039/_s_at			POLD1 Polymerase (DNA directed), delta 1,							+	}	
20000	M80397	poid1	catalytic subunit (125kD)	0	0.2	0	ō	0	0	0.1	C	C
M900/8 at	M926/8	picb2	PLCB2 Phospholipase C, beta 2	0	0	0	0	o	c	c	,	0
C80/137 F 24	757083		Fatty acid synthase {3' region} [human, breast					-			}	7
30043/ 3 dl	_		and Hepuz cells, mRNA Partial, 2237 nt]	0.4	0	0	0	0	0	0.7	1.3	0.2
U36787 at	U36787	hccs	Putative holocytochrome c-type synthetase		-	,	ľ		 -			
U51269 at	U51269	arvcf	Armadillo reneat protein mBNA	3 -	5 0	5 0	5	5	0	4.1	0.1	া
U51333_s_at				3	5	5	5	0	0	-	0 8.0	0.1
1	U51333	hk3	HK3 Hexokinase 3 (white cell)	1.5	9.0	0	-0	C	C	0 7	ō	α «
U51336_at_	U51336	itrpk1	Inositol 1,3,4-trisphosphate 5/6-kinase mRNA	0	0	c	0 5		0		-	
				,	,	>	5	>	5	5	7.7	7.7

U53446_at_ U53446	U53446	dab2	Mitogen-responsive phosphoprotein (DOC.2)	LC	C	-		_	-	-		(
			Mitochondrial NADH dehydrogenase-uhiguingne	5		1	1	3	5	5	0.7	
			Fe-S protein 8, 23 kDa subunit precursor									
			(NDUFS8) nuclear mRNA encoding									_
U65579_at_	U65579	ndufs8	mitochondrial protein		0	((-	
U72514 at	U72514		C2f mBNA	5	0.1	5	5	5	5	1.5	0	0
1177666 24	13266			5	0	-	0.3	0	0	0.5	αc	C
00/100 al	07/000		IRNaseP protein p30 (RPP30) mRNA	60	σ	c	7	C		2 0	0 0	7
			RIBONIICI FOSIDE DIPHOSPUATE DENLICTARE		2	5	\ .:\	5	5	0.0	0.8	4.0
VECTOR AS	24.70	,	TOOLS OF THE TOOL AND THE PROPERTY OF THE PROP			_	_	_		-	L	
A39343_at_ A59543	A59543	rrm1	MI CHAIN		-	C	ų		-	1	•	
			Cellular adhesion regulation, molecule [b.:.man		1	3	0.0	5	5	0.7	0	0
X6578/ s at [X6578/	1465787	,	- Dis 400 is								_	
700104 3 at	40700	car	mkina, 429 nt	C	α	2 1	-	_	_	((
X91257_at_ X91257	X91257		SERYL-TRNA SYNTHETASE	2 0		1.7	5	5	5	3.3	0.0	1.5
X92762 at	X92762		Totore oriental	/ 10	7.7	12.2	0.4	-	0	1.4	П	6.2
207750			ומומללוווא לוחופונו	2.8	0	0.5	0.7	c	Ĉ	c	u -	C
10//59_at_	10//59	myh12	Myosin heavy chain 12	7	0	1		7	7	2	7	٦
				, i	0.0	0.7	0	0	0	1.2	0.3	2.5
Z11559_at_ Z11559	Z11559	aco1	IREB1 Iron-responsive element hinding acceptance	,	(_	-	\vdash	
			וווווווווווווווווווווווווווווווווווווו	0.1	0.2	0.1	0	0	0	0.5	0	0 4
											1	;

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affylD	GBA	gene symbol	gene Name	feco	9900	2000		- 1			- 1	
X67325_at_	X67325	ifi27	INTERFERON ALPHA INDUCED 11.5 KD PROTEIN	700			bro	npra		ıcan	mcan	tcan
X02530 at	X02530	no 10	INP10 Interferon (gamma) induced cell line;	130.8	143.4	618.8	265.8	192.2	498.1	20	212.1	604.2
	$\overline{}$	25	1/128 Natural killer cell stimulaton, total	12.5	13.1	442.2	137.9	290.4	501.4	5.4	205.9	451.4
M65290_at	_	i12b/p40	(IL128)	712	261 5	225.7	Č	2 2	-	6		
1039280 at	028286	Itac	Beta-R1 mRNA, partial cds	34.9	1	237.0	201	20700	2400	32.8	9/-	412.7
M13090_8_at	M13690	clnh	CINH Complement component 1 inhibitor (angioedema, hereditary)				1	0, 10,	340.0	3.0	4.4/	389.7
U37518 at	U37518	iest	TNF-related apoptosis inducing ligand TRAIL	10.9	34.1	209.8	13.8	12.6	86.2	9.9	30.1	358.9
U29680_at	U29680	bcl2a1	Bcl-2 related (Bfl-1) mRNA	14.7		134.3	7	230.1	590.2	5.7	109.1	318.2
X72755_at_	X72755	mig	Humip mRNA	105.3	97.9	6/8.7	40.7	35.7	117.5	4	8.3	179.1
X07834_at_	X07834		SOD2 Superoxide dismutass 2 mitass	3.2	5.2	68.3	59.4	52.3	58.6	1.6	77.5	128.6
U88964_at_	U88964	5	HEM45 mRNA	2/./	104.1	240.9	34.7	92.1	91.6	6.6	17	116.5
				34.0	43./	191	27.2	15.5	73.3	8.8	43.4	116.1
X04602_s_at_ X04602	X04602	il6	IL6 Interleukin 6 (B cell stimulatory factor 2)	408 5	379.2	1267 E	70 5	7 7				
X65965 c at X65965	X65965	C	SOD-2 gene for manganese superoxide		3:()	777	0.0/	(0.0)	7.69.4	14.6	43	
M62403_s_at	2000		IGEBPA Institution like accounts for a	233.7	149.2	204	143.7	86.3	86.3	10.6	35.9	109.3
ţ	M62403	igfbp4	4	100	C L	1	;					
				10.3	2.2	32./	61.8	17.5	37.9	6.8	9.1	104.6
M33882_at_	M33882	mx1	MX1 Myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein 578)		(i	(1				
U52513_at_	U52513	ifit4	RIG-G mRNA	11.1	0.00	84.7	200	152.2	83.8	펀	397.3	102
M24594_at_	M24594	g10p1	IFIS6 Interferon-induced protein 56	7.07	29.3	36.2	92.1	84.6	98	13.2	39.1	94.7
			Signaling lymphocytic activation molecule	13.8	41/	//.5	90.8	266	141.1	18.6	248.6	89.6
U33017_at_	U33017	slam	(SLAM) mRNA	320.7	343.9	685.7	4.8	25.8	m	2.7	24.4	84.5
X02875_s_at_	X02875	oasl	OIAS (2'.5') oligoadenylate synthetase	16.7	30	48.7	41.5	58.8	117.7	4 2	0 0 1	2 0 0
at	98866X		MCP.2 gene	بر م	ű	0 90		8				
(VUUS94_at	V00594	lmt2a	Metallothionein isoform 2	1683.1	1698.4	143.4	371	82.6 414 5	107.8	8.6	23.8	79.5
							1	7	0:/01	0.0	707	74.7

Figure 3A

29.8 34.8 71.9 7.9 2.2 16.2 11 172.2 163.5 624.1 60.6 100.2 101.8 7 1 58.1 87.3 98.2 23.3 69.6 83.5 26.5 58.1 87.3 98.2 23.3 69.6 83.5 26.5 54.1 48.6 62.2 5.3 3.7 31.5 22.7 54.1 48.6 62.2 5.3 3.7 31.5 22.7 59.1 114.4 703.3 2 4.8 32.2 13.8 48.2 24.5 63.6 15.3 13.8 87.4 5 199.3 598.3 184.4 9.1 12.6 20.2 20.2 48.2 24.5 63.6 53.6 10.7 47.1 44.3 3.3 48.2 16.4 76.1 1 3.8 72.5 20.2 20.2 48.5 13.0 40.9 12.6				PTGIR Prostaglandin 12 (prostagyclin) receptor									
U77643 K12 K12 protein precursor mRNA 33 31 31 31 11 17 W31165 triaip6 PROTEIN TSG & PRECUSIOR INDUCIBLE 1722 1635 6241 606 100 101 7 L31854 cc77 CMKBR7 Chemokine (C-C) receptor 7 581 87.3 862 23.3 696 83.5 26.7 U37546 Ciap2 IAP homolog C (MHC) mRNA 54.1 486 62.2 5.3 3.7 31.5 22.7 U04636 cox2 Cycloxygenase 2 (MCx2) gene 110 120 6086 15.3 13.8 87.4 5.2 M57731 gro2 GRO2 GRO2 oncogene 110 120 6086 15.3 13.8 87.4 5.2 W57731 gro2 GRO2 GRO2 oncogene 110 120 6086 15.3 13.8 87.4 5.2 W57731 gro2 GRO2 GRO2 Gycloxygenase 2 (MCx2) gene 15.8 3.2 28.6 35.2 26.7 21.2	D38128_at	D38128	ptgir	(IP)	00 00	37.0		٢	C	,		,	
M31165 TUMOR NERROSIS FACTOR-INDUCIBLE 1722 163.5 624.1 60.6 100.2 101.8 7.1 L31584 Cerr7 CMKRRY COmmonine (CO, receptor 7 58.1 87.3 60.6 100.2 101.8 7.1 L31584 Cerr7 CMKRRY COmmonine (CO, receptor 7 58.1 87.3 60.6 100.2 101.8 7.1 L31584 Cerr7 CMKRRY COmmonine (CO, receptor 7 58.1 48.6 62.2 5.3 3.7 31.5 22.7 L31584 Cerr7 CMKRRY Commonine (CO, receptor 7 10.0 120.8 608.6 15.3 13.8 87.4 5.5 L3158 Cerr7 CMKRRY Commonine (CO, receptor 7 13.0 114.4 703.3 2 4.8 32.2 13.8 L315 Cerr5 Coccocygenase 2 (hCox.2) gene 110 120.8 608.6 15.3 13.8 87.4 5.5 L325 L115 Cerr5 Cerr5 Cerr5 Cerr5 Cerr5 Cerr5 Cerr5 13.8 L325 L115 Cerr5 L326 Cerr5 L326 Cerr5	U77643_at	U77643	k12	K12 protein precursor mRNA	25.0	0.4.0	71.9		7.7	16.2		2.1	65.6
M31165				TUMOR NECROSIS FACTOR: INDUCIBLE	,	3.5	0.00		7	11.4	4./1	9.4	63.3
U37546 Ciap2 IAP homolog C (MIHC) mRNA	M31165_at	M31165	tnfaip6	PROTEIN TSG-6 PRECURSOR	172.2	163.5	624.1	60 6	1002	α []	7	u u	0
U37546 ciap2 IAP homolog C (MIHC) mRNA 54.1 48.6 62.2 5.3 3.7 3.1.5 2.2.7 U04636 cox2 Cyclooxygenase-2 (hCox-2) gene 110 120.8 608.6 15.3 13.8 87.4 5 M57731 gro2 GRQ2 GRQ2 encogene 39.1 114.4 703.3 2 4.8 32.2 13.8 U72882 iri35 Interferon-induced leucine zipper protein (iFP33) 23.2 58.9 39.5 22 26.7 21.2 20.3 U56527 BRCA2 region, mRNA sequence CG018 5.9 16.4 76.1 1 3.3 18.4 3.3 2.0 L05072 iri1 IRF1 interferor regulatory factor 1 48.2 24.5 63.6 63.7 38.2 29.4 3.4 XA5500 ilib ILB Interferior regulatory factor 7 (humirf) mRNA 42.6 63.6 53.6 10.7 47.1 44.3 13.3 M28380 iri7 Interferior regulatory factor 7 (humirf) mRNA 42.6 53.6 </td <td>1137546 e at</td> <td>+</td> <td>ccr/</td> <td>CMKBR7 Chemokine (C.C) receptor 7</td> <td>58.1</td> <td>87.3</td> <td>98.2</td> <td>23.3</td> <td>9.69</td> <td>83.5</td> <td>26.5</td> <td>0.0</td> <td>20.0</td>	1137546 e at	+	ccr/	CMKBR7 Chemokine (C.C) receptor 7	58.1	87.3	98.2	23.3	9.69	83.5	26.5	0.0	20.0
March Marc	=	_	ciap2	IAP homolog C (MIHC) mRNA	1 73	9	(3
U04636 cox2 Cyclooxygenase 2 (hCox.2) gene 110 120.8 608.6 15.3 13.8 87.4 5 W57731 gro2 GRO2 GRO2 GROZ oncogene 39.1 114.4 703.3 2 4.8 32.2 13.8 U72882 iii35 mRNA, partial cds mRNA, partial cds 23.2 58.9 39.5 2 26.7 21.2 20.3 U50527 iri1 RF1 Interferion-induced leucine zipper protein (FP35) 23.2 58.9 39.5 2 26.7 21.2 20.3 U50527 iri1 RF1 Interferion regulatory factor 1 48.2 24.5 63.6 36.7 3.2 24.4 3.3 MX4500 ii1b LL1B Interfeukin 1, beta 199.3 588.3 184.4 9.1 12.6 20.2 24.4 3.3 MX4500 ii1b LL1B Interfeukin 1, beta 199.3 588.3 18.4 9.1 12.6 10.7 47.1 44.3 13.3 MX500 iri7 Interferion regulator	U04636_rna1	-			24.1	48.6	62.2	5.3	3.7		22.7	34	55.9
M57731 gro2 GRO2 GRO2 oncogene M57731 gro2 GRO2 GRO2 oncogene M57731 gro2 GRO2 GRO2 oncogene MRNA, partial cds MRNA, partial cds MRNA M807935 MRNA M808	_at_	ᅱ	cox2	Cyclooxygenase-2 (hCox-2) gene	-	1200	000		(
M57731 gro2 GRO2 GRO2 encogene 39.1 114.4 703.3 2 4.8 32.2 13.8 U22882 ifi35 ifi35 ifi35 ifi35 ifi35 ifi35 ifi35 ifi35 ifi35 ifi36 ifi35 ifi35 ifi35 ifi36 ifi35 ifi35 ifi36 ifi36 <t< td=""><td>M57731_s_at</td><td></td><td></td><td></td><td></td><td>120.0</td><td>908.5</td><td></td><td>13.8</td><td>87.4</td><td>2</td><td>4.7</td><td>54.9</td></t<>	M57731_s_at					120.0	908.5		13.8	87.4	2	4.7	54.9
U72882 ifi35 Interferon-induced leucine zipper protein (FP35) 23.2 58.9 39.5 22 26.7 21.2 20.3 U50527 BRCA2 region, mRNA partial cds BRCA2 region, mRNA sequence CG018 5.9 16.4 76.1 1 3.3 18.4 3.3 L05072 iri1 IRF1 Interferon regulatory factor 1 48.2 24.5 63 63.7 38.2 29.4 3.4 L05072 iri1 ILB Interferon regulatory factor 7 (humirf) mRNA 48.5 29.6 53.6 10.7 47.1 44.3 13.3 M28915 mtap44 protein p44 protein p44 protein p44 42.6 130 46 38.8 72.5 49.2 51.4 M253830 irf7 interferon regulatory factor 7 (humirf7) mRNA 42.6 130 46 38.8 72.5 49.2 51.4 13.3 M201121 rantes SCVA5 Small inducible cytokine A5 (RANTES) 78.7 42.6 40.9 82.6 115.3 113.6 M202031 I	-	 +	gro2	GRO2 GRO2 oncogene	30.1	110	5 607	·	-	0			
U72882 ifi35 mRNA, partial cds 23.2 58.9 39.5 22 26.7 21.2 20.3 U50527 BRCAZ region, mRNA sequence CG018 5.9 16.4 76.1 1 3.3 18.4 3.3 L05072 irf1 IRF1 Interferon regulatory factor 1 48.2 24.5 63 63.7 38.2 29.4 3.4 X04500 il1b IL1B Interferon regulatory factor 7 (humirt7) mRNA 42.6 130 46 38.8 72.5 24.2 24 598.3 184.4 9.1 12.6 20.2 24 3.4 D28915 mtap44 protein p44 mtorein p44 protein p44 42.6 130 46 38.8 72.5 14.3 13.3 M21121 rantes SCVAS small inducible cytokine A5 (RNITES) 728.7 661.7 83.4 71.7 396.6 11.6.6 10.0 47.1 44.3 13.3 M22910 tnfa TMX MXZ Myovirus (influenza) resistance 2, homolog 21.4.4 61.3	U72882_s_at	_		Interferon induced leucine zipper protein (IFP35)	1.5	111	0.00	7	δ.	32.2	13.8	11.7	53.6
U50527 irf1 IRF1 Interferon regulatory factor 1 48.2 24.5 63.7 38.2 29.4 3.3 M20502 irf1 IRF1 Interferon regulatory factor 1 48.2 24.5 63.7 38.2 29.4 3.4 X04500 iiib ILLB Interferon regulatory factor 1 48.2 24.5 63.7 38.2 29.4 3.4 D28915 mtap44 Protein p44 protein p44 protein p44 p4.6 130.3 184.4 9.1 12.6 20.2 24 M21321 rantes SCYA5 Small inducible cytokine A5 (RANTES) 728.7 61.7 83.8 72.5 14.4 31.3 13.3 M22910 trint Interferon regulatory factor 7 (humirt7) mRNA 42.6 130 42.6 16.0 82.5 51.4 42.5 13.8 72.5 13.4 M22910 trint TNF Tumor necrosis factor 52.7 18.4 61.3 16.2 15.2 12.2 14.4 17.8 16.5 13.7 13.6 13.7 <td>1150527 c at</td> <td>--</td> <td>ifi35</td> <td>mRNA, partial cds</td> <td>23.2</td> <td>58.9</td> <td>39.5</td> <td>22</td> <td>26.7</td> <td></td> <td>203</td> <td>20 2</td> <td>7,0</td>	1150527 c at	- -	ifi35	mRNA, partial cds	23.2	58.9	39.5	22	26.7		203	20 2	7,0
Interferon regulatory factor 1 AB AB AB AB AB AB AB	19-5- /3000											2	34:3
LO5072 irfl IRF1 Interferon regulatory factor 1 48.2 24.5 63 63.7 38.2 29.4 34 X04500 ii1b IL1B Interleukin 1, beta 1, beta 199.3 598.3 184.4 9.1 12.6 20.2 24 34 D28915 mtap44 protein p44 mtap44 protein p44 2.6 130 46 38.8 72.5 49.2 51.4 M21321 rantes SCYA5 Small inducible cytokine A5 (RANTES) 72.8 76.1 38.8 72.5 49.2 51.4 M21321 rantes SCYA5 Small inducible cytokine A5 (RANTES) 728.7 66.1 83.8 72.5 49.2 51.4 M22910 tnfa mxZ MXZ Myxovirus (influenza) resistance Z, homolog 21 74.4 42.6 40.9 82.3 50.4 19.8 M220310 tnfa TNF Tumor necrosis factor 144.1 225.5 115.7 73.8 58.6 48.5 27.2 M22032 tnfa Tap1	ŗ	02025/		BRUAZ region, mkina sequence CG018	5.9	16.4	76.1	1	3.3	18.4		13.9	50.7
X04500 illb ILLB Interleukin 1, beta 1913 598.3 184.4 9.1 12.6 20.4 3.4 D28915 imtap44 Hepatitis C-associated microtubular aggregate 8.5 29.6 53.6 10.7 47.1 44.3 13.3 M21321 rantes Brotein p44 mitap44 protein p44 42.6 130 46 38.8 72.5 49.2 51.4 M21321 rantes SCYA5 Small inducible cytokine A5 (RANTES) 728.7 661.7 83.4 717 396.6 115.3 113.6 MX2 MX2 Mx2 must inducible cytokine A5 (RANTES) 728.7 661.7 83.4 717 396.6 115.3 113.6 MX2 Mx2 mx2 of murine mX2 mx2 of murine mx2 of murine 74.4 42.6 40.9 82.3 50.4 19.8 M202030 trif TNF Tumor necrosis factor 144.1 225.5 115.7 73.8 58.3 27.2 M203031 unknown Phorbolin I mRNA, partial cds 134.3 42.3	L05072_s_at_	L05072	irf1	IRF1 Interferon regulatory factor 1	0		(0					
D28915 mtap44 Protein p44 Protein p46 Protein p46 Protein p46 Protein p46 Protein p46 Protein p47 Pro	X04500_at_	X04500	1115	IL1B Interleukin 1. beta	100.2	0.47	20.0	63.7	38.2	29.4	3.4	34.5	50.5
D28915 mtap44 protein p44 Drotein p44 Protein p45 Pro				Hepatitis Cassociated microtilibiliar aggregation	133.3	298.3	184.4	9.1	12.6	20.2	24	11.1	48.7
U53830 irf7 Interferon regulatory factor 7 (humirt7) mRNA 42.6 23.0 53.0 47.1 44.3 13.3 M21121 rantes SCYA5 Small inducible cytokine A5 (RANTES) 728.7 661.7 83.4 71.5 49.2 51.4 M30818 mx2 of murine 21 74.4 42.6 40.9 82.3 50.4 19.8 M202910 tnfa TNF Tumor necrosis factor 144.1 225.5 115.7 73.8 58.6 48.5 27.2 D42073 rcn1 Reticulocalbin 5.7 18.4 61.3 10 7.5 13.7 9.2 N57522 tap1 TAP1 Transporter 1, ABC (ATP binding cassette) 34.3 42.3 48.3 76.1 53.3 47.7 11.6 AB000115 unknown mRNA Phorbolin I mRNA, partial cds 43.8 28.9 21.9 18.9 8.4 26.9 28.7 3.4 M97935 stat1 TRANSCRIPTION 1-ALPHA/BETA 4.1 7.9 10.5	D28915_at_	D28915	mtap44	protein p44	O	0	C	- 1					
M21121 rantes SCYA5 Small inducible cytokine A5 (RANTES) 728.7 661.7 83.4 71.5 49.2 51.4 M30818 mx2 MX2 Myxovirus (influenza) resistance 2, homolog 21 74.4 42.6 40.9 82.3 50.4 19.8 X02910 tnfa TNF Tumor necrosis factor 144.1 225.5 115.7 73.8 58.6 48.5 27.2 D42073 rcn1 Reticulocalbin 5.7 18.4 61.3 10 7.5 13.7 9.2 X57522 tap1 TAP1 Transporter 1, ABC (ATP binding cassette) 34.3 42.3 48.3 76.1 53.3 47.7 11.6 M8000115 unknown mRNA Phorbolin I mRNA, partial cds 43.8 28.9 21.9 18.9 28.9	U53830_at_	U53830	irf7	Interferon regulatory factor 7 (humirf?) mPNA	0.00	23.0	33.0	10.7	4/.1	44.3	13.3	15.5	48
MA30818 mx2 MXZ Myxovirus (influenza) resistance 2, homolog 21 74.4 42.6 40.9 82.3 50.4 19.8 X02910 Infa TNF Tumor necrosis factor 144.1 225.5 115.7 73.8 58.6 115.3 10.8 X02910 Infa TNF Tumor necrosis factor 144.1 225.5 115.7 73.8 58.6 18.7 19.8 X57522 tap1 TAP1 Transporter 1, ABC (ATP binding cassette) 34.3 42.3 48.3 76.1 53.3 47.7 11.6 AB000115 unknown mRNA Phorbolin I mRNA, partial cds 43.8 28.9 21.9 189.3 58.3 23.3 4.4 M97935 stat1 TRANSCRIPTION 1.ALPHA/BETA 4.1 7.9 10.5 2.5 5.3 12.2 9.8 104164 1ii17 RPS3 Ribosomal protein S3 /wrong name 25.8 57.2 37.7 34.5 45.6 79.3 11.5	M21121_at_	M21121	rantes	SCYA5 Small inducible cytokine A5 /BANTEC	72007	130	40	32.8	72.5	49.2	51.4	43.1	47.5
M30818 mx2 of murine 7.5 19.8 50.4 19.8 X02910 tnfa TNF Tumor necrosis factor 144.1 225.5 115.7 73.8 58.6 48.5 27.2 D42073 rcn1 Reticulocalbin 5.7 18.4 61.3 10 7.5 13.7 9.2 X57522 tap1 TAP1 Transporter 1, ABC (ATP binding cassette) 34.3 42.3 48.3 76.1 53.3 47.7 11.6 AB000115 unknown Phorbolin I mRNA, partial cds 43.8 28.9 21.9 189.3 58.3 23.3 4.4 AB000115 unknown mRNA Phorbolin I mRNA partial cds 9.8 13.1 24.9 8.4 26.9 28.7 3.4 M97935 stat1 TRANSCRIPTION I.ALPHA/BETA 4.1 7.9 10.5 2.5 5.3 12.2 9.8 M97464 ifil7 RPS3 Ribosomal protein S3 /wrong name 25.8 57.2 37.7 34.5 45.6 79.3 <t< td=""><td></td><td></td><td></td><td>MX2 Myxovirus (influenza) resistance 2 homolog</td><td>/50./</td><td>/100</td><td>83.4</td><td>/17</td><td>396.6</td><td>115.3</td><td>113.6</td><td>87.4</td><td>43.7</td></t<>				MX2 Myxovirus (influenza) resistance 2 homolog	/50./	/100	83.4	/17	396.6	115.3	113.6	87.4	43.7
X02910 Infa TNF Tumor necrosis factor 144.1 225.5 115.7 40.3 50.4 19.8 D42073 rcn1 Reticulocalbin 5.7 184.1 225.5 115.7 73.8 58.6 48.5 27.2 X57522 tap1 TAP1 Transporter 1, ABC (ATP binding cassette) 34.3 42.3 48.3 76.1 53.3 47.7 11.6 AB000115 unknown Phorbolin I mRNA, partial cds 43.8 28.9 21.9 189.3 58.3 23.3 4.4 AB000115 unknown mRNA 9.8 13.1 24.9 8.4 26.9 28.7 3.4 M97935 stat1 TRANSCRIPTION 1.ALPHA/BETA 4.1 7.9 10.5 2.5 5.3 12.5 9.8 A164 ifi17 RPS3 Ribosomal protein S3 /wrong name 25.8 57.2 37.7 34.5 45.6 79.3 11.5	M30818_at	M30818	mx2	of murine	-10	74.4	12.6	0	0		(
V42073 Ircn1 Reticulocalbin 5.7 18.4 61.3 7.0 7.5 13.7 9.2 X57522 tap1 TAP1 Transporter 1, ABC (ATP binding cassette) 34.3 42.3 48.3 76.1 53.3 47.7 11.6 AB000115 unknown mRNA Phorbolin I mRNA, partial cds 43.8 28.9 21.9 189.3 58.3 23.3 4.4 AB000115 unknown mRNA 9.8 13.1 24.9 8.4 26.9 28.7 3.4 M97935 stat1 TRANSCRIPTION 1.ALPHA/BETA 4.1 7.9 10.5 2.5 5.3 12.2 9.8 J04164 ifi17 RPS3 Ribosomal protein S3 /wrong name 25.8 57.2 37.7 34.5 45.6 79.3 11.5	702910 at	X02910	tnfa	TNF Tumor necrosis factor	144.1	225.5	1157	73.0	586	20.4 70.4	20.70	39.4	43.2
X57522 tap1 TAP1 Transporter 1, ABC (ATP binding cassette) 34.3 42.3 48.3 76.1 53.3 47.7 11.6 U03891 unknown Phorbolin I mRNA, partial cds 43.8 28.9 21.9 189.3 58.3 23.3 4.4 AB000115 unknown mRNA SiGNAL TRANSDUCER AND ACTIVATOR OF Statt 9.8 13.1 24.9 8.4 26.9 28.7 3.4 M97935 statt TRANSCRIPTION 1.ALPHA/BETA 4.1 7.9 10.5 2.5 5.3 12.2 9.8 J04164 ifi17 RPS3 Ribosomal protein S3 /wrong name 25.8 57.2 37.7 34.5 45.6 79.3 11.5	0450/3_dl_	042073	rcn1	Reticulocalbin	5.7	18.4	61.3	10	7.5	13.7	9.75	110	43.4
U03891 unknown Phorbolin mRNA, partial cds A38 28.9 21.9 189.3 58.3 23.3 4.7 11.6 AB000115 unknown mRNA SIGNAL TRANSDUCER AND ACTIVATOR OF A1 7.9 10.5 2.5 5.3 12.2 9.8 13.1 24.9 8.4 26.9 28.7 3.4 28.7 3.4 26.9 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.7 3.4 28.	X57522_at_	X57522	tap1	TAP1 Transporter 1, ABC (ATP binding cassette)	34.3	42 3	0 0 0	1 27	5		;		
AB000115 unknown mRNA SIGNAL TRANSDUCER AND ACTIVATOR OF 13.1 24.9 8.4 26.9 28.7 3.4 M97935 stat1 TRANSCRIPTION 1.ALPHA/BETA 4.1 7.9 10.5 2.5 5.3 12.2 9.8 J04164 iii17 RPS3 Ribosomal protein S3 /wrong name 25.8 57.2 37.7 34.5 45.6 79.3 11.5	UU3891_at		unknown	Phorbolin I mRNA, partial cds	43.8	2000	210	1001	23.3	4/./	9.11	31.7	41.3
AB000115 unknown mRNA SIGNAL TRANSDUCER AND ACTIVATOR OF 4.1 7.9 10.5 2.5 5.3 12.2 9.8 13.1 24.9 8.4 26.9 28.7 3.4	AB000115_at				2	20.3	41.3	109.3	28.3	23.3	4.4	9.6	39.3
M97935 stat1 TRANSCRIPTION 1-ALPHA/BETA 4.1 7.9 10.5 2.5 5.3 12.2 9.8 J04164 iff17 RPS3 Ribosomal protein S3 /wrong name 25.8 57.2 37.7 34.5 45.6 79.3 11.5	-	AB000115	unknown	mRNA	σ	13.1	24 0	α	0 00	1	,	,	
105 301 16.5 2.5 5.3 12.2 9.8 105 10.5 2.5 5.3 12.2 9.8 105 10.5 2.5 10.5 2.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10	M9/935_s_at	M97935	1+0+0	SIGNAL TRANSDUCER AND ACTIVATOR OF				T O	20.3	7.07	4.5	-i	3/.6
11.5 37.7 34.5 45.6 79.3 11.5		104164	statt ifi17	PRS3 PIROS 1.4LPHA/BETA	4.1	7.9	10.5	2.5	5.3	12.2	8.6	17.2	36.7
			, , , , , ,	In 33 ribosoffial protein 53 /wrong name	25.8	57.2	37.7	34.5	45.6	79.3	11.5	603	35.1

· P.CEP	onse of Denamine Cens to u
Inventors:	Nir Hacohen, et al.

							11	nv	ento	ors:			Nır I	laco	hen	, €	t a	1.									
	34.3	33.8	33.4	22.4	30.4		31.9	30.8	5	30.7	2000	787	28.5	0 7 0	07/7	24.6	24.1	23.9		23.5	23.2		22.8	226	217	217	20.9
	208.8	10.0	10.8	Ľ	5 00		23.6	13.5	,	1 0	6.4	120	04	C	7	19.3	4.4	12.3		19.1	11.5		14.6	4 7	122	26	2.5
1000	302.1	5.0		,	273	2	6.1	5.1	5	2.4.3	0	٣	48,3	0 7		14.1	2.2	2.7		7.5	6		4.6	ſ.	11.5	6 7	5.2
	1001	7.8	65.8	206	112		6.3	15.1	-	7 7	9.7	3.4	11.4	0 4		4.6	12.4	24.4		6.1	15	1	7.5	12		86	
2	200	6.7	122.8	3124	3.5		9.6	13.3	7	17	2.3	α [~	7.7	0		16.8	5.9	10.5		3.5	13.7		3.2	10.1	6.1	3.1	27.2
, c	200	333	40.2	901	5.6		12.9	16.9	0	250	4.1	20.5	13.4	=	1	22.8	13.5	10.4		11.4	27.5		9.9	2.9	4.1	2.4	21
[15.0	85.6	83.4	27.0	212		32.4	33.6	306	48.8	26.4	104 2	16.9	120		47.2	26.2	16.1		47.1	55.8	1	644.5	19.1	11.4	7.4	807.3
7 24 2	25.0	64.4	154	25	19.5		20.6	17.9	10,0	31.1	10.1	39.7	11.4	0		233.7	15.2	9		16.1	36.8		130.6	13.4	9.7	29.6	88.9
1,4,1	4 5	46.3	53.2	σ .c.			30.6	23.1	127	43.8	5.8	29.6	7.4	LC.		166.9	24.7	5.2		30.7	61.7		43.0	3.6	3.8	5.6	82.7
G1P2 Interferon, alpha-inducible protein (clone	RGS1 Regulator of G-protein signalling 1	BF B-factor, properdin	Histone H2A.2 mRNA	ISG-54K gene (interferon stimulated gene) encoding a 54 kDA protein, exon 2	Mac-2 binding protein mRNA	iš -	CM. 1 APZ, LMPZ, LMP7 and DOB	CW.I MKINA	PROBABLE G PROTEIN.COUPLED RECEPTOR LCR1 HOMOLOG	Ninjurin1 mRNA	P63 mRNA for transmembrane protein	B94 PROTEIN	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	BONE MARROW STROMAL ANTIGEN 2 (BST.2)		Activin beta-A subunit (exon 2)	FACL1 Long chain fatty acid acyl coA ligase	Hou mRNA	INTERFERON INDUCED GUANYLATE-BINDING	PROTEIN Z	IL7R Interleukin 7 receptor	Melanoma growth ctimital	Melanolina growni sunnualory activity (MGSA)	Putative copper uptake protein (hCTR2) mRNA	Nuclear phosphoprotein mRNA	Dual specific protein phosphatase mRNA	PTX3 Pentaxin-related gene, rapidly induced by IL·1 beta
iso15	ier1	bf	h2a	g10p2	mac2bp	(404	Tap2	terer	cxcr4	ninj1	p63	tnfaip2	stat1	bst2		activinba	fac12	nmi	000	2100	il7r	aro1	1019	copt2	unknown	dusp4	ptx3
M13755	S59049	L15702	L19779	M14660	L13210	Y66401	700401	Пэперэ	L06797		01669X	M92357	M97936	D28137	1 1		D10040	U32849	MEGEAS	04000M	M29696	X54489	100	U83461	L22342	U48807	M31166
M13755 at	S59049_at	L15702_at_	L19779_at_	M14660_at_	L13210_at_	X66401_cds1	-d1-	Donoo3_at_	L06797 s at		X69910_at_	M92357_at_	M97936_at_	D28137_at	1 1	ᅫ	D10040_at_	U32849_at_	MERENO	WOOD#5 46	M29696_atx54489_rna1	24 - CO	-10-	_at_	L22342_at_	U48807_at_	M31166_at_

J05582 muc1 L41690 tradd X59892 wars L07633 pa28a L07633 pa28a X16396 MTHFD2 Z35278 admR D26579 adam8 U50648 pkr D42043 KIAA0084 M72885 GOS2 AF005775 flip CAR2200 starf50 M87434 oas2 U67963 huk5 U67963 huk6 M55067 ncf1 M55807 nk4 M55807 nk4 M55807 nk4 D14874 adm NA59807 nk4 D14874 adm NA59807 ninor	000					_	_	-	_				
Fig. 200 Tradd Tractor Tract	J05582_s_at_	J05582	muc1	MUC1 Mucin 1, transmembrane	3.6	מ	16.9	2	α				C
Victoria Properties Victoria Victori	L41690_at_	L41690	tradd	TNF receptor 1 associated protein (TRADD) mRNA, 3' end of cds	C	1 2	-	2 0					20.5
National	X59892_at	X59892	wars	TRYPTOPHANYL-TRNA SYNTHETASE	0.0	10.7	19.3	77.0	3.5	5.5	4.6	6.8	20.2
MTHFD	L07633_at	L07633	pa28a	INTERFERON GAMMA UP. REGULATED 1-5111	7.01	00.0	32.3	7.00	28.5	25.2	12.8	18	20.2
Mathematical Control					5.1	8.1	13.1	2			2.3	4.3	20.1
235278 amile PEBPZaci acute myeloid leukaemia mRNA 1.2 5.5 6.5 2.5 2.5 2.5 2.5 2.5 3.2 0.9 2.5 3.2 D26579 adam8 Transmembrane protein 5.5 6.5 3.5 1.5 2.2 0.9 2.5 3.2 U50648 pkr kinase (Pkr) gene kinase (Pkr) gene partial cds 24.8 14.1 27.1 7.1 3.1 4.5 8.8 J04080 c1s kinase (Pkr) gene partial cds 24.2 12.6 6.1.6 5.6 8.9 31.4 3.7 6.4 1 M72885 G0S2 gene extracted from Human GOS2 gene, 5 126.1 38 44.9 10.8 6.2 5.3 10.4 11.3 1 M72885 GOS2 flink and cds flink and cds 4.2 126.1 38 4.4 10.8 6.2 5.3 10.4 11.3 1 M82200 start50 Start50 mRNa Glary mRNa, a	X16396_at_	X16396	MTHFD2	MTHFD NAD-dependent methylene tetrahydrofolate depydrogenase anglebydrofol	1	1	i	<u>-</u>				<u> </u>	
D26579 adams Transmembrane protein D26579 adams Transmembrane protein D26579 adams Interferon-inducible RNA-dependent protein D42043 LACOBA Gene, partial cds D42043 LACOBA Gene, partial cds D42043 LACOBA Gene, partial cds D42040 LACOBA Gene, partial cds D40080 LACOBA Gene, partia	235278_at_	235278	am12	PEBP2aC1 acute myeloid leukaemia mRNA	2.7	5.5	15.2	2.5	2.2	6.0	2.5	3.2	19.8
USOG48 pkr National Color Interferon-inducible RNA-dependent protein USOG48 pkr Naturase (Pkr) gene C1S Complement component C1S Complement C1S Comp	726579_at_	D26579	adam8	Transmembrane protein	7 4	100	7.77	15.0	3.3	23.4	7.6	4.2	19.6
UBOG648	J50648_s_at			Interferon inducible RNA-dependent protein		0	0	6.3	7	4.2	2.1	2.6	19.3
Classification Clas	A2043 at	U50648	pkr	kinase (Pkr) gene	19.8	28.4	22.3	17.8		22.1	40 1	24.8	10
104080 C1S Customponent 1, s C1S Component 1, s C1S Component 1, s C1S Component 1, s C1S Component 2, subcomponent 2, subcomponent 3, subcompon	75-010	2127	4	NIAAUU84 gene, partial cds	24.8	14.1	27.1	7.1	3.1	4.5	83	8 6	10
M22885 GOS2 gene extracted from Human GOS2 gene, 5° 126.1 38 44.9 10.8 6.2 5.3 10.4 11.3 AF005775 flip (clarp) mRNA, alternatively spliced staffo staffo staffo staffo staffo mRNA M87434 0as2 GSFI G.rich RNA sequence binding factor 1 0.5 4.4 5.2 1.5 4.5 3.1 5.3 4.5 3.1 M57607 M87434 0as2 GSFI G.rich RNA sequence binding factor 1 0.5 4.4 5.2 1.5 3.1 5.3 4.5 3.1 M57607 ncf1 GRSFI G.rich RNA sequence binding factor 1 0.5 4.4 5.2 1.7 0.5 5.1 5.3 4.5 M55067 ncf1 disease protein CDS8 antigen (GD28 antigen igand 2, B7. 1.6 2.1 2.1 2.1 2.1 2.1 2.1 2.1 2.1 M5907 nk4 PRECURSOR M40renomedullin 18 20.1 46.2 3.4 4.5 10.4 2.5 5.2 M10gen induced nuclear orphan receptor M12767 minor (MINOR) mRNA M1020	04080_at_	-	c1s	cus complement component 1, s subcomponent		- 0			1 6				
National States Continued and cds Caspase-like apoptosis regulatory protein 2 Caspase-like apoptosis regulatory protein 3 Caspase-like apoptosis regulatory apoptosis regulatory appropriate apoptosis regulatory appropriate apoptosis regulatory appropriate apoptosis regulatory appropriate apoptosis regulatory receptor Caspase-like apoptosis regulatory receptor Caspase-like apoptosis regulatory regulatory Caspase-like apoptosis regul	472885_rna1		0000			15.0			20,			6.4	18.9
AF005775 flip (clarp) mRNA, alternatively spliced x82200 starf50 starf50 mRNA alternatively spliced 5.82200 starf50 starf50 mRNA, alternatively spliced 5.82200 starf50 mRNA sequence binding factor 1 0.5 4.4 5.2 1.7 0.5 5.1 5.3 4.5 0.07231 GRSFI G-rich RNA sequence binding factor 1 0.5 4.4 5.2 1.7 0.5 5.1 5.3 4.5 0.05201 mk5 blosphospholipase homolog (HU-K5) mRNA 2.5 1.2 6.2 1.7 0.5 5.1 5.3 4.5 0.004343 cd86 2 artigen) M55067 ncf1 disease protein CD28 antigen ligand 2, B7. 1.6 8.1 6 1.7 2. 2.9 9.7 4.6 0.004343 cd86 2 artigen) M65807 nk4 PRECURSOR M65807 nk4 ADM Adrenomedullin 18 20.1 46.2 3.4 4.5 10.4 2.5 5.2 0.1 3.1 minor (MINOR) mRNA 13.7 24.6 17.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1	S_at_	_	G0S2	flank and cds	126.1	3	44 9	α ()	, u			;	(
X82200 Lysophospholipase homolog (HU-K5) mRNA 11.8 8.6 21.2 15.4 16.7 2.1 3.1 M87434 oas2 69/ATRONA sequence binding factor 1 10.5 4.4 5.2 15.4 16.7 2.1 3.1 M87434 oas2 69/ATRONA 11.8 8.6 21.2 15.4 16.7 2.1 3.1 U07231 GRSF1 G-rich RNA sequence binding factor 1 0.5 4.4 5.2 1.7 0.5 5.3 4.5 U67963 huk5 Lysophospholipase homolog (HU-K5) mRNA 2.5 1.6 0.2 8.1 6.5 1.7 0.5 5.1 5.3 4.5 M55067 ncf1 disease protein 2.5 12.6 24.2 19.1 28.5 22.1 4.4 9.8 M55067 ncf1 disease protein CD86 CD86 antigen (CD28 antigen ligand 2, B7. 1.6 24.2 19.1 28.5 22.1 4.4 9.8 M59807 nk4 PRECURSOR ADM Adrenomedullin	NFUU5//5_at		ej.	poptosis regulatory protein		3		0.01	9.6		10.4	11.3	18.7
M87434 oas2 69/13 minor 1007231 1.8 8.6 21.2 15.4 33.1 16.5 2.5 5.3 4.5 5.2 6 3.1 4.4 5.2 5.2 5.2 1.4 4.6 5.2 1.4 4.6 5.2 1.4 4.6 5.2<	(82200 at	X82200	staf50	Chalp) IIIRIVA, alternatively spliced	7.8	18.5	37.9	0.7	5.9	5.4	m	7.6	18.4
U07231 GRSF1 Crich RNA sequence binding factor 1 0.5 4.4 5.2 15.4 33.1 16.5 2.5 5.3 4.5 U67963 huk5 Lysophospholipase homolog (HU-K5) mRNA 2 3.7 16.6 0 2.8 2.6 5.1 4.5 4.4 5.2 4.5 4.5 4.5 4.5 4.5 4.5 4.5 4.4 5.2 4.4 5.2 4.4 5.2 4.5 4.4 5.2 4.4 5.2 4.4 5.8 4.5 4.5 4.4 5.2 4.6 4.4 5.2 4.4 4.6 4.8 4.6 4.8 4.6 4.8 4.8 4.6 4.8 4.8 4.8 4.8 4.8 4.8 4.8 4.8	187434 at	M87434	oas2	69/71 KD	2	7	13.1	7.8	15.4	16.7	2.1	3.1	18.1
M55067 huk5 Lysophospholipase homolog (HU-K5) mRNA 2 3.7 16.6 0 2.8 2.6 6 3.1	107231_at	U07231		GRSF1 Grich BNA cogniscon Einding	11.8	8.6	21.2	15.4	33.1	16.5	2.5	5.3	17.5
M55067 ncf1 disease protein CD28 antigen (CD28 antigen ligand 2, B7. 1.6 0 2.8 2.6 6 3.1 M04343 cd86 2 antigen) 2 antigen 1.6 8.1 6 1.7 2 2.9 9.7 4.6 M59807 nk4 PRECURSOR ADM Adrenomedullin 18 20.5 2.5 10.6 11.1 4.6 1.6 4.8 Mitogen induced nuclear orphan receptor Mitogen induced nuclear orphan receptor 49.2 39.4 17.1 37.8 19.7 17.3 24.6 17.3	167963_at	U67963	huk5	Vsophospholipase homolog (HT) VS		4.4	5.2	1.7	0.5	5.1	5.3	4.5	17.5
M55067 ncf1 disease protein CD86 CD86 antigen (CD28 antigen ligand 2, B7 1.6 24.2 19.1 28.5 22.1 4.4 9.8				NCF1 47 kD autosomal chronic granulomatous	2	3.7	16.6	0	2.8	2.6	9	3.1	17.3
CD86 CD86 antigen (CD28 antigen ligand 2, B7. 15.1 25.2 22.1 4.4 9.8 (AFC) (MATURAL KILLER CELLS PROTEIN 4 (AFC) 20.5 2.5 10.6 11.1 4.6 11.4 2.6 4.8 (AFC) (MINOR) mRNA (MINOR	155067_at_	M55067	ncf1	disease protein		126	0 70	101	000	,	_		
M59807 nk4 PRECURSOR NATURAL KILLER CELLS PROTEIN 4 20.5 2.5 10.6 11.1 4.6 11.4 2.6 4.8	104343 at	1104343	80	6 antigen (CD28 antigen ligand 2,			7.2	1.2.1	60.0	77.77	4.4		17.2
M59807 nk4 PRECURSOR D14874 adm ADM Adrenomedullin 18 20.5 2.5 10.6 11.1 4.6 11.4 2.6 4.8 Mitogen induced nuclear orphan receptor (MINOR) mRNA 49.2 39.4 17.1 37.8 19.7 13.7 24.6 17.3		2	0000	0 1 10 0 1 1	1.6	8.1	9	1.7	7		9.7	4 6	16.0
D14874 adm ADM Adrenomedullin 20.3 20.3 10.5 11.1 4.6 11.4 2.6 4.8	159807_at_	M59807	nk4	LER CELLS PROTEIN	300			:					
WilnoR) minor (MINOR) mRNA (49.2 39.4 17.1 37.8 19.7 13.7 24.6 17.3 15	14874_at_	D14874	adm	ADM Adrenomedullin	20.2	2001	0 0	7-1-1	4.0	11.4	2.6	4.8	16.3
- 1012/0/	12767 at	7926111	300	Mitogen induced nuclear orphan receptor	2	20.1	7.04	3.4	t.5	10.4	2.5		16.1
	15/0/ al	101710	ITITIO	(MINOK) MKNA	49.2	39.4	17.1	37.8	19.7	13.7	24.6	17.3	15.7

Macmorche
MacHialchs
Metallothionein
MHC-encoded proteasome subunit gene LAMP7. E1 gene (proteasome subunit LMP7) extracted from H.sapiens gene for major histocompatibility
Transcription factor mRNA
Thyroid receptor interactor (TRIP10) mRNA, 3' end of cds.
Protein tyrosine phosphatase mBNA
Mch3 isoform alpha (Mch3) mRNA
Inhibitor of apoptosis protein 1 mRNA
GI VOVI DEDTINE N
TETRADECANOYLTRANSFERASE
SCYA4 Small inducible cytokine A4 (homologous to mouse Mip-1b)
KIAA0160 gene, partial cds
Syntaxin mRNA
extracted from Human 2,3-cyclic-nucleotide 3:-
PLATELET GLYCOPROTEIN IB ALPHA CHAIN
PRECURSOR
PML Probable transcription factor PML (alternative products)
(
CBB Carbonyl roductors
BZin profein B.ATF mBNA
עם יייסיס יש שיים יי

Figure 3E

					и
I	nvors:	Nir	Hacohen,	et al.	

Mail	HG1102. HT1102_at	HG1102- HT1102	ras-related	Ras-Related C3 Botulinum Toxin Substrate	1.9	3.7	13.4	1.8	1.2	4.1	4	2.1	10
NOO324 IR INTERLEUKIN 8 PRECURSOR S91 234.5 40.9 9.8 131 8.4 8.2 1.9	062002_81	022002	IXIA	INUCIEAR Orphan receptor LXR-alpha mRNA	1.5	7.3	9.6	34.8	11.4	9.4		3.1	10.9
AF000234 P2x4 P2x purinoceptor mRNA 2.5 32.4 8.5 1.9 2 1.5 6 M81750 mnda antigen an	Y00787_s_at_	Y00787	8 <u>!</u>	INTERLEUKIN-8 PRECURSOR	89.1	234 5	40.9	σ	12.1	0	0	9	
MABLY MADA Myeloid cell nuclear differentiation 0 2.2 0.4 3.7 7.4 7.8 1.7 H72324	AF000234_at	AF000234	Dy.Cu	AINO - Actoriogistic VCO			2)		j.	0.6	10.0	10.5
HG2339		10700 11	777	MANDA Macing and	2.5	32.4	8.5	1.9	2	1	5.6	4.5	10.4
HG2239	M81750_at_	M81750	mnda	minum injeroid cell nuclear differentiation antigen		0	7	r c	,	r			
Februaries Chemokine receptor X (CKRX) mRNA 3.6 9.2 36.3 3.7 5.3 6.6 5.1	HG2239. HT2324 at	HG2239- HT2324		Potaccium Channel Destain / Ch. 211 FOF		7.7	0	o o	4.	χ.		2.4	10.4
AF014958 ccr6 Chemokine receptor X (CKRX) mRNA 3.6 9.2 36.3 3.7 5.3 6.5 5.1 V05721 kynu L-kynucenine hydrolase mRNA 25.2 32.5 20.4 5.9 6.7 1 3.5 1 X70340 tgfa TGFA Transforming growth factor, alpha 2 7.3 1.1 0 0 3.3 1 3.6 9.5 20.4 5.9 6.7 1 3.5 1 1 0 0 0 3.3 1 1 0 0 0 3.3 1 1 0 0 0 3.3 1 1 0 0 0 3.3 1 1 0 0 0 3.3 1 1 4 9 2.0 4 4 6 4 4 6 4 4 6 4 4 6 4 4 6 4 4 6 4 4 6 4 <td< td=""><td>AF014958_at</td><td></td><td></td><td>Cacation Channel Florent (GD:11363)</td><td>20,0</td><td>2</td><td>1.2</td><td>0.7</td><td>0.3</td><td>0</td><td>1.7</td><td>2.6</td><td>10.1</td></td<>	AF014958_at			Cacation Channel Florent (GD:11363)	20,0	2	1.2	0.7	0.3	0	1.7	2.6	10.1
1.		AF014958	ccr6	Chemokine receptor X (CKRX) mRNA	3	0 0	36	4	ų	9 9	u	,	
Topic Topic Topic Topic Transcriptional Coactivator Protein Topic Topic Transcriptional Coactivator Protein Topic Topic	U57721_at_	U57721	kynu	L-kynurenine hydrolase mRNA	25.2	32.5	2000	2 4	ı	0 -	1.0	4.	10
Material BTG1 B-cell translocation gene 1, anti-	X70340_at	X70340	tgfa	TGFA Transforming growth factor, alpha	1	7.3	111	ה	o	70	3.5	1	200
Mc6899 ews EWISH Flating sarcoma breakpoint region 1 4.9 2.9 7.5 7.3 1.3 4.2 2.3	X61123 at	x61123	htg1	BTG1 B cell translocation gene 1, anti-							0.0	4.4	χ.
Professional Region of Earth Fagure 1	X66899 at	66899X	ews	FWSR1 Fwing sarroms broakmat to a 1	30.4	26.8	14.4	8.4	4.6	4.4	3.6	7.4	9.7
Froteasome-like subunit MECL.1 gene extracted strong through the contracted subunit (MECL.1) chymotrypsin-like protease (CTRL.1) and protein serine kinase (PSK.H1) last a 20 TNFAIP1 Tumor necrosis factor alpha inducible a 2.6 4.4 3.1 1.1 0 1.2				Designation of the second of t	y.9	2.9	7.5	7.3	1.3	4.2	2.3	4.4	9.7
X71874 Imp10 (CTRL-1) and protein serine kinase (PSK-H1) last exon 3.4 5.6 4.4 3.1 1.1 0 12 M59465 a20 TNFAIP1 Tumor necrosis factor alpha inducible 87 158.7 41.1 65.3 73.5 22.9 7.6 HG4297. TCPC4 Transcriptional Coactivator Pc4 2.6 2.7 4.8 6.4 4.5 6.3 2.5 V00594 mt2a Metallothionein isoform 2 167.1 337.3 15 64.9 122.8 34.8 69.4 M24283 icam1 human rhinovirus receptor 70.6 32.4 20.7 28 11.1 3.4 9.5 HG4069- Monocyte Chemotactic Protein I 2.5 2.5 2.8 38.4 16.9 10.3 2.5 L69546 RNA binding protein Etr-3 mRNA 2.5 7.1 6.4 3.1 2.1 2.1 2.1 2.1 2.1 2.1 2.1 2.1 2.1 2.1 2.1 2.1 2.1 2.1 <td></td> <td></td> <td></td> <td>Proteasome-like subunit MECL-1 gene extracted from H.sapiens genes for proteasome-like subunit (MECL-1), chymotrybsin-like profease</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>				Proteasome-like subunit MECL-1 gene extracted from H.sapiens genes for proteasome-like subunit (MECL-1), chymotrybsin-like profease									
M59465 a20 TNFAIP1 Tumor necrosis factor alpha inducible 3.4 5.6 4.4 3.1 1.1 0 12 M59465 a20 Protein A20 Transcriptional Coactivator Pc4 2.6 2.7 4.8 6.4 4.5 6.3 2.5 HT4567 TCPC4 Transcriptional Coactivator Pc4 2.6 2.7 4.8 6.4 4.5 6.3 2.5 V00594 mt2a Metallothionein isoform 2 167.1 337.3 15 64.9 122.8 34.8 69.4 M24283 icam1 human rhinovirus receptor 70.6 32.4 20.7 28 11.1 3.4 9.5 HG4069- HT4339 mcp1 Monocyte Chemotactic Protein I 2.5 2.1 6.4 3.1 5.1	X71874_cds1			(CTRL-1) and protein serine kinase (PSK-H1) last									
TNFAIP1 Tumor necrosis factor alpha inducible 87 158.7 41.1 65.3 73.5 22.9 7.6 HG4297.	_ar_	X/18/4	lmp10	exon	3.4	5.6	4.4	رب د			12	2	0
HG4297. Transcriptional Coactivator Pc4 2.6 2.7 4.8 6.4 4.5 6.3 2.9 7.6 HT4567 TCPC4 Transcriptional Coactivator Pc4 2.6 2.7 4.8 6.4 4.5 6.3 2.5 V00594 mt2a Metallothionein isoform 2 167.1 337.3 15 64.9 122.8 34.8 69.4 M24283 icam1 human rhinovirus receptor 70.6 32.4 20.7 28 11.1 3.4 9.5 H74339 mcp1 Monocyte Chemotactic Protein 1 2.9 2.5 2.8 38.4 16.9 10.3 2 U69546 RNA binding protein Etr-3 mRNA 2.5 7.1 6.4 3.1 6.1 3.1 2.1	M59465_at_	M59465	a20	TNFAIP1 Tumor necrosis factor alpha inducible protein A20	10	1507	;	(5 8	71	7	9.
HT4567 TCPC4 Transcriptional Coactivator Pc4 2.6 2.7 4.8 6.4 4.5 6.3 2.5 CV00594 mt2a Metallothionein isoform 2 167.1 337.3 15 64.9 122.8 34.8 69.4 CAM1 Intercellular adhesion molecule 1 (CD54), Post 10.0 10.3 10.3 10.3 10.3 10.3 10.3 10.3	HG4297-	HG4297.			ò	138./	41.1	65.3	/3.5	22.9	7.6	5.9	9.6
V00594 mt2a Metallothionein isoform 2 167.1 337.3 15 64.9 122.8 34.8 69.4 M24283 icam1 human rhinovirus receptor 70.6 32.4 20.7 28 11.1 3.4 9.5 HG4069- Monocyte Chemotactic Protein I 2.9 2.5 2.8 38.4 16.9 10.3 2 H69546 RNA binding protein Etr-3 mRNA 2.5 7.1 6.4 3.1 2.1	HT4567_at_	HT4567	TCPC4	Transcriptional Coactivator Pc4	2.6	2.7	4.8	6.4		7	0	~	C
M24283 icam1 human rhinovirus receptor	V00594_s_at_	V00594	mt2a	Metallothionein isoform 2	167.1	237.2	1	3	2	3			
HG4069- HT4339 mcp1 Monocyte Chemotactic Protein 1 2.9 2.5 2.8 38.4 16.9 10.3 2 16.9 10.3 2 2 2 2 2 3 3 3 4 16.9 10.3 2 2 2 2 3 3 4 16.9 10.3 2 2 2 3 3 4 16.9 10.3 2 3 3 4 16.9 10.3 2 3 3 4 16.9 10.3 2 3 3 4 16.9 10.3 2 3 3 4 16.9 10.3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	M24283_at_	M24283	icam1	ICAM1 Intercellular adhesion molecule 1 (CD54), human rhinovirus recentor	9			5	166.0	χ. Σ	4.60	27.7	9.4
HG4069- HT4339 mcp1 Monocyte Chemotactic Protein I 2.9 2.5 2.8 38.4 16.9 10.3 2 U69546 RNA binding protein Etr.3 mRNA 2.5 71 6.4 3.1 2.1 5.1 2.1	HG4069.			000000	2	32.4	7.07	87	11.1	3.4	9.5	9	9.3
U69546 RNA binding protein Etr.3 mRNA 2.55 7.1 6.4 3.1 2.1 2.1 2.1	HT4339_s_at	нG4069. НT4339	mcp1	Monocyte Chemotactic Protein 1	0	7	α	38	9	10.3		,	(
	U69546_at	U69546		RNA binding protein Etr-3 mRNA	2.5	7 1	6.4	7	2 -	7	2 1	7.0.7	200

7.4 0.0 0.9 0.6 0.2.6 1 8.
7 10.9 20.7 9.
10.5 6.2 1.7 5.4
3 2.1 0.5
10.9 2.4 1.8 0
4.2
25.2 8 12.7 6
9.6 19.9 4.9 5.9
4 1.1 0.6 1.3
40.6 0 1.4 6.5
2 2.2 0.9 0.3
7 0 0 7 8
1.1 2.3 0
2
30.
6.3 13.7 7.8 50.6
2.8 0.5
1.3
2 6.7 8.1 4.1

	esponse of Dendritie (clis to	
Invemor	s: Nir Hacohen, et al.	

Z11697_at_	Z11697	cd83	CD83 ANTIGEN PRECURSOR	18.7	12.6	9.8	19.6	9.5	9	4.1	10.4	7.2
M16038_at_	M16038	lyn	LYN V.yes.1 Yamaguchi sarcoma viral related oncogene homolog	6.2	5.6	0	11 6	6 7		-	7 4	7 1
			Myleoid differentiation primary response protein									
U70451_at_	U70451	myd88	MyD88 mRNA	2.2	7	2.8	6.3	17.2	7.1	1.6	2.4	7.1
Y08682_rna1												
_s_at	Y08682	cpt1b	Carnitine palmitoyltransferase I type I	0.3	1.8	6.0	9.9	m	6.1	80	4.5	7.1
HG544.	HG544-											
HT544_at_	HT544	ecgf	Endothelial Cell Growth Factor 1	5.9	15.3	4.8	10.4	5.2	2.1	26.7	16.5	7
			ANPEP Alanyl (membrane) aminopeptidase									T
			(aminopeptidase N, aminopeptidase M,								_	
M22324_at_	M22324	anpep	microsomal aminopeptidase, CD13)	5.4	10.4	7.5	1.9	1 9	C	22	۲.	7
U43185_s_at			STAT5A Signal transducer and activator of									T
	U43185	stat5a	transcription 5A	7.6	8.5	14.5	1.2	0.8	1.1	15.9	10.5	7
			Protein tyrosine phosphatase PTPCAAX1									
U48296_at	U48296	ptp4a1	(hPTPCAAX1) mRNA	2.4	3.7	14	2.8	3.2	14.7	7	2.3	6.9
D43949_at_	D43949		KIAA0082 gene, partial cds	2.7	6.7	5.6	0.3	0.7	2.6	6.5	٣	89
			PML Probable transcription factor PML						r			
M79462_at_	M79462	myl	{alternative products}	3.1	8.9	6.2	2.7	6.7	6.2	κ. κ.	8	89
U28014_at_	U28014	casp4	ICH.2 PROTEASE PRECURSOR	13.5	4.4	9	9.5	1.5	3.2	7.2	7.2	8 9
			PML Probable transcription factor PML								İ	
X63131_s_at_X63131	X63131	myl	{alternative products}	9.9	4.7	4	4	0.5	5.8	4.3	10.3	89
M23178_s_at			MACROPHAGE INFLAMMATORY PROTEIN 1.									
П	M23178	mip1a	ALPHA PRECURSOR	73.8	125	11.4	52.8	73.8	8.5	7.4	9.6	6.3
M37435_at_	M37435	mcsf	CSF1 Colony-stimulating factor 1 (M-CSF)	7	12.8	9	37.5	12.1	4.0	4.1	9.6	6.3
HG2917.	HG2917.		Major Histocompatibility Complex									
HT3061_f_at_ HT3061	HT3061	hla	(Gb:M21533)	5 7	7 6	0	ц	u C		,	c	ú
			Modulator recognition factor I (MRF 1) mRNA, 3		?	1	?		7	5.7	0.0	7.0
٦	M62324	mrf.1	end	4.8	8.6	10.2	7.9	6.1	14.3	1.8	3.4	6.2
- 1	070660	atox1	Copper transport protein HAH1 (HAH1) mRNA	3.8	8.1	6.0	1.8	2.2	4.0	13.5	6.1	6.2
U76189_at_	076189	ext12	EXTL2 (EXTL2) mRNA, partial cds	0.7	7.3	13.5	1.7	0.2	0.1	4.4	5.3	6.1
D79206 s at D79206	079206	sdc4	SDC4 Syndecan 4 (amphiplycan ryndoran)	7	σ	21 1	17.0	1.1	1.0	7 0	,	٥
				?	,	77.77	10.1	7.1.	+ O +	7.7	7.7	٥

Figure 3H

r.cep	onse of Dendrine Cens to a
Inventors:	Nir Hacohen et al

								lnv	. cr	ito	rs:			Νı	r ŀ	łac	col	1ei	1, 6	rt a	ıl.									
(υ υ		5.7		5.6		5.6	5.6	5.5	1			5.5	3		5.3	5.2		5.1	5.1		5.1	5		4	4.6	4.6	-	2 4	4 4
,	4.0	7	2.2		3.6		4.4	1.6	17.3	2.7			15.6	18		4.2	18		3.2	5.9		5.4	2.1		3.7	3.1	3.9	7	; -	9.9
,	4.		1.4		1.8		3.6	3.6	34.3	3.2			13.1	1.5		1.5	1		2.3	4.2		1.5	1.9		4.3	3.2		C		
9	12.1		7		2.8		1.7	2.7	5.7	5.8		_	13.7	0		7.8	8.3		2.9	9.5		2.8	0		4.7	27.1	0	7 %		0
-	7-1		7.7		4.2	Ī	0	10.7	8.2	3.2			97.1	1.5		7.1	9.3		1.9	15		4.2	1.4		9.5	20.6	6.0	1.5	000	
	8.8	, ,	7.7		5.8		0.4	13.9	17.1	1.2			70.6	1.8		3.7	5.5		4.7	10.6		1.6	2.9		14.8	16.7	2.9	171	3 6	
	0 4	2	1.0.1		80.		1.9	5.7	6.2	2			5.8	6.5		9.9	4.9		10.3	9.1		7.3	1.2		11	15.4	3.7	2 6		38.5
- 7	7 7 7	1	/:/		6.3		0	2.1	17.2	2.7			68.2	3.9	-	11.3	1.9	-	3.2	14.1		15	7.7		19.6	σ	3	3.1	10	39.6
7 7	13	1	0.0		6.1		0	9.7	13.1	0			115.3	2.8		2.4	1.1		4	9.5		1.6	2		23.9	4.4	4.1	6 1	90	43.5
SSB Sjogren syndrome antigen B (autoantigen	TRAF interacting protein I-TRAF mRNA	EIF5 Eukaryotic translation initiation factor 5	(circ)	Major Histocompatibility Complex, Class I, E	(Gb:M20022)	Receptor protein tyrosine kinase (HEK5) mRNA,	3' end	PLECKSTRIN	Proteasome activator hPA28 subunit beta	KIAA0239 gene, partial cds	6-16 gene (interferon-inducible peptide	precursor) extracted from Human interferon-	inducible peptide (6·16) gene	RagA protein	DNA-binding protein CPBP (CPBP) mRNA,	partial cds	14.3.3 PROTEIN TAU	MACS Myristoylated alanine-rich C-kinase	substrate	IL10R Interleukin 10 receptor	Variant urokinase plasminogen activator	receptor (uPAR2) mRNA, partial cds	PMP22 Peripheral myelin protein 22	MAJOR HISTOCOMPATIBILITY COMPLEX	ENHANCER-BINDING PROTEIN MAD3	X BOX BINDING PROTEIN: 1	Glutathione S-transferase homolog mRNA	Galectin	Proteasome subunit z	Poliovrus Receptor
ç	itraf	ję Ł	2		hla		drt	plek	pa28b				g1p3			bcd1	tan		macs	il10ra		plaur			ikba	xbp1		gals9		cd155
X14684	U59863	927671	00000	HG2915.	HT3059					087076			U22970	U41654		U44975	X56468		D10522	U00672		X74039	D11428		M69043	M31627	U90313	249107	D38048	НG3415. HT3598
X14684 s at X14684	U59863_at	1149436 at	- D- C-		HT3059_f_at_		at		D45248_at_	D87076_at_		U22970_rna1	_s_at_	U41654_at			X56468_at_		D10522_at_	U00672_at		X74039_at_	D11428_at_		M69043_at_	M31627_at_	U90313_at	Z49107_s_at_	D38048_at_	HG3415. HT3598_at_

recp	onse of Dendritie Cens to a
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								Inver	itors:		Nı	r Hac	ohen,	e	t al.							
4.5	4 4	4	43	4.2	4	5.	4	9	ď	88	38	3.7		3.7	3.6	3.6	3.6	7	, c	3.5	6 6	3. 4.
3.1	1	2.2	22	1.7	2 1	3.3	7 7	2.6	3.7	3.1	3.8	11.2		3.5	3.5	3.1	2.4	0	; m	14.8	, ,	5.4
2.9		200	2.5	2.9	1.9	6.2	4.3	1.6	27					3	4.1	9.5	5.9		4	3.4		18.3
4.5		1.5	0	5.2	5.1	3.1	4	 0.3	c	6.	0	9		2.4	0.5	3.3	5.3			0	0 4	
0.3	3.2	0	1.9	9.5	1.5	0	14.4	1.8		0.5	1.4	4.3		10.7	0.3	m	6.0		4	0		0.1
2.4		0.8	-	8.2	0.3	0	28.7	1.3	3.3	3.9	0	10.5		12.5	0.2	2.1	3.1	-4		0	7 7	
5.2	3.2	8:	10	4.2	6:1	4 3	6.9		6.0		6.2	m		14.5	3.3	0.2	3.7	0		0	7 4	0.1
2.1	m	0.3	8.1	2.4	2.8	1.5	26.4	1.2	3.1	2.4	11.8	4.5		26.9	5.6	3.7	1.3	1	4.4	0	r.	
0.8		0.4	7.9	2.8	0.1	03	65.5	0	8.4	14.6	2.9	6.1	ı,	-	0.5	0.7	1.6	80	8.3	0	22	0.9
LOT1 mRNA	Globin gene	CD19 CD19 antigen	EX:1	PROTEASOME COMPONENT C8	KIAA0151 gene	Fork head domain protein (FKHR) mRNA, 3' end	IL1RN Interleukin 1 receptor antagonist	METALLOPROTEINASE INHIBITOR 3 PRECURSOR	Novel glucocorticoid receptor associated protein	ID2 Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	ZNF151 Zinc finger protein 151 (pHZ-67)	GAPD Glyceraldehyde-3-phosphate dehydrogenase	Urokinase-type plasminogen activator receptor gene extracted from Human urokinase type	pidsiminogen receptor	IL3RA Interleukin 3 receptor, alpha (low affinity)	KIAA0226 gene	Phosphatase 2A mRNA, partial cds	Phosphotyrosine independent ligand p62 for the Lck SH2 domain mRNA	SERUM PROTEIN MSE55	Clones 23549 and 23762 mRNA	HLA-A MHC class I protein HLA-A (HLA-A28, B40, -Cw3)	MMP2 Matrix metalloproteinase 2 (gelatinase A; collagenase type IV)
ļ 		cd19	iex-1	psma3	IKKE	fkhr	illrn	timp3	bag1	id2b	znf151	psma4	<u> </u>	Diaur	il3ra			p62			hla·a	6dmm
U72621	M69023	M28170	581914	D00762	D63485	U36922	X53296	U14394	235491	M96843	U20647	D00763	1109937	100000	D49410	D86979	303802	U46751	M88338	80606N	D32129	105070
U72621_at_	M69023_at_	M28170_at_	S81914_at_	D00762_at	D63485_at_	U36922_at_	X53296_s_at_	U14394_at_	Z35491_at_	M96843_at_	U20647_at_	D00763_at_	U09937_rna1	-2-a!	!	D86979_at_	J03805_s_at_	U46751_at_	M88338_at_	U90908_at_	D32129_f_at_	J05070_at_

								In	vent	OI	s:	Nir l	Hac				t a	ıl.	ε ι	0.									
3.4	7	?	3.1	3.1	m		6.1	C	0.7	2.9	2.8	a c	2	2.8	2.7		2.7	2.6	2.6	Γ	2.5	2.5		2 4	2 0	100	200	3	2.3
1.6	2.3	î	3.9	2.6	4.1	-	1.6	9 4	-	1.4	1.6	, c	3	12.4	1.3		5.6	3.4	3.4	\mid	1,9	œ	+	ď		27	, 17	?	2.1
C1.	~		6.1	6.4	1.9		5.6	0		6./	4.2	2.7		21.8	2.3		4.9	2.3	2.7		1.8	38		0	32	200	4 6	?	2.7
3.7	3.4	5	2.8	5	0		0	4		4.4	7.8	c	;	4.3	7.		0.7	9.0	0.2			7.9		2.5	c	0	10		1.4
9.2	126		ci ci	5.7	0.4		=	1.7		14.	3.6			8.	S. S.		2.8	m	1.1	-	2.1	18.4	-	3.3	03	m C	000		0.8
o	α		4.5	11.4	1.3		σ: ∞	70.3		797	4.1	4 8		5.3	O	-	1.2	7.5	4.2		6.0	16.8		00	2.4	1	4 4		8.4
27.9	8			8.2	2.7		3.1	5.7		10.1	4.7	ب ب		5.2	<u>ن</u>	,	3.1	0.1	0		3.3	5.2		0	0	4	3.7		1.9
9.2	7.8		51	10.7	8.0		2.8	42.2	-	1//.0	2.5	6		8.4	7.7		84.9	2.9	1.3	-	3.6	39.5		6.0	1.2	-	2.1		0.7
3.3	3.7		2.5	29.4	1.4		11.4	<u>~</u>		36.1	7	66		12.7	0		14.6	1.8	0	_	2.1	22.4		9.0	3.3	6.0	4.1		38.2
Receptor 4.1BB ligand mRNA	76 kDa tyrosine phosphoprotein SLP.76 mRNA	VIVO (1017) (0)	IFL (IFL) MRINA	64:2 protein mikiya	GARS Glycyl-tRNA synthetase		Nuclear Factor Nf-116	SCYA4 Small inducible cytokine A4 (homologous to mouse Mip.1b)	DUAL SPECIFICITY PROTEIN PHOSPHATASE		Fas-binding protein (DAXX) mRNA, partial cds	U30999 Homo sapiens MV3 melanoma Homo sapiens cDNA clone memd, mRNA sequence	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F	KIAA0122 ggg gatist ad	MANALES Belle, partial cus	MMP12 Matrix metalloproteinase 12		26S PROTEASE REGULATORY SUBUNIT 4	FRG1 mRNA	Uridine diphosphoglucose pyrophosphorylase	mRNA	TXN Thioredoxin	PTPRC Protein tyrosine phosphatase, receptor	type, c polypeptide	Rit mRNA	KIAA0070 gene, partial cds	Homologue of yeast sec7 mRNA	ID2 Inhibitor of DNA binding 2, dominant	negative helix-loop-helix protein
41bbL	lcp2	<u></u>	2 7	2.40	gars		ntilb	mip1b	Cusin	adapa.	daxx	cd166	0 1	Illa-cual z		mmn12	""""p12	psmc1	frg1		ugp2	txn		cd45		kars	d17s811e		id2
965500	U20158	A FOOT 204	AF001234	002100	009587	HG3494.	H13588	J04130	111329	2222	AF006041	666080	200517	A17093	22000	1 23808	2000	LU2420	L76159		U27460	X77584		Y00062	Y07566	D31890	M85169		M97796
U03398_at_	U20158_at_	AF001294_at	103106 24	T	at		H13688_at_	J04130_s_at_	111329 at	7.0000	Ar000041_at	U30999_at_	1- 00000	T	1	123808 31	Ţ	1	L76159_at_			X77584_at_		-		D31890_at_	M85169_at	M97796_s_at	

Figure 3K

									ln	vei	ntors	:	N	ir Ha	co	hen,	et i	al.											
2.3	2.3	C1		ci ci	0		0	0		1 9	0		1 7	1 7	1 7		-	2			14		1.4	T	1.4		-		1.1
13.4	1.8	2.6		3.4	2.1		2.9	28		6.3	α		2		212		4	6.19			2.2		4.4		6.5	2.8	90		
32	1.5	1.7	-	2.3	1.9		7.3			1.4	C		27	80	33		4	4.1			3		2.5		2.6	2.2	1.5		
14.1	0	2.1		1.2	7.3		0	8		1.2	C		C	3.7	17		3.6	0			C		3.6	Ī	0	0	2.7		0.6
10.4	-	2.7		2.4	3.5		6.0	2.8		5.3	r.		1	9.9	1.2		2.3				0.7		3.3		m	0.5	0.4		1.1
4.1	2.6	2.3		5.6	9		0	3			7.		^	3.9	3.1		6.5				2.1		2.6		-	2.7	2.1		0.8
8.4	1.5	4.5		5.1	6.8		9.0	3.7		0.5	7 0		× 5	1.0	3.7		33	3.3			80		0.5		1.3	7	0.8		0.5
27.5	2.2	2.4		9.5	2.9	-	1.3	6.3		S	9		9.7	3.7	3.4		5.8	12.4	-			-	0.4		1.4	8.1	0.4	-	1.9
59.8	1.4	3.7		12	1.3		1.1	3.8		2.1	99		13.1	6.0	1.9		7	16.3			0.8				4.4	7.4	1.2	_	0.4
Actin bundling protein mRNA	ERK3 protein kinase mRNA	RPL3 Ribosomal protein L3	CDKN1A Cyclin-dependent kinase inhibitor 1A	(p21. Cip1)	Serine/threonine protein kinase		Ras-Like Protein Tc10	Nrf2		Osteopontin gene	mRNA fragment encoding beta-tubulin. (from clone D-beta-1)		Epican, Alt. Splice 1	Bak protein mRNA	CRFB4 Cytokine receptor family II, member 4	Major Histocompatibility Complex. Class I	(Gb:X12432)	I kappa B epsilon (IkBe) mRNA	YWHAZ Tyrosine 3-monooxygenase/tryptophan 5	monooxygenase activation protein, zeta	polypeptide	PAGA Proliferation-associated gene A (natural	killer-enhancing factor A)	Partial cDNA sequence, farnesyl pyrophosphate	synthetase like-4	Cytoplasmic antiproteinase 2 (CAP2) mRNA	RPL8 Ribosomal protein L8		Ribosomal Protein S4, X-Linked
snl		sui1		cpne5	dyrk1a			nrf2		osteopontin	tubulinB like		cd44	bak1	illorb		hla	ikbe			cirbp		рава			cap2	rp18		
U03057	X80692	L26247		009579	D86550	HG1879.	HT1919	S74017		U20758	V00599	HG2981.	HT3125	116811	217227	HG3597.	HT3800	091616			D78134		X67951		247055	L40377	228407		HG33·HT33
		L26247_at_			at_		_at	ĺ	U20758_rna1	_at_	V00599_s_at_ V00599	HG2981. HT3125_s at HG2981		at	Z17227_at_	HG3597.	HT3800_f_at_ HT3800	U91616_at			D78134_at_		X67951_at_		Z47055_s_at_ Z47055	at		HG33.	HT33_at_

Figure 3L

							Inv	r entors	espoi s:		ir Ha						IS	to a	•						
0.8	0.7	0.5	0.5	0.4	0 4	C		0.0	1 0	0.2	0	0	0	0	0	0	C		7	0		7	Ĉ	ि	
6.0		9.0	0.7	0	-	c	-	y	- c	0	0.5	90	0	0	0.3	9.0	C		3	0.4	-	,	C	0.7	0.2
1.7	80	0	1.3	0	90			5 6	2 0	0	0.5	0	0.4	-	0	0	.5	C	j	1.1	0	3	0 4		0
0	0.5	0	0	0	0	6		5	0 4		0	0	0	0	0	0	0			0	C	,	Ĉ	0	0
1.1		1.3	9.0	0.2	0.5	0				0.5	1.7	0.3	2.8	0.8	0	0.3	0	C C		0.8	7 0		6.0	0.2	1.5
0	0.5	0	0.5	0	0.2	9.0	-	5 6	0 0	0	1.3	0	0	0	0	0	0	C		3.6	C	1	0	0	0
2.2	9.0	0	0	0	0	0	-		4	0	0	0	0	0	0	0	0	C		Ö	C	+	0	0	0
4.7	7.7	0	0.2	0	0.8	0.8	0	0, 6		9.0	1.5	0	9.0	-	0.4	6.0	0	-		1.8	C		9.0	0	1.1
0.4	0.5	0	0	0	0.7	0				0	0	0	9.0	0	0	0	0	C		0	6		0	0	0
Adenosine triphosphatase mRNA	RpS8 gene for ribosomal protein S8	PUTATIVE PROTEIN PHOSPHATASE 2C	KIAA0232 gene	Skeletal beta-tropomyosin	Plectin (PLEC1) mRNA	KIAA0159 gene	GNAS1 Guanine nucleotide binding protein (G	RET ligand 2 (RETL2) mRNA	Oncoprotein 18 (Op18) gene	Acetolactate synthase homolog mRNA	Hematopoietic progenitor kinase (HPK1) mRNA	HRH1 Histamine receptor H1	KIAA0112 gene, partial cds	NADPH-flavin reductase	Rhodanese	KIAA0246 gene, partial cds	KIAA0264 gene, partial cds	Male Enhanced Antigen	SPTAN1 Spectrin, alpha, non-erythrocytic 1	(alpha fodrin)	IMPDH1 IMP (inosine monophosphate) dehydrogenase 1	TKT Transketolase (Wernicke-Korsakoff	syndrome)	ADORA3 Adenosine receptor A3	Endogenous retrovirus envelope region mRNA (PL1)
atp2b1	rps8	pp2c-like		tmsb			ard1	gdnfrb	lap18			hrh1		blvrb	rds	kiaa0246				sptanl	impdh1		tkt	adora3	PL1
104027	X67247	D13640	D86985	M12125	U53204	088890	X77588	AF002700	M31303	U61263	U66464	234897	D25218	D26308	D87292	D87433	D87453	HG1869. HT1904		J05243	105272		L12711	L77730	M11119
П.	.at_	D13640_at_	D86985_at_	M12125_at	U53204_at_	D63880_at_	X77588 s at	AF002700_at	M31303_rna1 _at_	U61263_at_	U66464_at_	Z34897_at_	D25218_at_	D26308_at_	D87292_at_	D87433_at_	D87453_at_	HG1869. HT1904_at_	0	J05243_at_	J05272_at_		اليد	L77730_at_	M11119_at_

0720 022												
14117/60_11146	002011		L-myc gene (L-myc protein) extracted from		_		_		-	-	-	
al	M19720	ımyc	Human L·myc protein gene	0	0	0	0.3	0	0	Ô	0	C
M2319/_at_	M23197	cd33	CD33 CD33 antigen (differentiation antigen)	0	-	0	0.5	1.6	0	60	000	
			PTGS1 Prostaglandin endoperoxide synthase 1				-		+	-	+	7
			(prostaglandin G/H synthase and				-				_	
M59979_at_	M59979	cox1	cyclooxygenase)	C	-		-1	0	-		_	-
M95678_at_	M95678	plcb2	PLCB2 Phospholipase C. beta 2	0 0		0	5		5 0	5 6	5 0	5
U06631_at_	U06631	H326	ILEF SSP 9502 mRNA		5 0	5 0	5 6	5 6	3 6	5 0	5	7
			Mitogon concentration and an arrangement of the concentration of the con	5	5	7.0	2	1.3	5	Σ.Ο	O	0
U53446_at_	U53446	dab2	mitugeii:responsive phosphoprotein (DOC:2)						C	-	0	(
				2	5	5	5	5	5	D	0.7	5
			PACE Paired basic amino acid cleaving enzyme									
X17094_at_	X17094	fur	(furin, membrane associated receptor protein)	6.0	0.6	C	1 4	C	C	-	7	_
			FES Feline sarcoma (Snyder-Theilen) viral (v.		-	+	+	?	3	+	<u>}</u>	7
			fes)/Fujinami avian sarcoma (PRCII) viral (v·fps)	_								
X52192_at_	X52192	fes	oncogene homolog	0	- <u>-</u>	C	- <u>-</u>	4 0		0		- 6
			Ung gene (uracil-DNA-glycosylase, UNG2)			1			5	7.7	1	7
X89398_cds2			extracted from H.sapiens ung gene for uracil									
_at	X89398	dgu	DNA glycosylase	0	C		C		- 1	· ·	_	
X95735_at_	X95735	zyx	Zyxin	17)	10	200	2 0	1	7 0	3	5
X97335 at	X97335	akap1	Kinase A anchor protein		5 0	5 0	7.7	0.0	5	7.7	=	٦
-			TOWN T	0	D	5	0	0	0	0.5	0	0
1	1		I FM1 Tropomyosin alpha chain (skeletal	_	-		-		-	-	-	Γ
224/2/_at	224/2/		muscle)	0		0	0	1.7	0	-	c	
250/49_at_	250/49	ppplr7	Sds22-like mRNA	0	0	c	C 0	90	c) [7-0	
						,	5	5	:			:

Figure 3N

affyID	GBA	gene symbol	gene Name	feco	heco	teco	fpr8	hpr8	tpr8	ican	mcan tcan	can
V00594_at_	V00594	mt2a	Metallothionein isoform 2	1683.1	1698.4	143.4	371.1	414.5	107.8	3.3	261	74.2
X64177_f_at_ X64177	X64177	mt1h	Metallothionein	761.9	728.2	93.6	73.7	6.99	27.4	10.4	27.4	14.9
X04500_at	X04500	illb	IL1B Interleukin 1, beta	199.3	598.3	184.4	9.1	12.6	20.2	24	11.1	48.7
J03910_rna1 _at_	103910	mt1g	(clone 14VS) metallothionein-IG (MT1G) gene	602.9	500.2	138.9	1.1	1.9	0	0	2.7	0.3
X04602_s_at_ X04602	X04602	91	IL6 Interleukin 6 (B cell stimulatory factor 2)	408.5	379.2	1267.5	70.5	76.5	269.4	14.6	43	111
U33017_at_	U33017	slam	Signaling lymphocytic activation molecule (SLAM) mRNA	320.7	343.9	685.7	4.8	25.8	е.	2.7	24.4	84.5
M65290_at_	M65290	ii125/p40	IL12B Natural killer cell stimulatory factor (IL12B)	71.2	261.5	825 7	0	23	4.7	32.8	9/	412 7
Y00787_s_at_ Y00787	Y00787	118	INTERLEUKIN-8 PRECURSOR	89.1	234.5	40.9	9.8	13.1	8.4	8.2	10.8	10.5
X57579_s_at_ X57579	X57579	activinba	Activin beta-A subunit (exon 2)	166.9	233.7	47.2	22.8	16.8	9.4	14.1	19.3	24.6
L11329_at_	L11329	dusp2	DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1	52.1	177.6	16.1	16.2	14.7	2.4	7.9	1.4	2.9
X54489_rna1 _at_	X54489	gro1	Melanoma growth stimulatory activity (MGSA)	49.6	130.6	644.5	0.9	3.2	7.5	4.6	14.6	22.8
X54925_at_	X54925	mmp1	MMP1 Matrix metalloproteinase 1 (interstitial collagenase)	74.3	127.2	147.8	0.5	0	0.4	4.0	0.4	0.7
U04636_rna1 _at_	U04636	cox2	Cyclooxygenase-2 (hCox-2) gene	110	120.8	608.6	15.3	13.8	87.4	2	4.7	54.9
M57731_s_at	M57731	gro2	GRO2 GRO2 oncogene	39.1	114.4	703.3	2	4.8	32.2	13.8	11.7	53.6
M28130_rna1 _s_at_	M28130	118	Interleukin 8 (IL8) gene	109.8	107.8	333.5	6.2	8.3		2.6	1.9	9.2
M26311_s_at 	M26311	qgeo	Cystic fibrosis antigen mRNA	45.8	106.5	303.7	6.0	4	0.2	2.3	0	0.6
U29680_at_	029680	bcl2a1	Bcl-2 related (Bfl-1) mRNA	105.3	97.9	678.7	40.7	35.7	117.5		8.3	179.1
M10942 at	M10942	mt1e	Metallothionein-le gene (hMT-le)	50.5	90.3	63.6	1.4	9	1.8	0.8	9.0	0.2

Figure 4A

		0,40	PTX3 Pentaxin related gene, rapidly induced	82.7	88.9	807.3	21	27.2	122.2	5.2	2.5	20.9
M31166_at	M31166	ptx3	MMP12 Matrix metalloproteinase 12	0 4 5	0 50	2		2 0	0.7	6.4	5.6	2.7
L23808_at_	L23808	mmp12	(macrophage elastase)	14.0	76.5	44.5	8.6		8.8	2.4	4.4	13.4
U15932_at_	U15932	çdsnp	Protein tyrosine phospilatase mons	, ;	1		000	200	95.7	C	15.8	39.3
Y00081_s_at_ Y00081	Y00081	ji6	IL6 Interleukin 6 (B cell stimulatory factor 2)	144.3	0.17	1683	6.7.5	6.6	20.8	0.2	34.9	132
D84276_at_	D84276	cd38	CD38 CD38 antigen (p45)	36.4	2.5	85.6	23	7.9	7.8	5.4	6.5	33.8
L15702 at	L15702	þť	BF B factor, properdin	40.3	יו ל ל ל ל	2000	2 6	Ca	44 4	-	8.4	83.6
1131628 at	U31628	il15ra	IL15RA Interleukin 15 receptor alpha chain	13	22.2	214.3	11.0	5		+		
			Pi Protease inhibitor 1 (anti-elastase), alpha-1	47.3	55.4	72.2	4.7	5.7	2.9	6.0	4.7	3
K01396_at_	K01396	aat	antitrypsin							-		_
Y53800 s at	x53800	gro3	GRO3 GRO3 oncogene	10.9	51.8	49.2	2	5.5	5.4	1.7	9.0	m
M60974_s_at		gadda5	DDIT1 DNA-damage-inducible transcript 1	30.7	43.6	78.3	0.4	4.4	5.1	1.4	=	6.7
HG3415.	HG3415-	2		43.5	39 6	38.5	1.7	- 0	0	4.2	9.9	4.5
HT3598_at_	HT3598	cd155	Pollovirus Receptor	5.5							-	
M72885_rna1	M72885	G0S2	GOS2 gene extracted from Human GUS2 gene, 5' flank and cds	126.1	38	44.9	10.8	6.2	5.3	10.4	11.3	18.7
X60673_rna1	+		Control of colored and a land of colored	ŗ	8	35.3	4.5	7.4	0.3	3.6	10.5	6
at	X60673	ak3	AKS mkinA for agenylate killase 3	57	37.4	8.9		8	2.1	1.1	0.2	0
X76717_at_	X76717	mtII	WILL MEIGHOUNDING 15									
12 02300 1	0/00/1	trin10	Thyroid receptor interactor (TRIPTO) IIIRIAA, 3' end of cds	34.8	37.1	33	5.3	5.5	7.6	22.2	8.9	13.5
L403/9_dl_	C (CO+)		PTGIR Prostaglandin 12 (prostacyclin)	0 00	378	71.9	7	2.2	16.2	11	2.1	65.6
D38128_at_	D38128	ptgir	receptor (IP)	25.0	32.5		5.9		-	3.5	11.7	6.6
U57721_at_	U57721	kynu	L Kynurenine nydrolase mikiya	7:23	21							
	20000		ICAMI Intercellular adnesion molecule i	70.6	32.4	20.7	28	11.1	3.4	9 5	9	9.3
M24283 at	M24283	ICALLI.	1.MK 2	3.9	31.6	25.9	0.8	3.6	7.	1.9	1.1	10.9
D45906_at_	D45906	NITIKZ NIAE1	WM Vimentin	56.3			19.9	4.9	5.9	14.1	5.3	7.9
030/55_at_	030/00	10	BTG1 B-cell translocation gene 1, anti-		0 00	7 7 1	۵	7	4 4	٧	7	9.7
X61123 at	X61123	btg1	proliferative	4.00		1 10	ک اد			1.	1.4	8.5
U02020_at	002020	ppef	Pre-B cell enhancing factor (PBEF) mRNA	26.9	20.4		o					

In autors: Nir Hacohen, et al.

M100/2 24	M10010	* ***										
TO CHOOTE	C+COTIAL	11111	Metallothionein It gene (hM I - If)	5.5	26.1	26.6	o	0	27	-	00	C
			PTGS2 Prostaglandin endoperoxide synthase									
L15326_s_at_	L15326	cox2	Z (prostaglandin G/H synthase and cyclooxygenase)	30 6	7 00	C	Ċ	,	(
M86849_at	M86849	cx26	Connexin 26 (GJB2) mRNA	000	23.7	32.4		7:7	000	2.1	0	2.4
M21005_at_	M21005	caga	CALGRANULIN A	6.2	22.0	31.0	0.4	4	2.4	0.4	- -	4.5
M90657 at	M90657	m3s1	THIMOR ASSOCIATED ANTICENITE	0 C	47.77	9.691	5	1.4	5.6	0.8	0	0.9
M16750 s at	_		CHICK TO COLUMN TO THE THE TO	18.5	22.2	90.1	0.3	0.3	0	0	0	0
		pim1	PIM1 Pim-1 oncogene	7 80	0.00	0		1	(- (,
D86967_at_	D86967		KIAA0212 gene	2000	21.0	0.17	7.4	7,5	4.0	m	5.9	8.2
1100011	710001		TNFR2 Tumor necrosis factor receptor 2	2.23	4:17	7.7	7	ò	2	χ. S	7.7	4 0j
116/19/20	1164107	thirz	(/5kD)	49.5	20.7	28.5	0.3	0.5	9.0	5.4		2.5
D14874 at	014874	adm	ADM Administration of the control of	10.8	20.2	164.2	1.7	12.2	16.1	0	3.9	6.4
M36284 s at	+	200	Activi Adrenomedulin	18	20.1	46.2	3.4	4.5	10.4	2.5	5.2	16.1
W30204_3_4	M36284	Se Se	GYPC Glycophorin C (Gerbich blood group)	0	0	1	r	,	;	-		
			MTF-1 mRNA for metal-regulatory	†	13.3	7:	1	0.5	7.7	1.6	6.0	2.3
X78710_at_	X78710	mtf1	transcription factor	8.7	19.7	σ	0	Ľ			ų	,
			Nicotinamide N-methyltransferase (NNMT)					7	+	7	7	2.3
U08021_at_	008021	nnmt	mrna	3.7	19.6	1.7	0	o	C	α		
D17357 at	017357	\delta + \delta \delta + \delta \delta + \delta \delta +	Activin beta-A gene, regulatory sequence of							0	>	4
AF005775 at	100	2000	o upstream region	29.4	18.8	10.8	0.5	6.0	7.3	5.9	0	14
- 000/ J_at	AF005775	flip	Caspase-like apoptosis regulatory protein 2 (clarp) mRNA, alternatively spliced	7 0	0,	100		1	;		+	
AF008445_at			popular Comments	0:	0.01	5/5) - -	ن. ن	5.4	m	7.6	18.4
	AF008445	plscr1	Phospholipid scramblase mRNA	28.0	17.2	127	C	7		,		
U15460_at_	U15460	batf	BZip protein B-ATF mRNA	19.8	17.1	26/:1	7 4	0.0	20.0	7.7	5.0	88.5
X65724 at	X6572A	t t				2				7	0.0	=
Ţ	12000	201	CTATA C.	33.4	17.1	39.4	0	1.2	0	3.5	0.5	2.5
L78440_at_	L78440	stat4	STATE Signal transducer and activator of transcription 4	ų.	7 4	(-	:			-	
Z48481_at_	248481	mmp14	MT-MMP protein	1001	10.1	0.0	5 6	4 0	0.5	3.1	2.4	7.8
			G-CSF protein gene extracted from Human	7777	0.01	10.1	2	χ. α.α	7.7	7	0	2.4
X03656_rna1			gene for granulocyte colony-stimulating factor									
at	X03656	gcsf	(G·CSF)	19.4	15.2	37.6	r.	- 0	C	- -	-	-
				-]	5	<u>5</u>	7.7	5	=	5	ī

			WNT5A Wingless-type MMTV integration site	-				f			-	
L20861_at_	L20861	wnt5a	5A, human homolog	-	Ţ.		-			•	-	
M13792_at_	M13792	ada	ADA Adenosine deaminase	13.5	7 1	001	5 6	1 -	5 j	-10		4.6
X05232_at_	X05232	mmp3	MMP3 Stromelysin	13.3	7 7	100.1) i	0.	9.0	3.6	2.1	12.3
D87953_at	D87953	rto	RTP	4107	14.4	× 0	0.3	0.1	0.1	0	0	1.1
M54915_s_at	1			ν./Τ	14.2	50.6		6.0	0.5	1.2	0.8	5
	M54915	pim1	PIM1 Pim-1 oncogene	11	13.7	37.2	,		,	C	1	(
D12775 s at	012775	- Spunds	AMPD3 Adenosine monophosphate			1	7.,	1.3	7.0	2.0	3	U.
MERRAD at		an indicate	dealifilase (Isolorm E)	14.7	13.1	18.9	0.1	2.7	6.0	0.8	1 2	7
WIGOOTO AL	14100040	таоа	MAOA Monoamine oxidase A	11.2	13	11.7	0.8	3.4	0	70	1-0	2
M35999 at	M35999	itoha	11GB3 Integrin, beta 3 (platelet glycoprotein									3
		200	MITOCHONDRIA FLORICE	8.3	12.8	21.8	0.3	0	0	1.7	0.4	0
L37936_at_	L37936		PRECURSOR	6.1	12.5	196	9	r, r,	Č	0		
S66896 at	968998	sccal	SCCA1 Square all and submers 14778			2		3		9	0.0	0.
			SEDIME / TUDE ONLY CONTROL OF THE STATE OF T	87	12.3	47.6	0	0.2	ж Ж	0	0.2	1.5
X66363_at_	X66363	pctk1	PCTAIRE.1	11.2	1	30.3	C	,	-	-		l
D86968_at_	D86968	map3k4	KIAA0213 gene, partial cds	100	7117	36:3	5 6	3 0	7	5	5	5.2
U15174_at_	U15174	nip3	Nip3 (NIP3) mRNA	10.0		7.7	7.8	0.5		3.6	1.8	7.4
X90858 at	X90858	-	Listing phone has signed	9	11.4	27.3	0.6	2.1	0.8	0.3	1.7	111
		25	origine prospriorylase	13.1	11.4	10.9	2.4	1.8	0	4.5	1.9	8.3
			ANPEP Alanyl (membrane) aminopeptidase									
M22324 at	M22324	2000	(aminopeptidase N, aminopeptidase M,									
L08187 at	108187	ehi3	Cytoking recentor (EDI2)	5.4	10.4	7.5	1.9	1.9	0	2.2	3.1	7
HG2981.			Storing receptor (EDIS) HIRINA	17.4	10.2	54.9	0	9.0	3	0	2.1	12.5
HT3125_s_at HG2981	HG2981-				_						-	
-	HT3125	cd44	Epican, Alt. Splice 1	13.1	9 7	α	•		-	,	(·
			ETS2 V-ets avian erythroblastosis virus E26		;	5	7	† - -	1	7:7	2.3	-
J04102_at_	J04102	ets2	oncogene homolog 2	23.3	9.6	53.3	7	4.7	-	C	- u	C
1,407			COT Proto-oncogene c·cot (protein-				+		;	+	5	
U1449/_at_	014497	cot	serine/threonine kinase)	4.1	9.5	27	0	0	4 4	C.		,
1109579 2	0.2001	() ()	CDKN1A Cyclin-dependent kinase inhibitor 1A								7	1.6
1003012-at-	6/0500	caudo	(pz1, cip1)	12	9.5	5.1	5.6	C.	C	c,	۲.	2

Figure 4D

1.2554_s_at_ 1.2524	TFRC Transferrin receptor (p90, CD71) 26.3	8.9	13.7	0.3	2.6	0.5	1.2	4.9	8.6
XO7820 mmp10 U 19557 scca2 S81914 iex.1 M30894 tcrg M30894 tcrg M93056 ei U43522 iak2 M24069 csda X01057 il2r D61391 prpsap1 D8422 csta J04501 gys K01383 mt1a U76421 adarb1 U16720 i110 N8156 gap1m U42408 lad1	6.6	8.6	63.7	Ö	0	5.1	0.4	0.1	6
U19557 scca2 S81914 iex-1 M30894 torg M93056 ei L422 fak2 f	13.3	α	8 86	0	C	-	6	0	4 6
U19557 Scca2 S81914 iex-1 M30894 torg M93056 iex Iak2 M24059 csda M24059 csda M24059 csda M24059 csda M24059 csda M24501 gys M13a M13a M13a M13a M1520 i110 U16720 i110 U167408 iad1								+	;
S81914 iev.1 M30894 tcrg M93056 ei U43522 fak2 M24069 csda X01057 il2r D61391 prpsap1 D88422 csta J04501 gys K01383 mt1a U16720 il10 U16720 il10 AF001548 myh11 D78156 gap1m U42408 lad1	17.5	8.2	24.2	0	0.6	1.5	0	0.1	0
M30894 tcrg M30894 tcrg M93056 ei U43522 fak2 M24069 csda X01057 il2r D61391 prpsap1 D88422 csta J04501 gys K01383 mt1a L D28235 cox2 U76421 adarb1 U16720 il10 AF001548 myh11 D78156 gap1m U42408 lad1	7.9	8.1	10		19	0	2.5	22	43
M93056 ei U43522 fak2 M24069 csda X01057 il2r D61391 prpsap1 D88422 csta J04501 gys K01383 mt1a K01383 mt1a U76421 adarb1 U16720 il10 AF001548 myh11 D78156 gap1m U42408 lad1	6.8	8	40.3	0	0.7	m	8	0	1
U43522 fak2 M24069 csda x01057 il2r i	23.4		30.8	3.7	1.8	0.7	1.6	4 8	0
M24069 csda X01057 il2r D61391 prpsap1 D88422 csta J04501 gys K01383 mtla L D28235 cox2 U76421 adarb1 U16720 il10 AF001548 myhl1 D78156 gap1m U42408 lad1	A 5.2	7.	16.3	r	1.6	5.8	0	129	25.9
X01057 it2r D61391 prpsap1 D78501 gys C01383 mt1a D28235 cox2 U76421 adarb1 U16720 i110 D78156 gap1m U42408 lad1 lagaran Lagaran D78156 gap1m U42408 lad1 Lagaran La		7.8	12.1	0	0.8	0	0.3	0	0
D61391 prpsap1 D88422 csta J04501 gys K01383 mt1a L D28235 cox2 U76421 adarb1 U16720 il10 AF001548 myh11 D78156 gap1m U42408 lad1	9.3		39.3	0	9.0	0.3	2.8	0.4	12
U201.391 prpsap1 U201.391 prpsap1 U204501 gys K01.383 mt1a L D28235 cox2 U76421 adarb1 U16720 i110 AF001548 myh11 D78156 gap1m U42408 lad1									
L D28422 csta J04501 gys K01383 mt1a L D28235 cox2 U76421 adarb1 U16720 i110 AF001548 myh11 D78156 gap1m U42408 lad1	2.1	7.3	6.4	0	0.7	0	0	0	2.8
Marcol Sys Marcol Marcol Sys Marcol 12.8	7.1	6.5	3.8	-	-	2.2	0.5	0.5	
K01383 mt1a L D28235 cox2 U76421 adarb1 U16720 ii10 AF001548 myh11 D78156 gap1m U42408 lad1	9.8	6.9	4.1	0	0.8	0	1-1	0.3	2.2
K01383 mt1a L D28235 cox2 U76421 adarb1 U16720 i110 AF001548 myh11 D78156 gap1m U42408 lad1	guipos								
U76421 adarb1 U16720 i110 AF001548 myh11 D78156 gap1m U42408 lad1	3.7	6.5	23.6	0.4	6.0	1.6	1.2	6.0	0
U76421 adarb1 U16720 i110 AF001548 myh11 D78156 gap1m U42408 lad1	28.6	6.4	147.9	1.3	1.5	21.9	0	0.7	7 7
1 U16720 i110 N AF001548 myh11 D78156 gap1m U42408 lad1	<u> </u>								
AF001548 myh11 D78156 gap1m U42408 lad1	2.6	6.3	7.8	0	0	0	0	0.1	0.1
AF001548 myh11 D78156 gap1m U42408 lad1	171	6.5	83.6		0	2.2	-		,
AF001548 myh11 D78156 gap1m U42408 lad1					3	,		7,	\ \
AF001548 myh11 D78156 gap1m U42408 lad1) extracted								
D78156 gap1m U42408 lad1	sequence 3.7	6.1	30.6	0.7	0	4.5	0.0	0	7.
lad1	-	5.9	3.6		0	0	0		0
	6.3		67.8	0.3	4.5		60	90	0
	LONY.								
X17648_at_ X17648 gmcsfR CHAIN PRECURSOR	9	5.9	12.9	C	1	C	0	0	8

Figure 4E

			Mon both theta gramma can the little little						ŀ			
U83115_at_	U83115	aim1	(AIM1) mRNA, partial cds	00	4	103	-0	-	,	,	<u> </u>	0
Z24725_at_	224725		Mitogen inducible gene mig.2	4.8	5.2	17.8	; C	0.4	200	10	200	ο α
M31551_s_at			PAI2 Plasminogen activator inhibitor, type II				1	,	1	;	3	2
1	M31551	pai2	(arginine serpin)	1.3	ري د	94 7	C	C		C	C	C
X55740_at_	X55740	nt5	NT5 5' nucleotidase (CD73)	6.9	4 7	101	0	0	7	200	2 0	
M28983_at_	M28983	illa	IL1A Interleukin 1, alpha	5.1	4 2	17.4	1 0		i u	700	0 0	0.0
					!		2	5	27	 	3	0.0
D79984_s_at_D79984	D79984	supt6h	KIAA0162 gene	4.4	4.1	2.3	1.7	0	C	0	7 0	0
			Heparan N-deacetylase/N-sulfotransferase-2						,	1	<u>}</u>	1
U36601_at_	U36601	ncst2	mRNA	3.3	4.1	11.2	C	C.	Ċ	C		0
U34877_at_	U34877	blvra	Biliverdin-IXalpha reductase mRNA	5	3.7	4.7	-	6.0	0	0.3	1 4	200
U//180_at	0//180	mip3b/elc	EBI1-ligand chemokine	12.5	3.7	233.2	90	c	30.8	0.5	207	327
			SCYA1 gene (secreted protein I-309)				+	+	2	?	1	35.7
M57506_rna1			extracted from Human secreted protein (I									-
at	M57506	i309	309) gene	2.3	3.1	916	0	0	4 6		C	F
			CAB3b mRNA for calcium channel beta3						?	7	7	1
U07139_at_	U07139		subunit	~	0	r,		-1	7		- 0	C
HG3494.	HG3494.			1		5.	+	1.7		7	5	0.7
HT3688_at_	нт3688	nfil6	Nuclear Factor Nf-II6	11.4	000	۳,	σ	_	C	2	4	c
1			VDR Vitamin D (1,25- dihydroxyvitamin D3)				-	+	,	21	-	6.3
J03258_at_	103258	vdr	receptor	9.1	28	2 6	~		-	- <u>'</u>	,	,
X15306_rna1						1	?	1	1	1	1	11
_at	X15306	nefh	NF-H gene, exon 1 (and joined CDS)	∞	2.8	36.6	o		C	0	٠,	
X95325 c at X95325	YGE30E	1	o de divide de la companya de la com				+		-	2	-	
M13452 s at	03000	Cada	DIAR-BINDING PROTEIN A	37.7	2.7	7.2	1.7	1.1	0.5	1.7	1.7	0
	M13452	cmd1a	LMNA Lamin A	0	α	2,1	o c	C	u -	,	-	0
				1	5	7:7	j	J	0.1		_	5

_												
affyID	GBA	gene symbol	gene Name	feco	heco	tero	fors	ά, α,	o'r t		1	
M14660_at	M14660	g10p2	ISG-54K gene (interferon stimulated gene) encoding a 54 kDA protein, exon 2	1 0	ü					i cal	1	Ican
X02530 at	X02530	O Laci	INP10 Interferon (gamma) induced cell line;	2:3		67.3	103	312.4	907	2	C)	33.4
	222	010	TNE-related apparations and a second	12.5	13.1	442.2	137.9	290.4	501.4	5.4	205.9	451.4
U37518_at_	U37518	trail	mRNA	1/7	0.70	1040			0	1		
U59286_at_	U59286	itac	Beta-R1 mRNA, partial cds	37.0	27.6	224.3	- 1	- 1	230.5	5.7	109.1	318.2
140387 24	1 40307	1000	Thyroid receptor interactor (TRIP14) gene, 3' end	5	2)	6.762	0.102	8./02	340.8	200	74.4	389.7
-4030/ -al-	L+030/	oasi	of cds	4.6	7.5	43	105.3	185.2	124.5	1.7	0.4	13.6
Y00451_s_at_		alas1	ALAS1 Aminolevulinate, delta., synthase 1	17.8	α	17.	63	r C	6		,	
X/2/55_at_	X72755	mig	Humig mRNA	2,0	100	0.1	700	200	23.9	7.7	12.2	7.7
			IGFBP6 Insulin-like growth factor binding protein	3.5	7.0	58.3	29.4	52.3	58.6	9.1	77.5	128.6
M62402 at	M62402	igfbp6	9	0	0.1	41.4	60.4	49.8	979	2		Ċ
J00210 rna1			IFNA gene (interferon alpha d) extracted from					2		1	5	4
at	012001	ifns 13	numan leukocyte interferon (IFN-alpha) alpha-d			_						
V00535 rn32	4-	Illiato	allag	0.1	0	0	40.5	48.5	1923	_		č
s at	V00535	ifnhi	Interreron beta 1 gene extracted from Gene for							7	7	
J05037 at		रेपेंड	CEBINE DELIVERATION DETAIL	0.8	11.8	187.4	68.4	33.2	165.4	1.2	0	C
	وا	cvh5	CYBE CAROLOGIA F. F.	0	7	2.4	4.1	31.6	15.8	0.1	0	4 8
			ores cytocillorne p.s	2.9	4.2	2	5.5	30.2	4.6	-	2	n A
X94563_xpt2			Exon 1b; used only in type 2 transcripts from H.sapiens dbi/acbp gene exon 1 & 2./ntype=DNA									S
_r_ar_	X94563		/annot=exon	14.2	e	m	4.6	20	œ m	α		-
D90070_s_at_ D90070	020060	pmaip1	LRP1 ATL derived PMA-resonnsive (ADB)	-	7							-
U80073_at_	U80073	tap	Tip association protein (TAB) DNA		7	125.8	16.9	24.1	249.1	0	0.4	11.1
			PRG2 Proteoglycan 2 hong married	2.3	1.5	6.1	19.7	21.8	31.1	0.1	2.6	7.6
			cell activator, eosinophil granule maior basic									
Z26248_s_at_ Z26248		prg2	protein)	C	-	-	C		1	-		
HG2724.	HG2724.			7	7.7	1	2.3	21.3	2./	0	0	0
H12820_at	HT2820		Oncogene Tis/Chop, Fusion Activated	0	0	2	α α	9	000		-	
UU92/8_at_	009278	fap	Fibroblast activation protein mRNA	c	6	3 0	2 0	17:0	5 [5	0.0	101
				,	5	5	5 t	7.7	4	=	Ξ	3

HG4069.					_				-	-		
HT4339_s_at									-			
1	HT4339	mcp1	Monocyte Chemotactic Protein 1	2.9	2.5	20	38.4	16.9	10.3	C1	10.7	9.5
M62831_at_	M62831	etr101	Transcription factor ETR101 mRNA	4.6	20.4	4.3	9.3	16.6	11.2	9.0	0.5	1.2
10 00000	798864		Annexin II, 5'UTR (sequence from the 5'cap to the	,							-	
D20304_d1	020304		start codoti)	8.2	0.1	4.1	14.2	15.2	6.1	1.4	0	3.1
	D55696	prsc1	Cysteine protease	0	6.0	1.2	2.5	14.3	3.8	0.1	0.1	6.4
	X98253		ZNF183 gene	0	0	9.0	6.6	13.7	34.5	0.5	0	0
D86962_at_	D86962	grb10	KIAA0207 gene	2.2	1.7	37.1	19.5	12	108.7	1.3	1.3	9.5
X78992_at_	X78992	erf2	ERF.2 mRNA	0	6.0	1.5	20.6	11.9	24.9	0.2	0	0
U22662_at_	U22662	lxra	Nuclear orphan receptor LXR-alpha mRNA	1.5	7.3	9.6	34.8	11.4	9.4		3.1	10.9
U07802_at_	U07802	erf2	ERF-2 mRNA	0	2.6	2.2	6.4	11.3	21.6	0.7	0	C
HG3884.	HG3884.									1		T
at	HT4154	hpx42	Homeotic Protein Hpx.42	1	0	m	4.3	11	2.8	0	0	0
X97324_at_	X97324		Adipophilin	0	9.0	2.8	2	10.8	5.7	0	0	9.9
X07743_at_	X07743	plek	PLECKSTRIN	9.7	2.1	5.7	13.9	10.7	2.7	3.6	1.6	5.6
L01664_at_	L01664	clc	ICLC Charot-Leyden crystal protein	0.5	2.7	0.8	2.6	10.2	15.8	0.3	0.8	1.6
X57351_at_	X57351		RPS3 Ribosomal protein S3	0.8	Э	26.5	8.2	10	43	1.4	5	72.9
Z11518_s_at_Z11518	211518		HISTIDYL.TRNA SYNTHETASE	0.5	0.5	10.4	6	Ç	ά	-	C	7.2
										+		!
U70663_at_	U70663	ezf	Zinc finger transcription factor hEZF (EZF) mRNA	0	0	0	10.2	6.6	55.7	ਰ	0	0
U65093_at_	U65093	mrgl	Msg1-related gene 1 (mrg1) mRNA	0	0.7	0.4	7.2	9.6	10.4	0.2	0	0.4
U27699_at_	U27699	slc6a12	SODIUM- AND CHLORIDE-ÖEPENDENT BETÄINE TRANSPORTER	6.0	0	51.9	14.9	0	9	0.5	C	42 B
X05345_at_	X05345	hars	HARS Histidyl-tRNA synthetase	9.0	2.2	0	28.5	8.5	7.7	0	2.6	3.2
M95809_at_	M95809	gtf2h1	BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT	1	1.3	0.2	3.1	8.1	16.7	0	0.5	3.3
D14826_s_at_D14826	D14826	crem	CREM CAMP responsive element modulator	3.4	-2	6.3	13.7	7	50.6	5.1	1 9	7.4
U59748_at_	U59748	dhh	Desert hedgehog (hDHH) mRNA, partial cds	9.0	0	2.4	5.4	7.3	24.5	0	0	000
M16707_rna1 _s_at_	M16707		Histone H4 gene, clone F0108	0.3	8.0	1.4	8.4		2.8	4.0	0	1.7
S77154_s_at_ S77154	877154	nurr1	TINUR	0.2	5.1	0.3	8	8.9	8.6	0.7	o	7.0
				1						ŀ	,	

(A96/19_at_ A96/19	(490/19	aici	AICL (activation induced Citype lectin)	0	1.7	ō	4.9	<u>6</u>	5.9 0.5	0	6	<u></u>
			ACTIN, AORTIC SMOOTH MUSCLE (ALPHA-ACTIN							T		Γ
X13839_at_	X13839	acta2	(2)	0.1	0.7	1.2	7.5	5.8	5.6	0	5.4	3.4
J04111_at_	J04111	jun	C-jun proto oncogene (JUN), clone hCJ-1	2.2	4.2	2.4	19.1	5.6	13.4	1.6	0.5	4
Z14978_at_	214978		ALPHA CENTRACTIN	0.5	9.0	0	1.1	5.1	5.6	0	0	0
D42040_s_at_ D42040	D42040	ring3	RING3 PROTEIN	1.3	1.7	-8	7.3	Ľ	7	4	2	27
Y10032_at_	Y10032	sgk	Putative serine/threonine protein kinase	0	0	1.6	2.5	4	5.4	80		C
M63438_s_at			GLUL Glutamate ammonia ligase (glutamine		H	İ						
	M63438		synthase)	1.6	0.2	0.2	2.6	4.6	137.4	0	0	1.2
X92106_at_	X92106	blmh	Bleomycin hydrolase	-	1.4	0	1.6	4.5	5.5	0.3	1.4	0
S68271_s_at_ S6827	S68271	crem	CREM CAMP responsive element modulator		6	2 4	126	4	200	=	o C	α
M63838_s_at					1						-	8
1	M63838	ifi16	Interferon-gamma induced protein (IFI 16) gene	0	0.4	0	2.6	4	4	0.1	0.1	2.8
			Pre-mRNA splicing factor SRp20, 5'UTR								-	
.D28423_at	D28423		(sequence from the 5'cap to the start codon)	0	0	6.0	7.5	3.7	4	0.2	1.1	0.7
U04285_s_at			LIPA Lipase A, lysosomal acid, cholesterol							T		
	U04285	lipa	esterase	0	0.5	H	1.9	3.7	1.9	7	0	1.1
			CLN3 Ceroid-lipofuscinosis, neuronal 3, juvenile									
U32680_at_	U32680	bts	(Batten, Spielmeyer-vogt disease)	2.5	0.8	2.1	10.1	2.1	7.3	0.1	9.0	2.7
U94592_at_	U94592	ucp2	Uncoupling protein homolog (UCPH) mRNA	0	0.7	Ó	0.5	1.5	0	0	0.2	0
U50733_at_	U50733		Dynamitin mRNA		1.9	1.7	1.2	0.4	0	1.7	0	0.4
			Fatty acid synthase (3' region) [human, breast							T		
[S80437_s_at_]S80437	S80437		and HepG2 cells, mRNA Partial, 2237 nt]	0.4	0	0	0	0	0	0.7	1.3	0.0

Figure 5C

	GBA	gene symbol	gene Name	feco	heco	teco	fpr8	hpr8	tpr8	ican	mcan	tcan
V00594_at_	V00594	mt2a	Metallothionein isoform 2	1683.1	1698.4	143.4	371.1	414.5	107.8	3.3	261	74.2
X64177_f_at_ X64177	X64177	mt1h	Metallothionein	761.9	728.2	93.6	73.7	6.39	27.4	10.4	27.4	14.9
	M21121	rantes	SCYA5 Small inducible cytokine A5 (RANTES)	728.7	661.7	83.4	717	396.6	115.3	113.6	87.4	43.7
X04500_at_	X04500	ii1b	IL1B Interleukin 1, beta	199.3	598.3	184.4	9.1	12.6	20.2	24	11.1	48.7
M13755_at_	M13755	isg15	G1P2 Interferon, alpha-inducible protein (clone IFI-15K)	214 1	545 6	57.4	253	662	100.2	302.7	208.8	34.3
X04602_s_at_ X04602	X04602	il6	IL6 Interleukin 6 (B cell stimulatory factor 2)	408.5	379.2	1267.5	70.5	76.5	269.4	14.6	43	111
U33017_at_	U33017	slam	Signaling lymphocytic activation molecule (SLAM) mRNA	320.7	343.9	685.7	4.8	25.8	m	2.7	24.4	84.5
V00594_s_at_ V00594	V00594	mt2a	Metallothionein isoform 2	167.1	337.3	15	64.9	122.8	34.8	69.4	52.2	9.4
Y00787_s_at_ Y00787	Y00787	118	INTERLEUKIN-8 PRECURSOR	89.1	234.5	40.9	9.8	13.1	8.4	8.2	10.8	10.5
X57579_s_at_ X57579	X57579	activinba	Activin beta-A subunit (exon 2)	1669	233 7	47.2	22.8	16.8	4.0	14.1	19.3	24.6
X02910_at_	X02910	tnfa	TNF Tumor necrosis factor	144.1	225.5		1	1	4		1	43.2
L11329_at_	L11329	dusp2	DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1	52.1	177.6	16.1	16.2	14.7	2.4	7.9	4.1	2.9
M33882 at	M33882	mx.]	MX1 Myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible profein 678)	1 1 2	9 991	0	0	'	0		5	
M31165_at_	M31165	tnfaip6	TUMOR NECROSIS FACTOR:INDUCIBLE PROTEIN TSG-6 PRECURSOR	172.2	1	624.	9.09	100	-		1	"
M59465_at_	M59465	a20	TNFAIP1 Tumor necrosis factor alpha inducible protein A20	87			l	į.				1
L19779_at_	L19779	h2a	Histone H2A.2 mRNA	53.2	154	83.4	40.2	"	1		ľ	r
X65965_s_at_ X65965	X65965	sod2	SOD-2 gene for manganese superoxide dismutase	233.7	149.2	204	143.7	86.3	86.3	10.6	35.9	109.3
X67325_at_	X67325	ifi27	INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN	136.8	143.4	618.8	265.8	192.2	498.1	50	C1	

lit. Intors: Nir Hacohen, et al.

U53830_at	U53830	irf7	Interferon regulatory factor 7 (humirf7) mBNA	426	130	7	30 0	7.0	2	1		
M23178_s_at	M23178	mip1a	MACROPHAGE INFLAMMATORY PROTEIN 1. ALPHA PRECURSOR	<u> </u>	125	-	0 0 0	72.0	7, 0	7, 7	43.1	0.74
U04636_rna1 _at_	004636	cox2	Cyclooxygenase-2 (hCox-2) gene	110	120.8	9.809	15.3	138	87.4	, r.	0.7	20 2
	X07834	sod2	SOD2 Superoxide dismutase 2, mitochondrial	57.7	104.1	240.9	34.7	92.1	5	0	12	110
UZY680 at	029680	bc/2a1	Bcl·2 related (Bfl·1) mRNA	105.3	97.9	678.7	40.7	35.7	117.5	4	τα	1791
M31166_at	M31166	ptx3	PTX3 Pentaxin-related gene, rapidly induced by IL-1 beta	82 7	88.9	807.3	21	27.2	122.2	7.	0 0	20.0
L31584_at_	L31584	ccr/	CMKBR7 Chemokine (C.C) receptor 7	58.1	87.3	98.2	23.3	9.69	83.5	26.5	11	56.3
الب	X57351	ifitm2	RPS3 Ribosomal protein S3 / wrong name	13	84.2	13.1	15.3	81.7	30.3	55.9	20.8	7.5
013332_d1_	266610	cdsnp	Protein tyrosine phosphatase mRNA	57	76.5	44.5	9.8	11.1	8.8	2.4	4 4	13.4
M30818_at_	M30818	mx2	MX2 Myxovirus (influenza) resistance 2, homolog of murine	21	74.4	42.6	40.9	823	50.4	ά	30,	0.00
M24594_at_	M24594	g10p1	IFI56 Interferon-induced protein 56	19.8	71.6	77.5	8.06	266	141	18.6	248 6	20.6
1100070 770			6-16 gene (interferon-inducible peptide									2
s_at_	U22970	g1p3	precursor) extracted from Human interferon. inducible peptide (6·16) gene	115.3	689	ű	70.6	07 1	101		i.	i.
X59892_at	X59892	wars	TRYPTOPHANYL-TRNA SYNTHETASE	40.2	6 99	32.5	56.5	70 2	25.0	1001	0.01	0 0
L15702_at	L15702	ρţ	BF B-factor, properdin	46.3	64.4	85.6	333	6.7	7.67	5.4	0 1 0	33.8
U/2882_S_at	U72882	ifi35	Interferon induced leucine zipper protein (IFP35) mRNA, partial cds	23.2	ας	30 5	3	7 30	5	6	2 6) L
J04164_at_	J04164	ifi17	RPS3 Ribosomal protein S3 /wrong name	25.8	57.2	37.7	34.5	45.6	79.3	11.5	60.3	35.1
	98866X	mcp2	MCP-2 gene	0	1	0	,					3
U37546_s_at	1137546	Cario			5	20.3	7,7	07.0	y ,	χ.	23.8	79.5
M69203 c at	040,00	ciabz	IAP nomolog C (MIHC) mRNA	54.1	48.6	62.2	5.3	3.7	31.5	22.7	34	55.9
_	M69203	mip1b	SCTA4 Small inducible cytokine A4 (homologous to mouse Mip-1b)	164.9	44.6	19.3	372 7	8	10.5	4	, ,	116
U88964_at_	U88964	hem45	HEM45 mRNA	34.6	43.7	161	27.2	15.5	73.3	ά	100	116.1
XE7E22 34	757522	1	TAP1 Transporter 1, ABC (ATP binding				!		5.5	0	5	110.1
7	770/07	lapı	cassette)	34.3	42.3	48.3	76.1	53.3	47.7	11	31.7	413

_																																
	2.9	28.7	2.5	,	15.7	34.7	18.7		13.5	23.2	1	6.5		318.2		3500	2000	σ	20.00	200.0	15.6		80.4		48	21.7	39.3	3	0.	17.7	389 7	2000
	4.6	13.9	∞		5.71	39.1	113		000	11.5		۲,		109.1		30.1		9	0	5	11		20.5		15.5	2.6	9 6		27.8	1 4	74.0	F (*
	6.6	n	3.8		0.47	13.2	10.4		22.2	6	1	-		5.7	r	9	3	9.5	200	5	3.4		٠ţ ز j		13.3	9.7	4.4		40.1	1 -	1 ×	22.5
	6.5	34	7.9		13.7	000	27		7.6	15		16.2		590.2		86.2	3	3.4	7 4		16.9	-	117.7	:	44.3	8.6	23.3		22.1	0 4	340.8	171
i	51.6	χ. Σ. Σ.	18.4	0.5	7.61	0.10	6.9		5.5	13.7		C1		230.1		12.6		11.1	1.7	+	30.2		500		4/.1	3.1	58.3	+	6	0 4		
	70.3	ر 20.5	16.8	37.0	0. 00	75.1	10.8		5.3	27.5	T	7.9		171.9		13.8		87	cc	;	11.5		41.5		10./	2.4	189.3	İ	17.0	10 0	201.6	-
,	5.7	104.4	5.5	171	06.2	21.00	44.9		33	55.8		71.9		134.3		209.8		20.7	48.8	2	44.7	-	48.7	(23.0	7.4	21.9		22.3	196	ı	ı
-0	42.2	33.7	39.5	39.4	30.5	2	38	-	37.1	36.8	-	34 8	_	34.2		34.1		32.4	31.1	+	30	_	30	000	62.0	29.6	28.9		28.4	28.2	27.6	27.5
	81.9	69.0	22.4	49.2	25.1		126.1		34.8	61.7		29 8		14.7		16.9	-	70.6	43.8		19.2		16 7	0	0 0	5.6	43.8		19.8	56.3	34.9	59 R
SCYA4 Small inducible cytokine A4	B94 PROTFIN	TVN TF:0000	I AIN TRIBLEDOXIN	Mitogen induced nuclear orphan receptor (MINOR) mRNA	RIG-G mRNA	G0S2 gene extracted from Human G0S2	gene, 5' flank and cds	Thyroid receptor interactor (TRIP10) mRNA,	3' end of cds	IL7R Interleukin 7 receptor	PTGIR Prostaglandin 12 (prostacyclin)	receptor (IP)	TNF-related apoptosis inducing ligand TRAIL	MKINA	C1NH Complement component 1 inhibitor	(angioedema, hereditary)	ICAM1 Intercellular adhesion molecule 1	(CD54), human rhinovirus receptor	Ninjurin1 mRNA		Macmarcks		UIAS (2.5) oligoadenylate synthetase	Hepatitis Cassociated microtubular	Dual specific protein phosphates	Dual specific protein prospiratase mKIVA	Phorbolin I mRNA, partial cds	Interferon inducible RNA dependent protein	kinase (Pkr) gene	VIM Vimentin	Beta-R1 mRNA, partial cds	Actin bundling protein mRNA
min1h	tnfaip2	tva	IXI	minor	ifit4		G0S2		trip10	il7r		ptgir		Itail		clnh		icam1	ninj1		macmarcks		oası	mtap44	Ansh	10000	unknown		pkr	NAF1	itac	snl
			1001	U12767	U52513		M72885		L403/9	M29696		D38128	1127510	03/310		M13690		M24283	U/2661	HG1612.	HT1612	37000	2/0707	D28915			003091		U50648			U03057
J04130 s at J04130	M92357 at	Г	Ţ	,	U52513_at_	85_rna1	_s_at_		T	M29696_at_		D38128_at_	1127510 24	-	M1369U_S_at	_		7	at	HG1612.	HT1612_at	X02075 5 34	70707 3-3-d1	D28915_at	Γ	Τ	+	USUB48_s_at	T		7	U0305/_at[

Figure 6C

itors: Nir Hacohen, et al.

U09937_rna1 _s_at_	756600	plaur	Urokinase-type plasminogen activator receptor gene extracted from Human urokinase-type plasminogen receptor	17	26.9	14.5	12.5	10.7	2 0	~	۳	4
X61123_at_	X61123	btg1	BTG1 B-cell translocation gene 1, anti- proliferative	30.4	26.8	14.4	8.4	4.6	4	3,6	7 4	6
X53296_s_at_ X53296	X53296	ii1m	IL1RN Interleukin 1 receptor antagonist	65.5	26.4	6.9	28.7	14.4		2 4		
S59049_at_	S59049	ier1	RGS1 Regulator of G-protein signalling 1	4.5	25.9	15.9	2.2	28	9 1	99	10.8	34
M14660_at	M14660	g10p2	ISG-54K gene (interferon stimulated gene) encoding a 54 kDA protein, exon 2	5.9	25	27.9	109	3124	206	,	2	33.7
L05072_s_at_	L05072	irf1	IRF1 Interferon regulatory factor 1	48.2	24 5	2	627	38	0,0	1 .	0 7	t u
M16750_s_at	M16750	pim1	PIM1 Pim-1 oncogene	7 80	0 5	3		100			2	200
X66401_cds1	0	,	LMP2 gene extracted from H.sapiens genes	7.03	0.17	0.11	7.1	, ,	4.0	7	2.	8.2
at D14874_at	X56401 D14874	tap2	TAP1, TAP2, LMP2, LMP7 and DOB	30.6	20.6	32.4	12.9	9.6	6.3	6.1	23.6	31.9
			MA IOD HIGHOROGATIII	2	70.7	46.2	3.4	4.5	10.4	2.5	5.2	16.1
M69043_at	M69043	ikba	MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN MAD3	23.9	19.6	11	14.8	9.5	4.7	4.3	3.7	4
L13210_at_	L13210	тас2bp	Mac-2 binding protein mRNA	9	19.5	21	5.6	3.5	11.5	27.3	α	32 5
L06797_s_at_ L06797	L06797	cxcr4	PROBABLE G PROTEIN.COUPLED RECEPTOR LCR1 HOMOLOG	12.7	19.2	30.6	α	7 0	0	5	-	200
D42073_at_	D42073	rcn1	Reticulocalbin	5.7	18.4	61.3	10	7.5	13.7	0.0	110	30.7 11.5
D50663_at_	D50663	tctel1	CW.1 mRNA	23.1	17.9	33.6	16.9	13.3	15.1	1 -	135	2000
D45248_at_	D45248	pa28b	Proteasome activator hPA28 subunit beta	13.1	17.2	6.2	12	8	5 7	34.3		0 L
M55543_at_	M55543	GBP2	INTERFERON-INDUCED GUANYLATE.BINDING PROTEIN 2	30.7	1 2		=	C	1	5 1	? .	
M31724_at_	M31724	ptp1b	PTPN1 Tyrosine phosphatase 1	14.7	15.8	16.2	11.4	ς α	1	0.7	1.6.	23.5
U19261_at_	U19261	traf1	Epstein-Barr virus-induced protein mRNA	25.7	15.4	25.2	α	127	1 0	ια	200) c
HG544. HT544 at	HG544. HT544	ecpf	Endothelial Cell Growth Factor 1	L.	L		9		3		-	5
D10040_at_	D10040	faci2	FACL1 Long chain fatty acid acyl.coA ligase	2.07	15.3	2, 4, 0	10.4	2.5	7.7.7	26.7	16.5	
			Variant urokinase plasminogen activator	1	7.0.7	7.07		9.9	16.4	7.7	4.4	24.1
X74039_at	X74039	plaur	receptor (uPAR2) mRNA, partial cds	1.6	15	7.3	1.6	4.2	2.8	1.5	5.4	5.1
U42043_at_	D42043	KIAA0084	KIAA0084 gene, partial cds	24.8	14.1	27.1	7.1	3.1	4.5	8.3	8.6	19

2',3'-cyclic-nucleotide 3'-phosphodiesterase gene extracted from Human 2,3'-cyclic nucleotide 3'-phosphodiesterase gene extracted from Human 2,3'-cyclic nucleotide 3'-phosphodiesterase gene for nucleotide 3'-phosphodiesterase gene nucleotide 3'-phosphodiesterase gene nucleotide 3'-phosphodiesterase gene nucleotide 3'-phosphodiesterase gene nucleotide 3'-cyclic nucleotide 3'-phosphodiesterase gene nucleotide 3'-cyclic nucleotid 1'-cyclic nucleotid 1'-cyclic nucleotid 1'-cyclic nucleotid 1'-cyclic nucleotid 1'-cyclic nucleotid 1'-	U00672_at_	U00672	il10ra	IL10R Interleukin 10 receptor	9.5	14.1	9.1	10.6	151	9	4.2	5 0	4
D13146 Crip	D13146_cds1			2',3'.cyclic-nucleotide 3'.phosphodiesterase gene extracted from Human 2',3'.cyclic.									i)
Native copte Putative copper uptake protein (hCTR2) 3.6 13.4 19.1 2.9 10.1	at	D13146	cub	nucleotide 3'phosphodiesterase gene	15.9	13.4	25.3		4.4	10.1	5.6	8,	11.2
ABOOO115 Unknown mRNA	U83461_at_	U83461	copt2	Putative copper uptake protein (hCTR2) mRNA	3.6	13.4	191		101	5	u	7	2
INPTO Interferon (gamma)-induced cell line; 98 131 24.9 84 26.9 28 28 20 20 20 20 20 20	AB000115_at	AR000115	awoodan	\$ Z						77	0	1	44.0
Note		2110000		IIINING INDIO 1-1-4-	9.8	13.1	24.9	8.4	26.9	28.7	3.4	6.1	37.6
Udd080 C1S Complement component 1, s Udd080 C1S Cubs component 1, s Udd080 C1S Subcomponent 1, s Udd080 C1S Subcomponent 1, s UDG080 C1S CD83 ANTIGEN PRECURSOR Udd080	X02530_at_	X02530	inp10	INP 10 Interferon (gamma)-induced cell line; protein 10 from	12.5	13.1	4422	1379	290 4	20.1	T.	305	1 1
M55067 ncf1 NCF1 47 No autosomal chronic A.2 12.6 61.6 56 8.9 3	104080 at	104080		C1S Complement component 1, s						1	j.	503.7	4.101.4
M55067 ncf1 W3 147 No autosorial critique 2.5 12.6 24.2 19.1 28.5 2 211697 cd83 CD83 ANTIGEN PRECURSOR 18.7 12.6 9.8 19.6 9.5 211697 cd83 CD83 ANTIGEN PRECURSOR 18.7 12.6 9.8 19.6 9.5 M97936 stat1 TRANSCRIPTION 1.ALPHA/BETA 7.4 11.4 16.9 13.4 7.7 1 U44975 bcd1 DNA-binding protein CPBP (CPBP) mRNA, 2.4 11.1 12.7 10.9 20.7 L08069 hspt4 DNAJ PROTEIN HOMOLOG 2 12.8 11.1 12.7 10.9 20.7 U03105 bd-2 B4-2 protein mRNA 29.4 10.7 8.2 11.4 5.7 X69910 p63 P63 mRNA for transmembrane protein 5.8 10.1 26.4 4.1 2.3 L22342 unknown Nuclear phosphoprotein mRNA 3.6 9.2 36.3 3.7 5.3 AF014958 <td< td=""><td></td><td>200</td><td>212</td><td>MOET 47 kD automated</td><td>4.2</td><td>12.6</td><td>61.6</td><td>5.6</td><td>8.9</td><td>31.4</td><td>3.7</td><td>6.4</td><td>18.9</td></td<>		200	212	MOET 47 kD automated	4.2	12.6	61.6	5.6	8.9	31.4	3.7	6.4	18.9
Libby Cd83 CD83 ANTIGEN PRECURSOR 18.7 12.6 9.8 19.6 9.5 M97936 stat1 TRANSCRIPTION 1-ALPHA/BETA 7.4 11.4 16.9 13.4 7.7 1 U44975 bcd1 partial cds DNA-binding protein CPBF (CPBP) mRNA, 2.4 11.3 6.8 3.7 7.1 U08069 hspf4 DNA-Drotein mRNA 2.4 11.3 6.8 3.7 7.1 U03105 b4.2 B4-2 protein mRNA 29.4 10.7 8.2 11.4 5.7 U03105 b4.2 B4-2 protein mRNA 29.4 10.7 8.2 11.4 5.7 U03105 b4.2 B4-2 protein mRNA 29.4 10.7 8.2 11.4 5.2 X69910 p63 P63 mRNA for transmembrane protein 5.8 10.1 26.4 4.1 2.3 L22342 unknown Nuclear phosphoprotein mRNA 3.6 9.2 21.1 4.1 6.1 AF014958 ccr6 <td< td=""><td>,</td><td>M55067</td><td>ncf1</td><td>granulomatous disease protein</td><td>2.5</td><td>12.6</td><td>24.2</td><td>19.1</td><td>28.5</td><td>22.1</td><td>4 4</td><td>σ</td><td>17.0</td></td<>	,	M55067	ncf1	granulomatous disease protein	2.5	12.6	24.2	19.1	28.5	22.1	4 4	σ	17.0
M97936 stat1 FIGNAL I RANSDUCER AND ACTIVATOR OF TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA 7.4 11.4 16.9 13.4 7.7 1 U44975 bcd1 partial cds partial cds 2.4 11.3 6.8 3.7 7.1 L08069 hspf4 DNA-binding protein CPBP (CPBP) mRNA, partial cds 2.4 11.3 6.8 3.7 7.1 U03105 bd-2 B4-2 protein mRNA 29.4 10.7 8.2 11.4 5.7 U76764 cd97 CD97 cD97 antigen (leucocyte antigen) 14.8 10.7 3.4 14.5 2.8 X69910 p63 P63 mRNA for transmembrane protein 5.8 10.1 26.4 4.1 2.3 L22342 unknown Nuclear phosphoprotein mRNA 3.6 9.9 21.1 14.5 2.8 AF014958 ccr6 Chemokine receptor X (CKRX) mRNA 3.6 9.2 36.3 3.7 5.3 RMPC-encoded proteasome subunit LMP7 extracted from H.sapiens gene for major histocompatibility complex encoded	at	711697	cd83	CD83 ANTIGEN PRECURSOR	18.7	12.6	9.6	19.6	9.5	10	4.1	0.0	17.6
DNA-binding protein CPBP (CPBP) mRNA, 2.4 11.3 6.8 3.7 7.1	M97936_at_	M97936	stat1	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1.4LPHA/BETA	7.4	11.4	0 41	1.0	7		Ç	,	1 6
U44975 bcd1 partial cds 2.4 11.3 6.8 3.7 7.1 L08069 hspf4 DNAJ PROTEIN HOMOLOG 2 12.8 11.1 12.7 10.9 20.7 U03105 b4.2 B4.2 protein mRNA 29.4 10.7 8.2 11.4 5.7 U76764 cd97 CD97 CD97 antigen (feucocyte antigen) 14.8 10.7 3.4 14.5 2.8 X69910 p63 P63 mRNA for transmembrane protein 5.8 10.1 26.4 4.1 2.3 D79206 sdc4 SDC4 Syndecan 4 (amphiglycan, ryudocan) 6.3 9.9 21.1 15.2 11.2 1 L22342 unknown Nuclear phosphoprotein mRNA 3.6 9.2 36.3 3.7 5.3 AF014958 ccr6 Chemokine receptor X (CKRX) mRNA 3.6 9.2 36.3 3.7 5.3 HAP7-E1 gene (proteasome subunit LMP7) extracted from H.sapiens gene for major histocompatibility complex encoded 2.6 9.2 36.3 3.7 5.3 <td></td> <td></td> <td></td> <td>DNA-binding protein CPBP (CPBP) mRNA</td> <td>1</td> <td></td> <td>10.0</td> <td>‡.</td> <td></td> <td>7.1</td> <td>4α.α</td> <td>40</td> <td>28.5</td>				DNA-binding protein CPBP (CPBP) mRNA	1		10.0	‡.		7.1	4α.α	40	28.5
12.00 12.0	U44975_at_	U44975	bcd1	partial cds	2.4	11.3	89	3.7	7 1	ν		-	u
UV5105 D4-2 B4-2 protein mRNA 29.4 10.7 8.2 11.4 5.7 UV6764 cd97 CD97 CD97 antigen (leucocyte antigen) 14.8 10.7 3.4 14.5 2.8 X69910 p63 P63 mRNA for transmembrane protein 5.8 10.1 26.4 4.1 2.3 D79206 sdc4 SDC4 Syndecan 4 (amphiglycan, ryudocan) 6.3 9.9 21.1 1.2 1 L22342 unknown Nuclear phosphoprotein mRNA 3.8 9.7 11.4 4.1 6.1 AF014958 ccr6 Chemokine receptor X (CKRX) mRNA 3.6 9.2 36.3 3.7 5.3 MHC-encoded proteasome subunit LMP7. extracted from H.sapiens gene for major histocompatibility complex encoded 2.6 9.2 36.3 3.7 5.3 T14982 Imp7 proteasome subunit LMP7 2.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	L08069_at	690807	hspf4	DNAJ PROTEIN HOMOLOG 2	12.8	11.1	12.7	10.9	20.7		17	7 0	n a
U76764 cd97 CD97 CD97 antigen (feucocyte antigen) 14.8 10.7 3.4 14.5 2.8 X69910 p63 P63 mRNA for transmembrane protein 5.8 10.1 26.4 4.1 2.3 D79206 sdc4 SDC4 Syndecan 4 (amphiglycan, ryudocan) 6.3 9.9 21.1 15.2 11.2 1 L22342 unknown Nuclear phosphoprotein mRNA 3.8 9.7 11.4 4.1 6.1 AF014958 ccr6 Chemokine receptor X (CKRX) mRNA 3.6 9.2 36.3 3.7 5.3 MHC-encoded proteasome subunit gene LAMP7-E1 gene (proteasome subunit LMP7) extracted from H.sapiens gene for major histocompatibility complex encoded 2.6 9.2 36.3 3.7 5.3 Z14982 Imp7 proteasome subunit LMP7 2.6 0.0 </td <td>003105_at_</td> <td>003105</td> <td>D4-2</td> <td>B4-2 protein mRNA</td> <td>29.4</td> <td>10.7</td> <td>8.2</td> <td>11.4</td> <td>5.7</td> <td>2</td> <td>6.4</td> <td>200</td> <td>ب 1 (د</td>	003105_at_	003105	D4-2	B4-2 protein mRNA	29.4	10.7	8.2	11.4	5.7	2	6.4	200	ب 1 (د
Name	0/0/04_5_4[136361	2000										;
D79206 Sdc4 SDC4 Syndecan 4 (amphiglycan, ryudocan) 6.3 9.9 21.1 2.3	Т	X69910	,6n3	CUS/ CUS/ antigen (leucocyte antigen)	14.8	10.7	3.4	14.5	2.8	2.3	1.7	2.3	7.5
D79206 Sdc4 SDC4 Syndecan 4 (amphiglycan, ryudocan) 6.3 9.9 21.1 15.2 11.2	Т		202	rod IIIviva lot transmembrane protein	2.8	10.1	26.4	4.1	2.3	9.7	3.9	6.4	29.3
L22342 unknown Nuclear phosphoprotein mRNA 3.8 9.7 11.4 4.1 6.1 4.1 6.1 4.1 6.1 4.1 6.1 4.1 6.1 6.1 4.1 6.1 6.1 4.1 6.1	_	D79206	sdc4	SDC4 Syndecan 4 (amphiglycan, ryudocan)	9	σ	-1.10	л С		0,	,	7	Ι,
AF014958 ccr6 Chemokine receptor X (CKRX) mRNA 3.6 9.2 36.3 3.7 5.3 6. MHC-encoded proteasome subunit gene LAMP7-E1 gene (proteasome subunit LMP7) extracted from H.sapiens gene for major histocompatibility complex encoded Z14982 Imp7 proteasome subunit IMP7	L22342_at_	L22342	unknown	Nuclear phosphoprotein mRNA	800	0	111 4	7.51	2.1.2	10.7	1,2,1	77	ام
MHC-encoded proteasome subunit gene LAMP7-E1 gene (proteasome subunit LMP7) extracted from H-sapiens gene for major histocompatibility complex encoded Z14982 Imp7 proteasome subunit IMP7		AF014958	بردرو					ř	5	1		12.2	71.7
LAMP7.E1 gene (proteasome subunit gene LAMP7.E1 gene (proteasome subunit LMP7) extracted from H.sapiens gene for major histocompatibility complex encoded Z14982 Imp7 proteasome subunit IMP7			2	MUD SECTION A (CRRX) MRINA	3.6	9.5	36.3	3.7		9.9	5.1	4.3	10
histocompatibility complex encoded Z14982 Imp7 proteasome subunit I MP7				MnC-encoded proteasome subunit gene LAMP7-E1 gene (proteasome subunit LMP7)									
Z14982 Imp7 proteasome subunit I MP7	Z14982_rna1			extracted from H.sapiens gene for major histocompatibility complex encoded							_		
3.0 9.2 9.4 4.7 8.7 9		214982	Imp7	proteasome subunit LMP7	3.6	9.2	9.4	4	ά	σ	r.	0	0

Figure 6E

			BONE MADDOW STROMAL ANTICENS 2 SET	-	}							
D28137_at_	D28137	bst2	2)	ι.	6	12.0		ō	14 9	7	2	0 7 0
M31627_at_	M31627	xbp1	X BOX BINDING PROTEIN 1	4.4	6	15.4	16.7	20.6	27.1	2.0	7 - ~	0,14
M79462_at	M79462	ly#	PML Probable transcription factor PML (alternative products)	2,1	0	0	, ,			1 (1 6	
M62324 at	M62324	mrf.1	Modulator recognition factor I (MRF-1) mRNA,			7 0	, (ò	0.6		X)	8
M87434_at_	M87434	oas2	69/71 KD	1.0 0 0	0 0	210.7	V 7	32.1	14.3	8	3.4	6.2
X17093_at_	X17093	hla-cda12	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F ALPHA CHAIN PRECURSOR	10.7	2 5	5 2 5	j 0	1:00	0.01	0.7	2 .	0:/1
L07633_at	L07633	pa28a	INTERFERON GAMMA UP. REGULATED 1.5111 PROTEIN PRECURSOR	i u	5 0	2 0				0.17	16.4	7.8
M97935_s_at	M97935	stat1	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1.4I PHA/RETA	7	0 0		0 1		9 9	2,3	20 0	20.1
U20158_at_	U20158	lcp2	76 kDa tyrosine phosphoprotein SLP-76 mRNA	3.7	(c. / 8.7	8.6	0 0	12.6	3.4	χ m	7 6	3 %
HG2917- HG2917 HT3061_f_at_ HT3061	НG2917. НТ3061	hla	Major Histocompatibility Complex, Class I, E (Gb:M21533)	7.5	7 6	0	r,	n,	~	, ,	0 0	
M79463_s_at	8707W	7,00	PML Probable transcription factor PML		?	;	?	3		Ç.,	0.0	0.6
Ū22662 at	U22662	Ixra	Niclear orphan recentor I VD alaba menia	20.5	7.6	13.3	7	4.2	4.1	7.1	5.9	11.1
			Myleoid differentiation primary recond	1.5	ر. دز	9.0	34.8	11.4	9.4	8.4	3.1	10.9
U70451_at_	U70451	myd88	protein MyD88 mRNA	2.2		2.8	6.3	17.2	7.1	1,6	4	7
X82200_at_	X82200	staf50	Staf50 mRNA	10	7	13.1	7.8	15.4	16.7	2.1	3.1	18.1
HG2915. HT3059_f_at_ HT3059	HG2915. HT3059	hla	Major Histocompatibility Complex, Class I, E (Gb:M20022)	6.1	9	α:	ري (٥	c 4	α	α	'n	n n
S74017_at_	S74017	nrf2	Nrf2	3.8	6.3			C.1 (0)			0 00	0 0
Z35278_at_	235278	am12	PEBP2aC1 acute myeloid leukaemia mRNA	14.3	6.1	12:11	15.3	67	23	1 12	.1	0 0
U32849_at_	U32849	nmi	Hou mRNA	5.2	9	16.1	10.4	10.5	24.4	2.7	12.3	23.9
HG3597- HT3800_f_at_	HG3597- HT3800	hla	Major Histocompatibility Complex, Class I (Gb:X12432)	ć	5.8	6. 6.	ָםי נח	رغ 3	დ	-1	6,3	1 9

Figure 6F

			LYN Vives: 1 Yamapuchi sarcoma viral related	-	-			ŀ	ŀ			
M16038_at_	M16038	lyn	oncogene homolog	7.9	5.6	9.1	11.6	6.7	S	1.6	4 7	7 1
D32129_f_at_		hla-a	HLA-A MHC class I protein HLA-A (HLA-A28, B40, -Cw3)	α.	ر ب	7 4	ر 1	,	9	C	7	
U59863_at_	U59863	itraf	TRAF interacting protein I-TRAF mRNA	133	2 5	4.5	7 7	1 -	2,7	3,0		j (
HG4322. HT4592_at_	HG4322. HT4592	tubulinB	Tubulin, Beta	α α	, r	13.1	i	1 0	, u	1, 4	u c	9.0
U40369_rna1	9980771	÷	Spermidine/spermine N1-acetyltransferase		?		-	2.5	9	5	0.0	
M62403 s at	20001	381	ICEBM Inchilia like assumb factorial	5.	5.3	12.1	10.6	24 σ	9.8	6.3	4.1	8.1
	M62403	igfbp4	protein 4	15.9	r.	32.7	ά	7.	1.0	Ci U	-	0,01
X72755_at_	X72755	mig	Humig mRNA	3.2	5.2	683	59.4	5,7,3	2,85	0 0	17.7	1286
U67319_at_	U67319	casp7	Mch3 isoform alpha (Mch3) mRNA	1.9	4.7	12.2	3.5	0	9 1 9	7	7 (4	137
D00763_at_	D00763	psma4	GAPD Glyceraldehyde 3-phosphate dehydrogenase	6.1	4 5	,	C C	, c	2	,	2	2,0,0
D90209_at_	<u>090209</u>	atf4	ATF4 CAMP-dependent transcription factor ATF-4 (CREB2)	4 7	α) C	2 4	- 1	<u> </u>	0	11.2	0.0
000	0000		Protein tyrosine phosphatase PTPCAAX1		2		1			0.1	7:0	9.0
U48296_at_	048296	ptp4a1	(hPTPCAAX1) mRNA	2.4	3.7	14	c i	3.2	14.7	CI	2.3	6 9
D10522_at_	D10522	macs	MACS Myristoylated alanine-rich C.kinase substrate	4	3.0	10.2	7	0	000	, ,	0 0	5 1
740107 5 24	70107	0								5.7	3.6	0.1
HG4297.	HG4297.	- Kalso	galectin	6.1	3.1	2.6	17.1	12.1	3.7	2.7	5.7	4.6
at	HT4567	TCPC4	Transcriptional Coactivator Pc4	0	7.0	0	V	· ·	Ç	(•	(
AF006041_at	AF006041	> c			, ,	?	j		2	0.7	λ. Σ	y C.
HG4069.		3	da Sullaning Protein (DACA) main, partial cos	77	2.5	4.7	.1	3.6	ζ,	4.2	1.6	2.8
HT4339_s_at												
	HT4339	mcp1	Monocyte Chemotactic Protein 1	2.9	2.5	200	38.4	16.9	10.3	C	107	0
1	M59807	nk4	NATURAL KILLER CELLS PROTEIN 4 PRECURSOR	20.5	٥	100	=		-	1 (4. 0
D00762_at_	D00762	psma3	PROTEASOME COMPONENT C8	20.2	5,7	o €	1 C	0 0	1.1.1 1.0.0	0.0	201	10.5
L26247_at_	L26247	Sui1	RPL3 Ribosomal protein L3	3.7	12.4	4	100	2.7	2.1	U L	7 0	2.6
										-		1

AF001294 at												
		ldi	IPL (IPL) mRNA	7	,	v	~	0 0	0 0	C	,	7
X07743_at_	X07743	plek	PLECKSTRIN	9.7	2.1	5.7	13.9	10.7		3.6	1.6	5.6
D14826_s_at_ D14826	D14826	crem	CREM CAMP responsive element modulator	3.4	~	7	12.7	7	0			,
U90913_at_	U90913	unknown	Clone 23665 mRNA sequence	0	1.4	0	10	1.5	3	197	0 5	4.0
U26308_at_	D26308	blvrb	NADPH-flavin reductase	0	7	0	0	0.8	0			0
L13939_s_at_	L13939	ap1b1	Beta adaptin protein mRNA	0	1	0	0	0.7	0	0	0.5	10
	M23197	cd33	CD33 CD33 antigen (differentiation antigen)	0	Н	0	0.5	1.6	0	60	0	
U8/433_at_	U8/433	KI330246	KIAA0246 gene, partial cds	0	0.9	0	0	0.3	0		0.6	0
M22632_at_	M22632	got2	GOT2 Glutamic oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	0.1	60	c	c		c		c	
M93221_at_	M93221	mmr	M6PR Mannose receptor	0	6.0	0.3	0.8	8.0	0	1.2	0	ग्र
M59979_at_	M59979	cox1	P1GS1 Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	C	Č		-			,	-	
HG4312. HT4582 s at	HG4312.				S)	5	0.0	٥	5	5	ो
		TFliia	Transcription Factor Iiia	0	0			C		- 0		
X63422_at_	X63422	atp5d	ATP5D ATP synthase, H+ transporting, mitochondrial F1 complex delta subunit		3		5	7 (5	0	5	
	X78817	RhoGAP4	KIAA0131 gene, partial cds		7.0	5 0	1.4	\	5	0.6	0	0
at_	D13640	pp2c-like	PUTATIVE PROTEIN PHOSPHATASE 2C	0 0	1 0	5 C	0 0	110	5 0	5 0	0.1	0
D80001_at_	D80001	kiaa0179	KIAA0179 gene, partial cds	C	0	c		20	5 0	3 [1	0 -	<u>م</u> اد
D83597_at_	D83597	RP105	RP105	C	0	o	2 0	0 0	5 0	0.1	10	χij.
HG3730. HT4000_s_at HG3730.	HG3730.			-		-		9	0.0		2.0	4.1
	HT4000	syk	Tyrosine Kinase Syk	0	C	C	0	7	C		-	_
L36818_at	L36818	llogu!	INPPL1 Inositol polyphosphate phosphatase.			,		3	5		2	
L77730_at_	L77730	adora3	ADORA3 Adenosine receptor A3	3 C	5 6	5	0	0.0	0	0.7	6.0	0.3
M22638_at_	M22638	lyl1	LYL-1 protein gene	5 0	5 0	5 0	5 0	7.0	5	5	0.7	গ
				5	5	5	5	5	=	č	<u></u>	=

M95678_at_	M95678	plcb2	PLCB2 Phospholipase C, beta 2	0	0	0	0	0	0	0	0	0
U06631_at_	U06631	H326	IEF SSP 9502 mRNA	0	0	0.2	0.3	1.3	0	8.0	0	0
			Mitogen-responsive phosphoprotein (DOC.2)									
U53446_at_	U53446	dab2	mRNA	0	0	0	0	0	0	0	0.2	0
U70439_s_at												
	U70439	ssp29	PHAP12b protein	0	0	0	0.7	0.7	0	0	0.9	0.4
Z34897_at_	Z34897	hrh1	HRH1 Histamine receptor H1	0	0	0	0	0.3	0	0	9.0	0.1
Z50749_at_	250749	ppp1r7	Sds22-like mRNA	0	0	0	0.3	9.0	0	0.1	0.1	0

Figure 61

... esponse of Dendittic Cells to a...

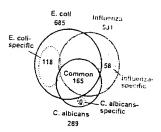


Figure 7A

Title. esponse of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

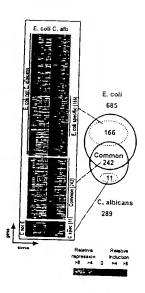


Figure 7B

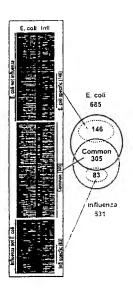


Figure 7C



Figure 7D



Figure 7E

Invo. .ors: Nir Hacohen, et al.

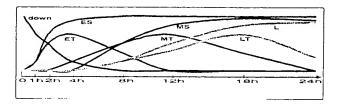


Figure 8A

Functional Category	E.A	ARLY	MIDD	LE	LA	TE
	Transient	Sustained	Transient	Sustained	Transient	· · ·
Phagocytosis		clathrin coat MMH		- Susanineo	11 at 1 sant 2	Sumained
Translation		ribosomal genes, sus t	wars		+	
innete immune response and inflammation	tnia, 85, mp1a, mp1b, a20, cox-2, oas2	#15, #8 histamineR cox1, rp105	il1m, ptor		 	
Cytoskeiston	macs, b-subulin,	sni	fctel f		 	
Apoptosis	pl	CIBC2, CBSD7	trail bol2-a1		-	
Receptors+sdhesion	ccr6	810ra cd33	471		cd97	nk4
Signaling	ptp4a1,lcp2, mknor, pkr.	ptp1b.pm1,traf1,lkbe dusp2, tes syk bra adenosineH.plcb2 lipk,ppp1r7,RhoGeo	mx1, mx2, dusp4, igfbp4, ecgt, igais9, myd88, lyn	adm, plaur, bst2 tnfaip6	-	7855
Transcription	ef1, topc4 nd2	ari4	statt, id7, id1, emi2, kt2, stat50	myl	 -	
rotein degradation			psma4. psma3		 	
F cell regulation		(cam1	rentes, slam, mcp1, inp10, mig		 	пср2
Cell stress and radical nomeostasia		neny1, ncf1	mi2a,hapi4,ron1	copt2, sod2,	milh	
Antigen presentation		pa28a	pa28b	hia, imp2, top1, tap2	<u> </u>	mp7, Na
Aigration to lymph node						cr7. cxcr4

Figure 8B

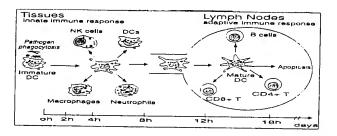


Figure 8C

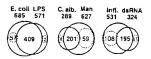


Figure 9A

In. Interes: Nir Hacohen, et al.

E. coli Man 685 627 E. coli daRNA 685 324

Figure 9B

Gene	GenBank accession no.	£. coti	C. albicans	Influenza
		Innate		
Neutrophil				
il8	Y00787	+++	+	+
gro 1	X54489	+++	+	+/~
gro2	M57731	. +++	+	+/-
gro3	×53800	++	+/-	+/~
Inflammation				
tnfa	402910	++	+	+
II16	(04500	+++	<u>.</u>	+
il6	X04602	++	+	
il 1a	M28983	+	Ŧ	+
gcsf	X03656		-	-
mip1b	M69203	++	-	-
mip3a/larc			+	++
	U64197	++	+/-	+/-
mip3b/elc	U77180	+	+/-	+/-
bf	L15702	+ +	+	+/-
Prostaglandin/leukotri	ene			
ptgir	D38128	++	+	+
ptger4a	L28175	_		+
cox2	U04€36	++	+	T
	001030		T	+
T cell: T _H 1		Adaptive		
il12b/p40	M65290	++		
itac			+	-
	U59286	+	+	++
mig	X72755	+	+	++
inp 10	X02530	+	+	+ +
ifnb1	V00535	+	-	+ +
ifna2	J00207	~	_	+
ifna 13	J00210	-	-	+++
ifna 14	V00533	-	_	+
ifna 16	M28585	_	_	+
rcell: T _H Z				
tarc	D43767	++		
mdc	U83171	T.T	+	+/-
	003171	т	+	+/-
Cell stimulation				
41bbL	U03398	++	_	+/-
slam	U33017	+++	+	+
cd86	U04343	+	+	+
icam 1	M24283	++	+	++
ebi3	L08187	++	+	
Antigen presentation			•	
b2m	300 10 5			
lmp 10		**		++
•	X7:874	+	+	+/-
cell				
ρbef	U02020	+++	+	÷
	lm	mune receptor		
il15ra	U31628	++	+/-	
il7r	M29696	++	+	Ŧ.
il2r	X01057	+		+
il4r			+/-	
	X52425	+	+	+/-
gmcsfr	X17648	+	+/-	_
il3r	D49410	+	+	-
41bb	U03397	+++	+/-	++
tnfr2	M32315	++	_	-
il13ra1	Y10659	++	++	_
cd155	M24406	+++		
cd83	Z11697	++	++	
•		ine transcription		7.7
nfkb p52	\$76638	++		
			+/-	+
nfkbp50	M58603	++	+/-	++
nfkb p65	L19067	+	+	+
nfkb_relB	M83221	+	+/-	-
stat\$a	U43185	++	+	

Figure 10A

Gene	GenBank	E. coli	C. albicans	1-0
	accession no.	E. COII	C. albicans	Influenz
stat4	L78440	++	+	
stat3	L29277	+	+	+/-
irf2	X15949	+		+/-
irf4	U52682	+	+/-	+/-
isgf3	M87503	+	+/-	
csda	M24069	++	-	+
		olysis and energy	_	-
eno1	M14328	+	_	ď
pk3	X56494	++		+/~
tpi	J04603	+	_	+/-
gys	J04501	+		- d
pgm1	M83088	+	+/-	ď
gk	×69886	+	+/-	-
pfkp	D25328	+		-
pgk1	V00572	4	-	+/-
g3pdh	X01677	·	_	+/-
ldh1	X02152		-	+/-
pgd	U30255	1	-	+/-
pgam1	J04173	+		+/-
hif1a	UZ2431	T	+	+
	042451	400000	-	+/-
nhibitor		Apoptosis		
pai2	M31551			
iex-1	S81914	++	-	-
tax1bp1	U33821	++	+	-
flip	AF005775	+	-	+/-
bag1	Z35491	++	+	+/-
ciap2	U37546	+	+	+/-
bcl2-a1	U29680	++	++	+
mcl1	L08246	++	+	+
tau	X56468	+,	-	+
	430408	+/-	+/-	++
ctivator				
casp4	U28014	++	+	+/-
nip3	U15174	++	+/-	_
trail	U37518	+	+	++
fas	X63717	+	+	+
casp5	U28015	+	-	+
bak1	U16811	+/-	+/-	+
pmaip1	D90070	+	-	++
casp10	U60519	+/-	+	+
		tors and receptors		
tgfa	λ70340	+	_	_
ndp	λ65724	+++		-
wnt5a	L20861	+++	+/-	-
activinba	X57579	+++	++	+
p2x4	AF000234	+	+	•
vdr	J03258	+	+/-	_
	Tissue	remodeling		
ттр9	J05070	+/-	+	_
mmp7	L22524	++		-
ттр3	X05232	+	_	_
mmp19	X92521	+	+/-	+/~
mmp14	Z48481	++		+/-
mmp12	L23808	++	- + - - -	+/-
mmp10	X07820	+		-
nmp1	X54925	+		-
ad1	U42408	<u>.</u>	_	+/
extl2	U76189	+/-	_	+/-
collagen-a 1	M55998	+	_	-/-
nr	X98085	+	_	+/-
	Cel	l stress		.,
nt1g	J03910	+++	+/-	+/_
	M10942	+++	+/-	1/-
nt1e				T/-
ntre rtg2	U72649	++	+/_	_
	U72649 L20941		+/-	_
tg2		++ ++ ++	+/- + +/-	-

Figure 10B

Gene	GenBank accession no	E. coli	C. albicans	influenza
ddit1	M60974	++	_	+/-
map3k4	D86968	++	+/-	+/-
mt1l	X76717	+ +	-	+/-
mt1h	×64177	+ +	+	+
mt2a	V00594	++	+	+
hspa1a	M11717	++	+/-	+ +
ninj1	U72661	++	+	++
sod2	×07834	++	+	+ +
atox1	U70660	+	+	-
hspa6	351757	+	+/-	-
krs1	U26424	+	+/-	-
mt1a	k01383	++	-	-
mt1f	M10943	+	-	-
rtp	D87953	++	+/-	-
cyp450db1	x07619	+	+/-	+/-
ast12	U46499	+	-	+/~
hsf4	D87673	+	-	+/-
hspa4	L12723	+	-	+/-
dusp1	×68277	+	-	+
mtf	¥78710	+	-	+
hsp70	U10284	+/-	-	+
hsp27	Z23090	-	+/-	+++
cbr1	104056	+/-	+	+
	In	nmune inhibitors		
тср1	\$69738	+	++	++
1110	U16720	++	-	-
hla-e	×.56841	-	-	+
gfrp	U7B190	ď	-	+
ido	M34455	++	+/-	+ +

Figure 10C

Interfeuchin Library (consideration) 105008		Gene Name	Gene Symbol	GBA	Score Ecoli	Score Candida	Score Indicates
Interleukin Beturation factor 2, cyctoxic L12B M65990 2449.1 7615.5 1	1520 s at	endothelin 1	FONT	IOEOOO	200	Score can	score_inituenza
High process	563_at	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic	1128	-	2770		113.7
State Microbia	- 1	lymphocyte maturation factor 2, p40)			2443		1.2
Brighton Brighton	4	Interleukin 8	=		0000		
Interfeukin 6 (riterferon, beta 2)	35822_at	B-factor, properdin	בונים	1	2300.		
SCYARO 1566.4 101.3 22 at pentaxin-related gene, rapidly induced by IL: 1 beta 1560.4 101.3 28.3 at pentaxin-related gene, rapidly induced by IL: 1 beta 150.2 at GRO2 oncogene 22.7 886.7 27.7 at small inducible cytokine subfamily B (Cys.X-Cys), member 11 150.4 101.5 101.5 at small inducible cytokine subfamily B (Cys.X-Cys), member 11 150.4 101.5 at cyclobydricase 100.5 101.5 101.5 at cyclobydricase 100.5 at cyclobydricase 100.5 at	38299_at	interleukin 6 (interferon, beta 2)	DL	L15/02	1635.	`	17.3
The protection of the protec	40385 at	Small inducible cytokine subfamily A (Ovs. Ovs.) mambar 30	1.0	X04430	1566.4		
Second Part	91636 at	OS JOSEPH CASTOS INCIDIOS ZO	SCYA20	U64197	943.4		
SCYGE Concogene CROS C	1491 at	Dentaxin-related gene rapidly induced by II 1 bota		AI652725	886.7		7
t tumor necrosis factor, alpha-inducible cytokine subfamily B (Cys-X-Cys), member 11 SCYB11 AF030514 655.1 844.8 77 tumor necrosis factor, alpha-inducible protein 27 174 AP030514 178.165 573.9 87.7 178.165 178.165 179.1 178.165 179.1 178.165 179.1 178.165 179.1 178.165 179.1 178.165 179.1 178.165 179.1 178.165 179.1 178.165 179.1 178.165 179.1 178.1 17		GROZ oncopene	PTX3	M31166	827.3		79
Interferon, beta Interferon Inter		small inducible cytokine subfamily B (Cyc. V.Cyc.)	GR02	M36820	785		
Interferon, alpha-inducible protein Control of the interferon is a protein Control of the interferon is a protein Control of the interferon is a protein Control of		tumor necrosis factor, aloba, induced protein 6	SCYB11	AF030514	655.1		7
BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-related protein AI BCL2-Related BCL2-Related A95.3 26.7 330.9	425 at	Interferon, alpha-inducible profein 27	INFAIP6	M31165	573.9		
SCA 192467 5478 65.2 192467 192467 54.8 65.2 192467 192	2002 s at	BCL2-related protein A1	IF127	X67325	565.5		
Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	37944 at	GTP cyclohydrolase 1 (dona.responsive dystonic)	BCL2A1	U27467	547.8		
and cyclooxygenase and cyclooxygenase and cyclooxygenase and cyclooxygenase and cyclooxygenase at the cy	1069 at	Drostaglandin-endoneroxide synthase 2 / prostaglandin 0 (1)	GCH1	U19523	505.4		
GRO1 oncogene (melanoma growth stimulating activity, alpha) GRO1 X54489 486.7 11.5 at hexabrachion (tenascin C, cytotactin)	1	and cyclooxygenase)	PTGS2	U04636	495.3		
GRO1 oncogene (melanoma growth stimulating activity, alpha) GRO1 AA641972 493 59 at hexabrachion (tenascin C, cytotactin)	77706_at			0.000			
at hexabrachion (tenascin C, cytotactin) description (tenascin C, cytotactin) at AF026941 486.7 11.5 at interfeukin 1, beta at 11.18 M15330 468.5 37.3 at interferon, beta 1, fibroblast 11.18 M15330 468.5 30.5 at interferon, beta 1, fibroblast 11.18 M15330 428.5 30.5 at small inducible cytokine subfamily A (Cys-Cys), member 19 SCYA19 AB000887 334.2 25.2 at small inducible cytokine subfamily A (Cys-Cys), member 19 SCYA19 AB000887 394.2 25.2 at interferon stimulated gene (20kD) MTIG J03910 370.2 20.5 at aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde ALDH9 A127172 326.5 3.6 at interferon-induced protein with tetratricopeptide repeats 2 IFIT2 M14660 320.5 145.5 at Stockhetical protein AB0 (calgranulin B) AA618602 280.5 16.5 at interferon, gamma	408_at			AA641972	493		
The example of the continuation (tenascin C, cytotactin)	38549_at		GROI	X54489	486.7	11	7.1
at interleukin 1, beta HXB X78565 474 9 37.3 at interferon, beta 1, fibroblast IL1B M15330 468.5 30.5 at small inducible cytokine subfamily A (Cys.Cys), member 19 SCYA19 AB000887 425 188.4 at interferon stimulated gene (20kD) MT1G J03910 370.2 25.2 at alrehyde dehydrogenase (20kD) MT1G J03910 370.2 20.5 at interferon-induced protein with tetratricopeptide repeats 2 at S100 calcium-binding protein A9 (calgranulin B) IFIT2 M14660 320.5 3.6 at hypothetical protein A (a) (calgranulin B) S100A9 AA618602 296.2 15.3 at interferon, gamma A (a) (calgranulin B)		hexabrachion (tenascin C. cytotactin)		AF026941	484.1		1149.
at small inducible cytokine subfamily A (Cys-Cys), member 19 at small inducible cytokine subfamily A (Cys-Cys), member 19 at interferon stimulated gene (20kD) at aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde at interferon-induced protein with tetratricopeptide repeats 2 at S100 calcium-binding protein A (Cys-Cys), member 19 at interferon-induced protein with tetratricopeptide repeats 2 at S100 calcium-binding protein A (Cys-Cys), member 19 at interferon-induced protein with tetratricopeptide repeats 2 at S100 calcium-binding protein A (Cys-Cys), member 19 at interferon-induced protein with tetratricopeptide repeats 2 at Interferon-induced protein A (Cys-Cys), member 19 at interferon-induced protein with tetratricopeptide repeats 2 at Interferon-induced protein A (Cys-Cys), member 19 and A (Cys-Cys), and A (Cys-Cys), and A (Cys-Cys) and A (Cys-Cys) and A (Cys-Cys) and			HXB	X/8565	474.9		1.
at small inducible cytokine subfamily A (Cys.Cys), member 19 at small inducible cytokine subfamily A (Cys.Cys), member 19 at interferon stimulated gene (20kD) at aldehydrogenase, E3 isozyme) at interferon-induced protein with tetratricopeptide repeats 2 at S100 calcium-binding protein A9 (calgranulin B) at hypothetical protein at interferon, gamma at interferon, g	1214 s at	14	118	M15330	468.5		
at small inducible cytokine subfamily A (Cys.Cys), member 19 SCYA19 A898319 425 188.4 at interferon stimulated gene (20kD) MTIG J03910 370.2 0.5 at aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme) ALDH9 A1127172 326.5 3.6 at interferon-induced protein with tetratricopeptide repeats 2 at S100 calcium-binding protein A9 (calgranulin B) IFIT2 M14660 320.5 145.5 at hypothetical protein AM000 W72424 313.3 0.5 at interferon, gamma IFING J00219 286.2 15.3 at interferon, gamma Interferon, alpha IL15RA AF035279 278 99.5	52615_at	٠.	IFNB1	V00535	433.9		540.3
metallothionein 1G 394.2 25.2 at interferon stimulated gene (20kD)	36067_at	Small inducible cytokine subfamily A (Cys. Cys. Cys.)		AA948319	425		
at interferon stimulated gene (20kD) at aldehydrogenase 9 (gamma-aminobutyraldehyde M 1G J03910 370.2 0.5 at aldehydrogenase, E3 isozyme) at chydrogenase, E3 isozyme) 320.2 200 10 at interferon-induced protein with tetratricopeptide repeats 2 at S100 calcium-binding protein A9 (calgranulin B) IFIT2 M14660 320.5 145.5 57 at hypothetical protein repeats 2 at interferon, gamma IFING M72424 313.3 0.5 15.3 1 at interferon, gamma IFING J00219 289.9 58.8 3 at interferon, gamma Interferon IL15RA AF035279 278 99.5 11	926_at	metallothionein 1G	SCYA19	AB000887	394.2		2.8
at dehyde dehydrogenase 9 (gamma-aminobutyraldehyde 15G20 U88964 327.2 200 at dehydrogenase, E3 isozyme) ALDH9 AI127172 326.5 3.6 3.6 at interferon-induced protein with tetratricopeptide repeats 2 at S100 calcium-binding protein A9 (calgranulin B) IFIT2 M14660 320.5 320.5 320.5 145.5 320.5 at hypothetical protein at hypothetical protein A9 (calgranulin B) AA618602 296.2 296.2 15.3 15.3 320.5 at interferon, gamma IFING J00219 289.9 58.8 58.8 at interferokin 15 receptor, alpha IL15RA AF035279 278 99.5 5	33304 at	interferon stimulated gene (20kD)	MrlG	J03910	370.2		1.5
dehydrogenase, E3 isozyme) ALDH9 A127172 326.5 3.6 interferon-induced protein with tetratricopeptide repeats 2 IFIT2 M14660 320.5 145.5 \$100 calcium-binding protein A9 (calgranulin B) \$100A9 W72424 313.3 0.5 hypothetical protein interferon, gamma Interferon, gamma IFNG J00219 289.9 58.8 interferon, alpha IL15RA AF035279 278 99.5	53579 at	aldehyde dehydrogenase 9 (gamma.aminobuturaldahuda	18620	U88964	327.2		103.7
Interferon-Induced protein with tetratricopeptide repeats 2 IFIT2 M14660 320.5 145.5 145.5 145.5 1400 calcium-binding protein A9 (calgranulin B) S100A9 W72424 313.3 0.5 15.3	2 000	dehydrogenase, E3 isozyme)	ALDH9	A1127172	326.5		2.1
S100A9 W72424 313.3 0.5 Interleukin 15 receptor, alpha IL15RA AF035279 278 99.5	41471 at	S100 calairm binding by Arthur tetratricopeptide repeats 2	IFIT2	M14660	320.5		
AA618602 296.2 15.3 Interferon, gamma Interleukin 15 receptor, alpha IL15RA AF035279 278 99.5 1	43853 at	hypothatical protein A9 (calgranulin B)	S100A9	W72424	313.3		
at interleukin 15 receptor, alpha 158.8 158.8 158.8 15.8 15.8 15.8 15.8 1	1021 at	interferon gamma		AA618602	296.2	1	186
IL15RA AF035279 278 99.5 1	41677 at	interleukin 15 recentor alaka	IFNG	J00219	6'682		36.2
	10 / /01	miterieumii 10 receptor, alpha	IL15RA	AF035279	278		1117

41531_at	transmembrane 4 superfamily member 1	TMACET	ALAAEAC.	010		
1097 c at		T JOHIAOL T	M443401	8/7	0.8	
1010	מומווים (ב.כ וווסנוו) ופנפויוס (CCR7	L31584	276.6	100.6	88.3
25577 24			AI970348	265	32.3	2 5
355//_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7	SERPINB7	AF027866	262.3	26.1	5.6
37219_at	monokine induced by gamma interferon	C. S.	23505			
34929 at	1	פוואו		201.6	704.2	182.7
2205E 24	integration 100 keeps recepted superiorities in the recepted to	INFRSF8	M83554	255.9	0	0.8
22327	interieuriii 12A (natural Riller cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)	IL12A	M65291	250.2	18.4	14.6
41096_at	S100 calcium-binding protein A8 (calgranulin A)	C10048	100110	,		
41468_at	T cell receptor gamma locus	STOCK OF THE PARTY	-	249.4	5	0.0
35000_at	tumor necrosis factor (ligand) superfamily, member 9	TNECED	M30694	245.1	200	
33705_at	phosphodiesterase 4B. cAMP-specific (dunce (Drospobile) homolog	0.00	000000	232.3	5.9	3.1
	phosphodiesterase E4)	PUE4B	L209/1	232.3	51.8	92.7
1403_s_at	small inducible cytokine A5 (RANTES)	SCYAS	M21121	2221		
48864_at	Interferon, alpha-inducible protein 27	70131	A100104E	232.1	30.0	200.3
33965 at	Small inducible cytokine A1 (1.309 homologous to mouse Too 3)	12117	A1991845	216.4	274.9	141.4
36116 at	thyroid hormone recentor interactor 10	SCYAI	M57506	216.3	0	7.8
1400 at		TRIP10	AJ000414	215.9	29.7	7
47855 at	inferlenting actor 2 (granulocyte-macrophage)	CSF2	M13207	210.9	0.1	
£1371 2	mitericanni 19	IL19	AA151656	205.5	0	0
1052 24	Cyclinic Diliging protein 1		AA555023	204	148	479 5
22700 at	fulfior flecrosis factor (TNF superfamily, member 2)	TNF	X02910	201.2	47.5	57
33709 at	Small Inducible cytokine A5 (RANTES)	SCYAS	AF088219	191 5	6.4.1	
45164 at	19A24 protein		W74027	189 7	74.5	2.1 2.0 E
02330 at			AI075407	185.9	169.1	1219
20504 at			AA947472	182.2	52	423.6
33513 24	interieron-induced protein with tetratricopeptide repeats 4	IFIT4	AF026939	179.4	153.2	1486
58018 24	Signaming lymphocytic activation molecule	SLAM	U33017	178.3	14.3	
30310 at			AA210892	176.1	VC	0 70
41104_at	small inducible cytokine B subfamily (Cys-X-Cys motif), member 13 (B-	SCYB13	AF044197	171.2	0	2.3
1334_s_at	colony stimulating factor 3 (granulocyte)	CCE3	YOSEEC	1631		
57761_at		5	A03030	/01	7.7	7.2
40159 r at	neutrophil cytosolic factor 1 (47kh chronic granulomatous disease	1014	AIS13233	191	90.6	33.7
	(autosomal 1)	NC-1	M55067	160.7	91	140.3
		_	_	_		_

31623_f_at	\Box	MTIA	X K01383	1603	JE 00	0,0
40323 at	CD38 antigen (p45)	CD38	1	160.1	10.00	107
41048 at	phorbol-12-myristate-13-acetate-induced protein 1	PMAIP	L	1001	102.0	18.5
1107_s_at	interferon-stimulated protein, 15 kDa		1	133.0	2.0	408.5
33364 at	similar to rat myomegalin		CC/51M	159	86.3	213.8
431 at	Small inducible cytokine subfamily B (Cyc. V.C.)			156	28.9	2.9
	RNA helicase	SCYB10	_1	152	390	545.7
49076 at	SGRE protein Interleukin 23 n.10 minit		A/807018	151.1	63	36.2
41870 at	ling type, cell membrane accorded along		AI796983	147.7	0.3	2.3
34666 at	superoxide dismitase 2 mitashandia		4	143.7	0	12
89884 at	metallothiopain 2A	SODZ	- 1	141.3	63.1	42.3
32114 s at	_	MT2A	AI991852	138	45.1	82.3
48919 at	notassium inwardly	ADORA2A		137.9	31	27.9
51725 at	recession man of receiping chainner, subjamily J, member 2	KCNJZ	_1	130	11.2	13.1
63335 at	Sorting nevin 10		AA521246	129.3	35.4	18
48753 at	6		AI285531	127.4	55.8	74.2
53508 at			N57259	126	7.9	14.7
63628 at	interletikin 7 recentor		AI247103	124.7	84.6	27.2
46468 at		IL7R		123.1	41.5	20.00
1548 c at	otarikin 10		AI735586	122.3	4.7	000
70458 : 24	ייובי ופתעוון דס	11.10		121.9	43	3.0
			AI654525	120.3	1743	1070
36174 24	Constitution of the contraction		AW014801	120.2	4	10.0
84995 at	macioniage invisionialed againne-rich C Kinase substrate		X70326	119.6	44.8	42
50978 at	Outstive correted linear Land		AA769482	117.4	12.2	9 9
609 f at	metallothionein 1D (functional)	hfjx	AI338625	117.2	3.8	3
51972 at	ubiquitin specific professor 10	MT1B	M13485	116.3	11.1	20 1
51546 at	and a second processes to	USP18	٦.	114.4	158.3	218
63066 at			AI498361	113.1	77.9	73.9
675 at	- 1 -		AA001735	113	12.6	96
71839 at	Transport induced transporter protein 1 (9.27)	IFITM1	J04164	112.7	140.9	1736
50827 at			AA251131	111.4	76.5	82.8
58957 at	hynothetical protain El 1206237		AW001213	109.2	52.4	9 9
36070 at			A1620475	108.9	42.7	283
33382 24	וויסוטן לבודייון וויסוטן לבודייון וויסוטן לבודייון וויסוטן לבודייון		AL049389	108.4	0	2.9
33505_at	Iddinin 1	LAD1	U42408	107.2	24	4.4

eining ion transport regulator 6	FXYD6	1 1	103.8	73.3	28.3
	CAIZ		103	0	
		AI819198	102.7	8.4	7.6
		`	102.4	C	, ,
	IL7R		102.3	30.8	25.20
subfamily VIIB (oxysterol 7 alpha-hydroxylase)	MT1F	_	101.8	13.1	32.6
, (oc) (oc) (ac)	CYP/B1	AF029403	99.5	17.6	1.2
zio dioxygenase	ODNI	AI302268	99.5	8 60	000
		AA932068	99.3	55.6	39.3
		AA678425	99.2	1.2	0.0
subfamily XXVIIB (25-hydroxyvitamin D.1-alpha.	Larcavo	AA766831	98.3	63.3	41.1
	10/2/0		98.2	17.2	2.9
		₩	98.2	26	9 9
	TRAF1		97.1	27	0.0
		. 1	96.4	20.4	0.0
	AKAP2		95.8	38.5	200
		AL047300	94.9	18.8	43.7
		AA873008	94.5	63.3	0.0
ytokine; neurotrophin-1/B-cell stimulating factor 3		A1936516	93.7	1.9	16.9
		AI040033	92.7	4.7	4
	MT2A	AI547258	92.5	37.3	. 50
GTP-binding protein	CLCNKB	230644	92.3	1	74.1
	BLR1	X68149	92	0.2	11 5
		AA733119	92	11.1	286
2,3 dioxygenase	HILM	R93527	91.6	9.4	26.1
kinase/fructose-2,6-biphosphatase 3	ONI	M34455	91.3	36.9	37.7
associated membrane glycoprotein	ZTKT B3	AI765775	91	6.2	11.2
metallothionein 3 (growth inhibitory factor (neurofronhic))		AB013924	6.06	50.6	16.1
growth arrest and DNA damage-inducible, alpha	MT3	M93311	90.7	15.1	10.1
(interstitial collagenase)	GADD45A	M60974	88.7	5	2.2
(App. 1)	MMFI	M13509	87.8	0	0.3
		AI/4205/	87.7	54.8	56

37407_s_at		MYH11	AF013570	87	17.5	7
	DKFZP586G0522 protein		AW008790	85.4	4.8	52.3
54982_at	pellino (Drosophila) homolog 1	PEL11	AL043980	85.4	6.2	54.5
45237 at	superoxide dismutase 2, mitochondrial	SODZ		84.4	32.6	17.7
38570_at	major histocompatibility complex, class II, DO beta	HLA.DOB	ŧ	84.2	55.5	30.1
91313_at			AA131041	84	77.5	157.1
84893_at			A1446168	83.4	119.5	160.2
1527_s_at			U50527	82.5	50.7	14.2
32775_r_at	phospholipid scramblase 1	PLSCR1	AB006746	81.8	68.4	32.6
1549_s_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4	SERPINB4	U19557	81.2	0.7	1.1
40679_at	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	SLC6A12	U27699	80.9	46.2	10.4
1693_s_at	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	TIMPI	D11139	79.8	-	0.0
60032_at			AI984197	79	0.0	0
36130_f_at	metallothionein 1E (functional)	MT1E	R92331	78.7	4.6	8
54594_at	KIAA0668 protein		AA009571	78.6	23.3	31.3
57711_at			AA576959	78.3	9.6	0.7
35844 at	syndecan 4 (amphiglycan, ryudocan)	SDC4	D79206	77.4	5.8	20.7
85561_at			AL079435	76.5	7.7	9.0
	KIAA0963 protein		AB023180	75.3	33.5	1.2
40687 at	gap junction protein, alpha 4, 37kD (connevin 37)	GJA4	M96789	74	13.5	4.2
44126_at			W28501	73.5	28.6	16.2
69142_at	- 1		A1635522	72.4	7.8	8.6
69818_at	hypothetical protein FLJ22318		AI250747	72.4	0	0
31540 at	tor superfamily, mem	TNFRSF9	U03397	72.27	7.8	19.5
35735 at	guanylate binding protein 1, interferon inducible, 67kD	GBP1	M55542	72.1	49.4	49.8
90958_at			A1660377	71.6	38.3	4.8
71013_at	interleukin-1 homolog 1		AI814314	71.5	4.1	2.3
39224_at	KIAA0580 protein		AB011152	71.4	27.4	2
41446 f_at	RNA helicase related protein		H68340	71.4	10.1	219
38111_at	chondroitin sulfate proteoglycan 2 (versican)	CSPG2	X15998	71.2	4.1	27.4
47483_at	similar to rat myomegalin		AI659612	71.1	8.6	11.8
50746 at			AA897516	71	20 1	430

42204 at						
668_s_at	matrix metalloproteinase 7 (matrilysin utering)			7.07	4.8	2
73455_f_at		MMP7	_	9.07	1.3	1
63675 at			H72723	70.4	82	1 X
37643 at	tumor necrosis factor recentor suportamily		1	69.2	, -	1.0
44513 at	adpending, mernoer b	TNFRSF6	X63717	69	174	2.1
39114_at	decidual protein induced by progesterons		AI760613	68.8	812	36.6
37641_at	interferon induced, hepatifis C. associated misratishings		AB022718	9.89	26.6	28.6
			D28915	68.5	51.1	43.6
49438_at						
32026_s_at	PDZ domain containing guanine nucleotide exchange factor/GFF)1		A1535730	68.4	21	15.8
63769 at	1/17/10/10/10		AB002311	68.3	25.1	16.6
71174 r at	K14A1682 2542iz		AI749656	67.8	100	
56070 21	lient portwell		A1921158	2,00	7 1	14.3
000 at	neparan sulfate (glucosamine) 3.0-sulfotransferase 3B1	HS3ST3B1	44780067	0/10	81.9	115.6
1000 at	matrix metalloproteinase 10 (stromelysin 2)	MMP10	000000	0.70	2.5	34.8
4/51/_at		OT IIAIIAI	07870	6/.5	2.4	3.6
1715_at	tumor necrosis factor (ligand) superfamily member 10		AA639645	67.1	51.4	33
59185 at	1	INFSF10	U37518	8.99	179.7	463.3
41475_at	ninjurin 1		AA926689	66.3	α.	200
595_at	tumor necrosis factor, alpha indirect extrained	NINJ1	U91512	65.2	35.7	7.7
1036_at	interleukin 15	TNFAIP3		65.1	11 4	76.7
77244_at	bHLH factor Hes4	11.15	- 1	64.7	16.6	20.02
286_at	H2A histone family, member 0		AI380603	64.7	15.4	22.5
38326_at	נוס ו	HZAFO	L19779	64.6	21	57.1
51015 at			M69199	64.6	20.8	6.5
75014 i at	KIAA1533 protein		AI655467	64.4	21.6	4 4
	tumor necrosis factor, alpha-induced protein 2		AW006583	64.4	37.7	3.6
at	NK homeobox (Drosophila) family 3 A	TNFAIP2	M92357	63.8	17.8	000
		NKX3A	AI557413	63.8	000	10.1
1717 s at	baculoviral IAP reneat containing 3		AF043129	63.4	α [ς	10.7
1		BIRC3	U45878	63.1	47.7	10.3
Г	hypothetical protein El 12076A		AA705165	62.7	3.6	7.02
39221 at	leukocyte imminoglobilin like receptor supfamily B Kinth The		AI684508	62.7	4.1	, , ,
'	ITIM domains), member 2	LILRB2	AF004231	62.6	6.1	17.8

Vets avian enghnoblastosis vizirs 505 and 1		AI823649	62	51.5	7.87
melanoma differentiation associated	ETS2		61.9	3.6	19.7
novel Ras family protein		AA134958	61.8	41.7	0.00
		AA133248	61.7	3.8	24.3
		A1244908	61.5	3.8	4.4
myxovirus (influenza) resistance 2 homolog of		AI928513	61.2	14.4	
	MX2	M30818	61.1	61	69
CD80 antigen (CD28 antigen ligand 1 B7 1 antigen)		Y13323	61	1	1.5
Snail 1 (drosophila homolog) zinc finger protein	CD80	M27533	61	26.5	15.7
	SNAI1	AA613301	8.09	0.3	2
NY-REN-18 antigen		AI525592	59.9	9.0	0.5
		AA587445	59.8	23.1	10
		AA115266	59.2	45	5.1
tryptophanyl-tRNA synthetase		AA127641	58.7	2.4	7.4
	WARS	X59892	58.2	45.4	45.6
	CCNA1	U66838	57.6	16	70.3
brain acid-soluble protein 1		AI347073	57.3	2.1	116
	BASP1	AA135683	56.9	17.8	
DKFZP586C1619 protein		AA776412	56.8	24.4	33.3
		AL050374	56.3	9.1	10.6
	GBP2	M55543	55.5	23.9	6 1
testis zinc finger protein		AI082042	55.4	14.7	1.9
annexin A8		AI798147	55.2	2.9	200
solute carrier family 1 (plial high affinity plutamate trans-	ANXA8	X16662	55.1	0	80
	SLC1A2	U01824	55	0	1.2
CASP8 and FADD-like apoptosis regulator					
signal transducer and activator of transcription 4	CTLAR	Ar 005//5	54.9	24.7	5.8
nuclear factor of kappa light polypeptide gene enhancer in B cells 1	SIAIA	L/8440	54.6	10.3	5.9
(p105)	INLYE	M58603	54.5	18.3	18
		41084027			
	MX2	AWOO1846	54.1	57.5	0
mitogen activated protein kinase kinase kinase 8	MAPAKR	014407	40 5	54.3	70.9
		A1246590	03.0	U.4	11.2
EH domain containing 1	1000	000000	0.5.0	8.9	10.2
		170001	2	(

64603_at			NA7335	537	F 7	60
37014 at	Imyxovirus (influenza) resistance 1. homolog of murine (interferon.	IVA	W22000	13.7	7.00	2.8
	inducible protein p78)	7.71	3000	0.5.0	65.3	2.60
649_s_at	chemokine (C.X.C motif), receptor 4 (fusin)	CXCRA	106797	5.3 E	70%	7
74633 at	tumor necrosis factor, alpha induced protein 2	TNEAIDS	A1005430	0.00	7 1	95
63382 at	interferon consensus sequence binding protein 1	100001	A1072004	03.0	12.5	0.1
47287 at		1000	AIA75472	03.0	35.7	χ.
36927 at	hybothetical protein expressed in osteoblast		A14/34/3	23.5	2.5	6.9
48676 at			AB000115	53.4	60.4	83.5
2719E at			AL040192	53.3	Ó	0
37.103_at	serine (or cysteine) proteinase innibitor, clade B (ovalbumin), member	SERPINB2	Y00630	52.6	0	0
40670_at	kynureninase (L·kynurenine hydrolase)	KYNU	AI148772	52.5	136	7.0
37137_at	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine	GZMB	M17016	523		0.41
	esterase 1)) !			1.0	0.01
80773_at			H15073	ν.	0	001
48025_at	NCK adaptor protein 2	NCK2	A1934552	51.5		15.9
63780_at	hypothetical protein FLJ11259		AA814195	21.7	200	6.0
222_at	exostoses (multiple) 1	EVT1	003063	1.00	0.61	7,07
37451 at			37,303,9	20.3	2	8.6
	VIAA1021 protein		AL109695	50.6	4.8	5.8
33143 at	NIAA1U31 protein		A1138605	50.6	24.1	4.6
24.25 at	Interieron regulatory factor 1	IRF1	L05072	50.6	35.4	27.2
34435_at		AQP9	AB008775	50.5	15.3	3.4
32814 at	interferon induced protein with tetratricopeptide repeats 1	IFIT1	M24594	50.5	70.1	76.97
3//16 at		MOX2	X05323	50.5	7	C
1/35 at	Insulin-like growth factor binding protein 6	IGFBP6	M62402	50.4	0	104.8
60527 at			AI016542	50.4	9.1	4.4
02332 at			AI821392	20	7	1 7
48505 at	= 1		AI358871	49.8	6.0	0.4
41/45_at	Interferon induced transmembrane protein 3 (1.8U)	IFITM3	X57352	49.6	74	6 69
510/5_at	pannexin 1	PANX1	AA115920	49.5	3.9	
3252/ at	$\overline{}$		AI381790	49.3	1.4	1 4
36412_s_at	interferon regulato	IRF7	U53831	49.2	415	54 1
35985 at	A kinase (PRKA) anchor protein 2	AKAP2	AB023137	49		24 6
/0460_t_at			AI654525	489	000	757

Figure 11H

	OCIN 11401 A01003	48.8	2.5	2.4
S100 calcium-binding protein A12 (calgranulin C)	S100A12 D83664	4 48 3	C	, 9
tullor liecrosis ractor receptor superfamily, member 1B	TNFRSF1B M32315		3 4	0.0
	AI830607	4	333	3,7
Carbohydrate (N. acetylali cacamina 6 00 - 1611	AI916948	18 46.9	13.9	44
receptor interacting sering threating binary	CHST7 N64774	4 46.8	23.4	1
regulator of Garotein signallian 16	RIPK2 AF117829	29 46.7	26.8	104 9
prostaglandin F evotbase	- 1	6 46.6	1.8	
retinoic acid induced 3		0 46.5	2	
	RAI3 A1990405)5 46.5	0.2	000
	A1129310	10 45.7	0.8	800
	AA149736	36 45.6	8.7	10.3
	A1161358	45.6	13.2	521
dual snecificity phosphatase E	AA442239	45.4	0.4	7 7
chataca	-	45	12.1	10.5
T proposition of the control of the	DUSP1 X68277	7 44.6	0.0	20.7
	AI590710	0 44.5	9.7	31
dual adaptor of phosphotyrosine and 3 phosphointil	W37880	0 43.8	0.1	
n FI 123375	AF150266	96 43.8	9.5	
	AI818808	8 43.4	18.3	62
Solute carrier family 1 (glist bigh afficity, glist		35 43.3	3.1	17
member 3	SLC1A3 W26838		7.2	4.8
erythrocyte membrane protein band 7.2 (stomatin)	FPR70 Y8E116			
plastin 3 (Tisoform)	1	0	21	21.9
	_[`	3 46.8	2.1	68.4
adenylate kinase 3	⋖		1.5	1.7
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase polyneptide 5	_1.		6.8	
applied for the state of the st	D4GALID AA133969	42.5	9.3	9.5
prostaglandin E synthase				
	r1GES AFU10316		0	1.2
KIAA1170 protein	N95225	42.1	4.1	808
	C14031	42.1	18.4	7.2
STAT induced STAT inhibitor 3	Al337136	6 42	18.5	15.7
_	11000011			

Figure 111

4		TIAM2	AI126294	41.6	25.5	8 9
Jan Serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1	e G (C1 inhibitor),	SERPING1	X54486	41.5	67.8	17.1
_			000:00:0			
48822_s_at adenylate kinase 3			_1.	41.5	10.4	
_	o Lineary	AK3	_1.	41.5	6.1	0.5
KIAA0172 protein	od Milase 4	MAP4K4	AB014587	41.4	2.7	9.0
			D79994	41.4	3.6	10.9
pre-B-cell colony.e			AB006624	41.3	5	5
Γ				41	8.3	16.3
		AIM2		40.9	18.1	16
58737 at			AA194980	40.7	35.3	101
44640 at			N27438	40.2	2.4	43
64333 s at lovrophosphatase (inorganic)			. 1	40.2	11.6	8.4
adenosine deaming		dd	٩١	39.9	10.9	5
Γ		ADA	X02994	39.7	4.1	3.2
GRO3 oncogene			٩	39.4	1.8	
Γ		GRO3		39.3	1.9	1.4
48014 at			C14904	39.3	13	22.8
38388 at [2,5] olippadenvlate synthetase 1 (40 45 km)			N54957	38.8	5.2	
inhibin, beta A (activin A activin	(chitacont	OAS1	M11810	38.7	54	103.7
at	(application)	INHBA	103634	38.6	4.9	5
54147_at pyruvate dehydrogenase kinase isoenzyme /			AI963642	38.5	33.4	11.9
Γ		PDK4	AI763378	38.3	4.5	9.0
			Al347001	38.2	44.7	11.3
68652_at			AF070570	38.1	14.3	8.7
67259_at			AI431778	38	3.8	9.0
51104_at			R56235	37.9	0	6.3
59283_at hypothetical protein FI 120035			A1937446	37.7	10.5	22.6
28kD interferon re-			AL042790	37.5	24.6	11.4
H2B histone family			AA651720	37.5	34	40
at JM5 protein		н2вғв	AJ223353	37.4	13.7	16.1
1			Z78315	37.4	27.2	
41045 at Iserreted and transmembrane 1			AA580047	37.3	29.6	43.2
ŧ		SECTM1	U77643	37.2	67.4	10.4
7	•	C 0	MODOCOM	1		

139070 at	Singed (Drosophila) like (sea urchin fascin homotog like)	INO	1102067	0 36	1200	1,0
34476 r at	enirequin	SINC	003037	30.9	73.0	31
38380 24	2' S' oligoadenylate synthetase 1 (A) AS VO)	200	20000	20.5	0.0	17.0
30305 at	2,3 -UIRUAUEIIYIALE SYIIIIIEIASE 1 (40-40 KD)	OASI	X04371	36.5	71.8	35
90421_at	conserved gene amplified in osteosarcoma		AA633203	36.5	35.1	8.6
1343_s_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3	SERPINB3	96899S	36.4	0	0.3
48331_at			AL041454	36.4	m	16.7
69876_at			AI825713	36.1	32.1	60.3
55634_at			AI040355	35.9	21	3.9
34916 s_at	tumor necrosis factor receptor superfamily, member 4	TNFRSF4	S76792	35.7	20.3	7.8
43456_at			AI299952	35.5	2.6	0
62214_at	hypothetical protein FLJ11354		A1583960	35.5	28.7	23.8
52729_at	CD44 antigen (homing function and Indian blood group system)	CD44	AA037772	35.3	3.3	9.0
45256_at	pre-B-cell colony-enhancing factor		AI271460	35.1	7.1	33.4
54823_at			AI651594	35.1	30	5.8
56169_at			W55852	35	2.2	29.4
64170_at			AI609751	35	3.2	0.5
32686_at	prostaglandin E receptor 3 (subtype EP3)	PTGEP3	96098G	34.9	C1 C1:2	2.2
			AI337231	34.9	10.4	1.6
53100 at	hypothetical protein FLJ10307		AA747448	34.8	5.3	1.3
46133_at	- 1		W60263	34.8	34.9	12.6
33305_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	SERPINB1	M93056	34.7	9.2	0
33730_at	retinoic acid induced 3	RAI3	AF095448	34.7		4.6
40153_at	ATP binding cassette, sub-family B (MDR/TAP), member 2	ABCB2	X57522	34.3	33	40.6
37294_at	B-cell translocation gene 1, anti-proliferative	BTG1	X61123	34.3	15.2	000
36609_at	solute carrier family 1 (glial high affinity glutamate transporter). member 3	SLC1A3	D26443	34.2	5.8	3.4
51550_at			AI681179	34	13.3	22 5
54769_at			AA203416	33.9		14.7
52255_s_at		COL5A3	AI984221	33.9	2.1	3.9
37305_at	enhancer of zeste (Drosophila) homolog 2	EZH2	U61145	33.6	10.9	2.4
53983_at	hypothetical protein PR02714		AI139975	33.6	13.8	0.3
55353_at			AA760977	33.6	6.9	9
848_at	TNF receptor associated factor 1	TRAFI	U19261	33.5	6.6	5.5

52183 at			H38110	33.5	9.1	5
73972 at			AA243659	33.5	15.4	188
1000			A1863446	33.1	17.3	0.00
52085 at			AA210833	33.1	2,7,5	200
30/60_at	Clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	CLU	M25915	32.9	5	8.7
59365_at			1			
56922_at			U59637	32.9	6.9	4.
51026_at	hypothetical protein PRO0813		AA211158	32.7	18.2	35.
47484 at			N30257	32.6	3.3	
1445 at	chemokine (C.C motif) recentor like 2		H17489	32.5	22.9	8.8
36543 at	Coagulation factor III (thrombonlastin tissue factor)	CCRLZ	٩	32.3	6.4	3.6
Γ		F3		32.3	6.6	4.3
	pim-2 oncogene		℄	32.2	3.6	3.6
41635_at	Wilms' tumour 1-associating protein	FINE	1	32	15.7	11.
63342_at	hypothetical protein		D14661	31.6	6.1	18.
		nypoprotein	AA150254	31.6	2.4	23.4
47113 at	Kruppel·like factor 5 (intestinal)		- !	31.5	0.1	14
	탈	KLF5	- 1	31.5	41.2	7.2
	glutamate decarboxylase 1 (brain, 67kD)		AB00/447	31.4	36.2	36.8
		GADI	AL042399	31.4	5	
	regulator of G-protein signalling 1		AI199418	31.2	19.8	24.7
Г	glycoprotein Ib (platelet), alpha polypentida	KGS1	S59049	31	46.9	16.7
	zinc finger protein 259	GP1BA	J02940	30.9	9.1	9.4
		ZNF259	AF019767	30.5	2.7	
Γ	small inducible cytokine Ad (homologous to manage Min 11)		AI655289	30.5	5.2	0.7
		SCYA4	J04130	30.3	13.4	13.3
60835_at			R37337	30.1	6.4	3.6
47076_at			AI831561	30.1	6	5.6
1	H2A histone family member G		W87690	29.9	2.6	3.4
	in FI 11130	HZAFG	280776	29.8	16.1	30.5
	ubiquinol-cytochrome c requetase (5 41/0) c.:his		AA854113	29.8	3.8	
Γ	Ithinitin-conjugating enzyme F21 &		AI480328	29.8	8.6	8.6
Ī	יים לייונל ויים מייי	UBEZLE	AA883502	29.7	38.7	20
			100000	1 00		

49339_s_at	49339 s_at reticulocalbin 1, EF-hand calcium binding domain	1400	L			
47318 at		KCN	_	29.7	11.9	6.9
			A1949175	29.7	5.4	1.3
38997 21	STAT induced STAT inhibitario		AA902134	29.7	55.3	39 5
53588 at	STAL INDUCED STAL INDIDITOR:Z		AF037989	29.2	6.3	α.
190 of at			A1967984	29.2	4.3	0.1
2007E 24	iluciear receptor subtamily 4, group A, member 3	NR4A3	L	29.1	24.6	25.3
4000 at			A1989871	29 1	26.0	12.0
40362_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NFKB2	<u> </u>	29	11.4	5.2
67764 r at			0000			
44729_at	hypothetical protein FLJ13855		AA0048/9	29	4.4	11.8
32863_at	similar to calcium/calmodulin dependent protein kingses		AI02/524	28.8	10.5	13.3
53010 at	care in the care i		AL023754	28.7	7.3	1.9
36139 at	DKFZP586G0522 protein		AI809925	28.6	4.2	29.8
1953 at	vascular endothelial growth factor			28.5	1.5	20.1
56999 at		VEGF	~1	28.4	6.2	7.2
53799 at	hypothetical protein similar to maise Desira		AI625959	28.4	11	3.4
89202 at			AA628434	28.3	2	0
40098 at	EH domain containing 1		AI347361	28.3	30.4	9.1
58941 at		EHD1	AF001434	28.1	9.0	3.9
42769 at	pridict Company of the Company of th		AI765967	28.1	24.1	11.5
81887 at			N46441	27.9	0.7	0.4
	RAD50 (S. cerevisiae) homolog		- 1	27.8	10.9	33.8
51278 at		KAUSO	`	27.8	17.5	30.9
49670 at			AI139543	27.7	2.8	2.6
37442_at			W96225	27.7	2.1	0
40268_at	FOS-like antigen 2		AL050378	27.6	5	11.8
47971_at	ferritin, heavy polypeptide 1	FOSEZ	X16706	27.6	1.7	2.1
54491_at		LHI	T92243	27.6	6.3	0.8
41872_at	deafness, autosomal dominant 5		AA043562	27.5	ĸ	3.1
48105_at		UFNAS	AF073308	27.4	24	1.3
63380_at	hypothetical protein DKFZp434P0531		AI6/2094	27.4	6.5	0.9
56500_at			AI732727	27.4	5.9	4.9
65628 at			AI241578	27.4	3.9	0
38617 at	LIM domain kinase 2		AW023171	27.4	1.6	3.4
		∑ 2 2 2 3	D45906	27.3	~ ~	,

34777_at	1 ~ 1	ADM	014874	0.20	0	ŗ
38/83_at	mucin 1, transmembrane	I CI I M	1	27.70	0.0	7.1
58873_at	neuropilin 2	COCIA	L	2.72	35.1	3.8
49249 s at	$\overline{}$	ואאו		27.2	18.8	1.1
44115 at	+		AA533079	27.1	2.8	2.5
87497 4 24	ייז איני ביינימן איניינימן אייינימן איניינימן איינימן איניינימן איינימן איינימן איניינימן איינימן	AA486504	27.1	3.1	a c	
-1 '			AI832016	27	21.1	10.0
20041 at	IIVer-expressed antimicrobial peptide		A1937227	70	101	/:/
52905_at	Rag C protein		0107010	7 2 2	1.0.1	7.5
86581_r_at			M27,3036	26.9	14.5	19.7
39263 at	2.5'oligoadenvlate synthetase 2		~	26.8	2.7	35.6
43817 f at	Т	OASZ	M87434	26.7	28	34.8
	2, testosterone-repressed prostate message 2, apolipoprotein J)	סרס	CLU AW008412	26.7	4	2
49117_at	interferon-induced protein 75, 52kD	111111111111111111111111111111111111111	- 1			
52958 at		11/5	٦,	26.5	24.4	71
38970 s at	Nef.accociated factor 1		N63458	26.5	0.8	C
74344 21	U2D higher femil		AJ011896	26.4	7.6	0 7
10406	y, mem	H2BFL	AA557205	26.4	300	4 0
5066E 21	complement component 1, s subcomponent	C1S		26.3	2.5	0.0
18 C002C			H16258	26.3		y.)
1/3/ s at	Insulin-like growth factor-binding protein 4	LOFEDA	MEDADO	20.3	0.0	5.6
46709_at	hypothetical protein from EUROIMAGE 1955967	5	14102403	7.07	7.7	18.6
1173 g at			AI80/1/0	26.2	0.8	0
37018 at	H1 histone family, member 2			26.2	15.6	19.2
41744 at	. 1	H1F2	- 1	26.1	2.3	10.1
ı	leurine zipport demains, Huntingtin interacting protein L; transcrption factor IIIA interacting protein L; transcrption		AF070533	56	45.9	21.1
64733 r at	Serine (or cysteine) proteinase inhibitor, clade D. Carella		- 1			
	9	SERPINB9	AA156247	26	12	6.4
48531_at			0.000			
56691 at			AA522816	26	6	3.6
33386 at	H1 histone family, member 0		AI935202	56	15.1	1.2
75000 at	.1	H1F0	297630	25.9	19.3	1.4
56871 24			AI735440	25.9	12.1	6.5
50105 24	mitonhandain a lista a silista		AI953847	25.7	8.6	128
20042 at	IIIIIOCITOITATI SOIUTE CAFFIEF		AI862097	25.7	4.2	2 1
39942_at	Dasic leucine zipper transcription factor, ATF-like	BATF	1	25.6	7.7	7.7

Figure 11N

62092 at 1 Figure for the period of the period	145146_at			0000000	7		
1	62992 at			A1693688	25.6	16.7	0
According to the interference of the interfe	56760 24	D7 U1 200421		AI214996	25.6	10	4.3
String 126560 25.5	26010 at			AA292201	25.6	α	6.1
Its sevent factor pathway inhibitor 2 24 25 25 3 3 3 3 3 3 3 3 3	30019 at	inase 19	STK19	L26260	25.5	90	10.
apolipoprotein L APOLI AA156784 25.3 1 at 2.50igoadenylate synthetase 2	3/388_at	vay inhibitor	TFPI2	D29992	25.5	0.00	10.4
at a polipoporate Laborate	60968_at			A1990212	5.51		1.2
2.5 Oigoadenylate synthetase 2	49459_at	apolipoprotein L	1 700V	AA150212	50.3	8.3	4.9
21-5 foligoadeny/ate synthetase 3	90662 at	synthetace	APOLI	AA156/84	25.2	18.2	17.4
Month March Marc	64450 at	synthetase	OASZ	AI340262	25.2	27.3	19
Application Application	35362 at	371111101030		AA135525	25.2	30.3	10.8
APP-ribosylation factor like 4 APP-ribosylation factor like 4 APP-ribosylation factor like 4 APP-ribosylation factor like 4 APP-ribosylation factor like 4 APP-ribosylation factor like 4 APP-ribosylation factor like 4 APP-ribosylation factor like 4 APP-ribosylation factor like 24.9	38788 21	100		AB018342	25.1	C	12
ARLA AND AND	30700 at	promiyerocytic reukernia	PML	M82827	25.1	203	0 0
Transfer Transfer	337.90_at	ADP-ribosylation factor like 4	ARL4	073960	24.9	1 1	0.0
Insulm-like growth factor binding protein 3	33924 at	- 1		AB029014	24.9	0.01	j -
CYSTATHIONIAN	1586_at	insulin-like growth factor binding protein 3	IGFBP3	M35878	0 70	0.0	3.1
A	///// at	cystathionase (cystathionine gamma-lyase)	HLO	A1955061	0 10	200	14.4
Second-color kinase	41658_at	Cdc42 effector protein 2		VED 000	0,1,0	2.8	0
Serum-inducible kinase	90749_at			ALCTO01430	24./	6.7	10.9
at protein tyrosine phosphatase, non-receptor type 2 Lat protein tyrosine phosphatase, non-receptor type 2 Rat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Aleast dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specific tyrosine-(Y)-phosphorylation regulated kinase 3 Lat dual-specific tyrosine-(Y)-phosphorylation	41544 at	Serum-inducible kinase		A1653230	24.7	4	1.5
AIR26091 24.6	76497 at			AF059617	24.6	0.2	19.4
Protein tyrosine phosphatase, non-receptor type 2 PTPN2 M25393 24.4	58702 at			AI826091	24.6	1	O
## dual-specificity tyrosine-prosphorylation regulated kinase 3 ## dual-specificity tyrosine-(Y)-phosphorylation	1265 g at			T55716	24.5	0	40
Additional part Additional part Additional part	74382 9 34		PTPN2	M25393	24.4	6.4	10
The control of the	39931 at	dual specificity tyrosing (V) phospholitic	_	AA568587	24.4	10.8	0
15 15 17 1882 24.3 3 3 3 3 3 3 3 3 3	464 s at	interferon indused protein 25	DYRK3	Y12735	24.3	0.2	0 -
tumor necrosis factor alpha-inducible cellular protein containing factor lilk-interacting protein L; transcrption factor IIIk-interacting protein L; transcrption factor IIIk-interacting protein L; transcrption factor IIIk-interacting protein L; transcrption at factor IIIk-interacting protein L; transcrption w27419 24.2 Aleczooz Aleczo	75652 at		IF135	U72882	24.3	35.4	12.9
Percentage Per	41742 s at	timor pocrocic factor alaminates		AI983437	24.3	2.9	9 9
at W27419 24.2 7 S_at human immunodeficiency virus type I enhancer-binding protein 2 HIVEP2 AL023584 24.2 7 at Al629027 24.2 17 at hypothetical protein AA131626 24.1 1 prostaglandin IZ (prostacyclin) receptor (IP) PTGIR D38128 24.1 7		leucine zioper domains; Huntingtin interacting protein L; transcrption factor IIIA-interacting protein L; transcrption		AF061034	24.3	28.1	8.7
s_at human immunodeficiency virus type I enhancer-binding protein 2 HIVEP2 M27419 24.2 7 at Al629027 24.2 17 at hypothetical protein AA131626 24.1 1 prostaglandin I2 (prostacyclin) receptor (IP) PTGIR D38128 24.1 11	36564_at			W27410	0	,	
at Advisible Advis	36175_s_at	iciency virus type I enhancer-hinding protein		W27419	7.47	9.7	2
at Adv. 3027 24.2 17 at hypothetical protein Adv. 31626 24.1 1 prostaglandin IZ (prostacyclin) receptor (IP) PTGIR D38128 24.1 7	48964_at			ALU23584	24.2	7	5.7
at hypothetical protein AA131626 24.1 1 prostaglandin I2 (prostacyclin) receptor (IP) PTGIR D38128 24.1 7	59133 at			AI629027	24.2	17.2	9.1
prostaglandin 12 (prostacyclin) receptor (IP) PTGIR D38128 24.1 7	48076 at	hypothetical protein	`	AA131626	24.1	1.2	0.7
Programment of Apropagation (II) Programment D38128 24 11	758 at	Infortaglandin 12 (proctacyclin) recentor (10)		A1949434	24.1	7.5	19.9
	100	International of (prostacyclin) receptor (if)	PTGIR	D38128	24	11.3	2.6

35094_f_at	35094_f_at leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	LILRA3	AF025527	23.9	6:2	1.5
83874_at			AI024818	23.9	7.8	4.4
46266_at	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8	SERPINA8	AI208913	23.9	15.5	6.6
39422_at	KIAA0477 gene product		AB007923	23.8	11.2	7.1
47899_at			AA056755	23.8	16.9	13.4
62217_at			T81422	23.7	7.2	15.8
55334_at			AI249019	23.7	2.3	0
32186_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	SLC7A5	M80244	23.6	3.5	2.3
44235_at			H82526	23.6	2	9.2
88550_at	hypothetical protein FLJ12929		AI468004	23.6	4.9	0
63017_at	pleckstrin homology domain containing, family A (phosphoinositide	PLEKHA4	AA521373	23.6	0.2	49.9
	binding specific) member 4					
54744_at			AA582287	23.5	8	m
37032_at	nicotinamide N-methyltransferase	LWNN	U08021	23.4	ō	1.2
32156_at	poliovirus receptor-related 2 (herpesvirus entry mediator B)	PVRL2	AF044968	23.4	5.9	8.9
34481_at	vav 1 oncogene	VAVI	AF030227	23.3	0	0
37028_at	growth arrest and DNA-damage-inducible 34		U83981	23.2	1.9	9.6
41503 at	KIAA0854 protein		AB020661	23.1	10.5	8.6
54610_at			AI479815	23.1	4.1	9.5
39839_at	cold shock domain protein A	CSDA	M24069	23	1.1	0
41142 at		DXCT	U62961	23	3.7	4.5
35718_at	interferon-induced protein 41, 30kD	1F141	L22342	23	37.3	14.5
1779_s_at	pim-1 oncogene	PIMI	M16750	23	3.5	9.9
34770_at	mitogen-activated protein kinase kinase 8	MAP3K8	Z14138	22.9	9.0	3.3
41472_at	phorbolin-like protein MDS019		AL078641	22.9	41	25.5
87811_at			AA868517	22.9	1.1	18
47870_r_at	hypothetical protein DKFZp761C169		AW003245	22.9	4	8.8
908_at	interferon induced protein with tetratricopeptide repeats 2	IFIT2	M14660	22.9	34	384.9
88906_at	KIAA1442 protein		AL110312	22.8	0	1.8
38281_at	caspase 7, apoptosis related cysteine protease	CASP7	U67319	22.7	14.4	4.9
54782_at			AI281068	22.7	9	1.1
87415_at			W73083	22.7	4.8	17.3

Response of Dendritie Cent to a...

Inventors:

Nir Hacohen, et al.

38582 at	Serine protease inhibitor. Kazal type 1	CPINKI	A1961220	1200	30	301
44906 at		TVIAL	1016676	22.00	0 0	0.01
84601 at			A1460960	22.00		7.7
1000	C	0	71403300	67.0	2.3	t
002 al		88511	M/3/80	22.5	2.1	1.2
36526_at	exostoses (multiple) like 2	EXTL2	AF000416	22.5	7.5	0
39119_s_at	natural killer cell transcript 4		AA631972	22.5	34.2	10.5
56979_at			AA133395	22.5	3.4	3.4
35036_at	complement component C1q receptor		U94333	22.4	1.2	6.0
41451 s at	SAR1 protein		W28498	22.3	2.8	3.6
64930 at	FN5 protein		AA587944	22.3	15.6	3.9
35957_at	stannin	NNS	AF030196	22.2	16.3	1.1
68355_at			AI655376	22.2	0	0.7
49364_at			AL041551	22.2	1.7	2.7
946_at	t-complex-associated-testis-expressed 1-like 1	TCTEL1	D50663	22.1	20.3	12.3
47544_at			AA741324	22.1	4.8	5.3
80151_at			AA031832	22	0.7	0.3
46175 i at			AA552969	22	8	m
36453_at	KIAA0711 gene product		AB018254	21.9	1.1	0.3
68002_at			AA503803	21.9	17.2	13.1
92145_at			AI703103	21.9	13.4	27.4
32529_at	transmembrane protein (63kD), endoplasmic reticulum/Golgi		x69910	21.7	23.9	6.8
0.000	mermediate compartment					
382/2_at	MKP-1 like protein tyrosine phosphatase		AF038844	21.7	2	0
62939 at			D12309	21.7	16.6	4
69197_r_at			AA508552	21.6	6.1	0
44087_at	HSPC018 protein		AI279029	21.5	20.8	2.1
58605_at	DNA segment on chromosome X (unique) 9928 expressed sequence	DXS9928E	A1697939	21.5	20.6	9.4
44092 at			AI862887	21.3	17.7	5.5
51016 s_at	phosphoserine aminotransferase		AI971498	21.3	13.6	9 5
1508_at	integrin, alpha 9	ITGA9	D25303	21.2	0	0.4
39660_at	defensin, beta 1	DEFB1	AI309115	21.1	7.8	15.1
91587_at			A1554946	21.1	4	1.9
51092_at	putative zinc finger protein NY-REN-34 antigen		AI950095	21.1	14.6	8.5
53757_at			AA131524	21.1	1.8	3.6

36933_at		NDRG1	D87953	21	23	2
25843 at	Jun dimerization protein p21SNFT		AI359117	21	8.4	
46152 at			A1750251	0000	7 0 0	0.1
51161_at	ras homolog gene family, member A	ARHA	ſ	20.00	12.0	200
1776_at	Ras-related associated with diabetes	CARA		20.5	2.6	20.3
39071_at	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen (CD51)	ITGAV	_	20.8	1.6	1.3
1237_at	immediate early response 3	IFB3	010103			
51637_at		ILINO	301314	20.8	4.7	0
41242 at	UDP-N-actevialucosamine pyrophosphomylase 1		666791	20.8	2.6	11.6
40852 at	tudor reneat associator with POTAIDE 2	UAPI	AB011004	20.7	1.9	1.2
61873 at	alvoard kipaca		AB025254	20.7	18.9	29.9
47500 24	Cimus promotor biodine and in	GK	AI741715	20.7	13.9	0.5
44370 at	curso bronder-bridging protein		AA805337	20.6	7.1	2.8
64247 at			AI 589469	20.6	0.3	2.5
10211 24			H40631	20.6	4	3 1
20517 24	1 0000 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -		AI458231	20.6	3.8	1.5
50057 at	10927		AF035313	20.5	14.3	16.0
13001 at	choride intracellular channel 4	CLIC4	AA142983	20.5		707
30623 24			AI435160	20.5	8.7	
100 of		NDP	X65724	20.5	ας	60
100 at	runt-related transcription factor 3	RUNX3	Z35278	20.4	71	21.5
34099 at	CUZ-associated protein	CD2AP	AL050105	20.4	120	11.3
36560 at	IKIAAU481 gene product		AB007950	20.4	1.0	0 0
1/29_at	INFRSFIA associated via death domain	TRADD	L41690	20.4	13.9	7
16567 24			W72194	20.3	80	7 1
40007 40447	Crici		AI732347	20.3		10
33291 24	acolor lyne	LPINZ	D87436	20.2	47.2	182
33157 24	inculing and processing process I (carcium and DAG-regulated)	RASGRP1	AF081195	20.2	2.4	27
301/12 at	IIIsumioria-associated 1	INSM1	M93119	20.2		Š
22142_4	increar factor of activated 1-cells, cytoplasmic, calcineurin-dependent	NFATC1	U08015	20.2	1.8	0
91350_at			AAGRGOR3	000	0.00	1
90629 at	cyclin K	CCNK	X84721	20.02	1 0	3.
53855_at			N36284	20.5	10.0	1.0
52875_at			A1888503	2001	7.7.7	16.0
			20000010	40.1	2.3	٥

53/27_at			00000			
61130 at			AI / 58508	50	7.8	1.7
50296 i at	anolinoprotein 1 3		٩	20	3.3	1.9
33243 at	TNE induced protein	APOL3	3 T63428	20	24.4	121
30640 24			AF099935	19.9	26	α /
48276 24	Biutainine-iructose-o-phosphate transaminase 2	GFPT2	AB016789	19.9	C	4.0
318 34	- 1		AI275691	19.9	9 9	100
250 24	-J (H1FX	1	19.8	7.9	7
63337 at	 Oligoadenylate synthetase-like 	OASL	Ļ		6.9	1107
51155 at			AA127696	19.8	11.7	11.0
53995 at	hypothetics protein		AL043669	19.8	6.2	87
54310 34	Typografical protein		Al346913	19.8		
45785 at	DKE7DEGED1346 SECTION		AA975511	19.7		10
74908 at	interferon induced protein 25		AL040982	19.7	8.6	3.4
64449 at		IF135	AW026462	19.7	35.8	σ
40388 at	discs large (Drosonkila) homela		AI810399	19.7	5.7	3.4
84220 at	Gises, raige (Prosopring) normolog-associated protein 1	DLGAP1		19.6	2.1	0
32965 f at	heat thook 7000 months 10		AI373122	19.6	0	1:5
38010 34	-4	HSPA18	W28645	19.5	C	1.1
35763 24		BNIP3	AF002697	19.5	2 0 0	2.4
71787 7 24	Indition Dux (expressed in ES cells) I	HESX1	AF059734	19.4	203	70.0
34039 at	Wmohow te antires 0/ (mounts)		AI312358	19.4	14.4	10.6
; ; ; ;	propried to an ideal 34 (illouse) Hornolog (activating NK-receptor; NK. (p46)	LY94	AJ001383	19.3	0	0.8
65738_at	TERA protein					
32640_at	intercellular adhesion molecule 1 (CD54), himae rhinainia		1	19.3	10.8	1.4
	receptor	CAMI	M24283	19.2	5.5	1.4
88541_at			30700814	0		
91017_at	baculoviral IAP repeat containing 3	COCIO	2000	13.5	0.2	0
63742_r_at	KIAA0635 gene product	בטאום	054/11	19.2	19.6	m
45602 at			AA910186	19.2	1.5	3.4
48018 at			AA195108	19.2	1.3	2
49283 at			AA700227	19.1	31.1	9.3
52696 at			AA158597	19.1	10.1	6.0
37615 at	growth factor recentor bound protein 10		AW024937	19.1	14.9	000
51771 at	בוסאנו ופרנחו וברבלוות: החתוות לווחובוון זה	GRB10	D86962	19	3.9	60.3
35.77			AA284560	10	000	-

55830_at			AA058686	19	13.5	88
82933_at			AI312873	18.9	12	800
54759_at			A1291314	18.9	3.7	1.5
44744_at	solute carrier family 12 (potassium/chloride transporters), member 7	SLC12A7	AI816843	18.9	1.9	0
82588_at	CASP8 and FADD-like apoptosis regulator	CFLAR	AI302459	18.9	11.6	1.6
38555_at	dual specificity phosphatase 10	DUSP10	AB026436	18.8	7.8	11.2
189_s_at	plasminogen activator, urokinase receptor	PLAUR	U09937	18.8	3.3	5.3
48740_s_at			AI973108	18.7	5.4	4.1
48081_at	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80k-L)	MACS	AA131320	18.7	7.3	8.2
36578_at	baculoviral IAP repeat-containing 2	BIRC2	U37547	18.6	4.9	13.5
73776_at			AI554044	18.6	13.5	14.8
53831_at	hypothetical protein DKFZp434F2322		AI632223	18.6	2.7	0.3
49626_at	Alg5, S. cerevisiae, homolog of		AA425251	18.6	4.7	3.8
47533 at			AI982765	18.6	12.9	14
38971 r at	Nef associated factor 1		AJ011896	18.5	5.4	1.5
39616_at			AL050227	18.5	0	4.8
32222_at			AA152202	18.5	14.2	4
73130_s_at	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CDKN2A	AI989792	18.5	2.6	4.9
1125_s_at	CD44 antigen (homing function and Indian blood group system)	CD44	L05424	18.5	0.6	
44207_at			AI422986	18.5	5.7	2
62113_at			AI674731	18.5	2.5	1.7
62561_at	DnaJ (Hsp40) homolog, subfamily B, member 4	DNAJB4	AI741503	18.5	4.6	26.4
53497_at	integrin, beta 8	ITGB8	AI129512	18.5	2	9.0
57733 at			AI652899	18.5	8.5	1.6
61428_at			AW014148	18.5	6.0	0.4
1292_at	dual specificity phosphatase 2	DUSP2	L11329	18.4	2.6	4
40074_at	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	MTHFD2	X16396	18.4	21	0
1702_at	interleukin 2 receptor, alpha	IL2RA	X01057	18.4	0.2	1.8
34877_at	Janus kinase 1 (a protein tyrosine kinase)	JAK1	AL039831	18.4	13.2	2.9
79520_at			AW022213	18.4	8.8	00
32193_at	plexin C1	PLXNC1	PLXNC1 AF030339	18.3	38	9.3

AR766 at Invocthation protein El 100001	X8	X82200	18.3	22.2	11
וואסמוובווים אוויסלגוו	AAO	AA011633	18.3	2.1	2
graphical coolers		A1928764	18.3	8.5	20.8
T	GUCY1A3 Y15	Y15723	18.2	3.1	m
6479K at	AI76	AI768334	18.2	0	60
hydethotical	A105	AI050855	18.1	6.1	
40422 at higherinerical protein FLJ1Z134	A143	AI431797	18.1	3.2	00
51510 r at	AA99	AA999894	18.1	2.5	6.6
יייין: יווייין:	192	192882	18.1	10.1	0.6
347.10_at IIISUIII-IIKE growth factor I receptor	IGF1R X04	X04434	18	m	7
24 5000000000000000000000000000000000000	A133	A1338290	18	22	-
	PML X6313.	131	17.9	49.4	18 9
53578 at	AA76	AA767436	17.9	3.4	2.6
200 at	W7(W70067	17.9	7.9	3.9
t Constant	D17	D17357	17.8	5.2	10.3
cystatili r (leukocy		AF031824	17.7	9.4	
ASOUT STATE SPETITION OF SPETITION OF SECURITIONS OF SECURITION OF SECUR	SAT AL05	AL050290	17.7	12	200
64530 at	AASO	AA502943	17.7	3.7	
42721 at	AA72	3927	17.6	23.2	15.8
63390 at KIAAN603 gene product	A126	AI261490	17.5	4.3	5.9
010 2112	AI94	AI948512	17.5	18.7	1
35682 at	N24987	987	17.5	9.4	1.6
sterile alpha motif a	AI13372	3727	17.4	1.4	32
59009 at	N95341	341	17.4	0.5	
43478 at hypothetical protein El 190373	AI98	AI982723	17.4	1	c
KIAA0942 protein	AW02	AW021103	17.4	9.0	5.2
12	- 1	AI073412	17.4	0.2	5
chemotactic proteir	SCYA8 Y16645	545	17.3	63.9	47.1
hypothetical proteir	AF070530	0530	17.3	5.7	
retinaldenyde denyd	AB01	AB015228	17.3	i a	0.0
55001 r at 5500 domain, 5H3 domain and nuclear localisation signals, 1	SAMSN1 AI823872	3872	17.3	11.4	4.0
45551 at	H15727	727	17.3	2	0.5
11/ F. (0.00 to 10.00	AI991958	8561	17.2	0.4	
3/02_at jiiyuruxysterula (11-beta) denydrogenase]	TOUT 101101				-

35153_at	Nijmegen breakage syndrome 1 (nibrin)	NBC1	AFORBEOG	17.	00.	
182_at	inositol 1,4,5 triphosphate receptor, type 3	TPB3		17.1	10.8	2.5
38040_at	splicing factor 30, survival of motor neuron related			1./.1	0.2	6.3
39108 at	1 %		1	17.1	2.2	3.1
50361 at	(State of the control	LSS	_1	17.1	14.6	4.4
	hypothetical protein El 11 2868		AI658662	17.1	24.2	11.4
167 24	Office in the contract of the		AI814485	17.1	3.4	17
5/0	This the state of	EIF5	U49436	17	4.3	
33230 dt	TIME receptor associated factor 5	TRAF5	AB000509	17		
1401_at	Inuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NFKBIA	1	17	6.4	6.3
76847_at			A1951161	7.1	-	
54029_at			1011000	/ 1	1.3	3.4
70591_at	hypothetical protein FL121162		AA948385	17	6.2	4
56331 at	hynothetical protein El 190650		AL046389	17	0.4	0.3
40082 24	fath soid Consum A list.		AA478923	17	3.7	1.4
30002 34		FACL2	D10040	16.9	11.5	7.7
18 COCCC	priospirationiositol glycan, class A (paroxysmal nocturnal hemoglobinuria)	PIGA	D11466	16.9	8.5	5.8
52786_at						
48372 at			AI266042	16.9	0.7	6
53773 at	through factorial factorial factorial		AA318275	16.9	6.3	38
64403 at	de la company de	TNFSF13B	AA682496	16.9	17.6	11.2
54063 at			AA195829	16.9	0.2	0.7
			AI801777	16.9	4.4	6.2
41386 i at	Klaan 346 protein		AI718148	16.9	7.1	3.6
40635 at	flotilia 1		AB002344	16.8	4.5	0.5
36671 at	asparapine synthetase	FLOT1	AF089750	16.8	13.6	1.2
	CD36 antigen (collagen type I recentor thrombognophic angiety)	ASNS	M27396	16.8	9.8	3.2
	2 (lysosomal integral membrane protein II)	CD36L2	D12676	16.8	30.9	9.5
55//6 at			WOODRO	16.0	0,00	
56805_at			NE2761	10.0	26.9	17.7
64769_at			V1200500	10.8	10.4	14.1
32668_at	Single-stranded-DNA-binding protein		A1200039	8.01	5.1	2.9
40960_at	UDP-Gal:betaGlcNAc beta 1.4. palantosyltransferase polygontide :		ALUSUU/6	16.7	4.5	3.8
	1 political increases and the brings 1	046AL 1	029805	16.7	6.4	3.9
196_s_at	caspase 5, apoptosis related cysteine protease	CASP5	U28015	16.7	60	C

67401 at			A1434675	16.7	16.1	14
55629 at			AI 040635	16.7	7.01	000
38797_at	KIAA0062 protein		D31887	16.6	0	2.3
58242_at	solute carrier family 21 (organic anion transporter), member 11	SLC21A11	AA053855	16.6	2.5	0
54819_r_at			AI720898	16.6	6.1	1.3
46655_at	transcription factor (SMIF gene)		AA131327	16.6	8	14.5
39986_at	DKFZP586D0919 protein		AL050100	16.5	4.2	4.9
37933 at	retinoblastoma binding protein 6	RBBP6	X85133	16.5	2.8	61.5
81932_at			AI659966	16.5	8.6	0
79721_at			AI733197	16.5	11.6	56.6
52675_at			AI581142	16.5	7.4	3.6
50375_at			AI091460	16.5	4.1	1.2
37416_at	ras homolog gene family, member H	ARHH	235227	16.4	15.5	11.5
39064_at	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate	MTHFS	L38928	16.4	2.4	16.3
35785_at	trinucleotide repeat containing 15	TNRC15	W28281	16.4	3.3	8
79053_at			AI962796	16.4	4.3	1.6
48556_at	HIV TAT specific factor 1	HTATSF1	AA581365	16.4	6.4	4.2
86536_at			AI740796	16.4	8.8	1.7
55692_at	hypothetical protein FLJ11656		W22924	16.4	4.3	2.7
35937_at	MHC class I polypeptide related sequence B	MICB	U65416	16.3	17.2	32.3
75007_at			AI079327	16.3	3.3	0.1
80084_at			AI889019	16.3	5.6	0.8
54990_at	hypothetical protein		AW009586	16.3	9	8.2
52062_f_at			Н98105	16.3	22.9	6.4
35113_at	solute carrier family 22 (organic cation transporter), member 1	SLC22A1	X98332	16.2	1.8	10.1
31883_at	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	MTRR	AF025794	16.2	5.2	0
35275_at	adaptor-related protein complex 1, gamma 1 subunit	AP1G1	AL050025	16.2	9.0	0.3
53661_at			AL038450	16.2	5	5.2
36398 at			W28729	16.1	1.1	25.8
49353 at	hypothetical protein FLJ20216		AI927837	16.1	0.3	0
72808_at			AI640523	16.1	6.1	32.6
39723 at	culin]	CULI	AF062536	16	6.5	4.8
296_at	tubulin, beta polypeptide	TUBB	X79535	16	12.7	2

JUIS.

Figure 11X

	multifunctional protease 2)	PSMB9	AA808961	15.2	15.8	8
73800_at			41890347	0 11		
80408_at ribosomal protein	protein L37a	API 37A	44961504		2.3	0.9
64879_at heparan sulfate 6-	ulfate 6.0.sulfotransferase	10001	4000004	13.2	0.3	٥
37732 at RING1 and YY1 bi	1 YY1 binding profein	10000	- 1	15.2	0.2	0
Γ		אומר	-1	15.1	4.6	5.3
63984 f at			AI885498	15.1	10.7	7.2
80945 f at			AA535914	15	16.4	9.5
48039 at			AI440145	15	12.7	2.5
51842 at			AI634580	15	16.9	9.4
41237 at major histocompa	ibility complex		AI570531	15	2.9	7.3
T	occurpationly complex, class 1, A	HLA-A	D32129	14.9	9.7	5.6
81035 i at			AI653152	14.9	3.1	11
56850 at			AI573275	14.8	7.8	1.9
87002 j.at			R08417	14.8	3.5	1.2
51923 at subingosine kinas	kinase 1		A1270476	14.8	28.7	63.7
Ī	hip 1 EF hand calcium hinding described	SPHK1	AI769914	14.8	e	1.6
Τ	at the second of	RCN1	D42073	14.7	9.7	5.4
62266 at hypothetical profe	al protein El 191079		A1694316	14.7	0.5	2.2
T	:		AI339505	14.7	6.1	1.7
52831 at			A1335361	14.7	4.2	3.4
			AI160811	14.7	0	29.8
л.			AA005281	14.7	16.7	12.4
40957 at KIAA0160 protein	nrotein		AI161358	14.7	5.7	16.9
te	osine kinase 2 heta	KIAA0160	D63881	14.6	17.7	5
Г		PTK2B	U43522	14.6	13.4	5
44008 at			AW007125	14.6	1.3	1.3
53389 at			AI921877	14.6	3.1	1.3
Τ	Calcium channel voltam denominate to 1- 2		H70631	14.6	1.9	3.7
Ī	ociated membrane matrix 6	CACNB3	U07139	14.5	0.1	3.3
_	chared inelibrate protein 3 (myobrevin)	VAMP5	AF054825	14.5	39.7	13.4
			AI125204	14.5	9	m
46699 at			AI819734	14.5	1.5	2.5
T			AI052110	14.5	0.2	4.2
Boo at Droille-rich profes	i protein with nuclear targeting signal		003105	14.4	0.0	0

E1054 24			AI922470	14.4	7.2	
21024 at	MAA1128 protein		AA424126	0 0 1	100	1 1
34887 at			NOOFA		0.0	0.0
62174_at	SWI/SNF related, matrix associated, actin dependent requistor of	CANA DO DA	04CZ6NI	14.3	6:/	1.4
		SIMPACE!	N63449	14.3	1.9	4.9
42537_at			00010044			
31680_at			AA201239	14.3	0.3	0.3
38649 at	KIAA0970 protein		M55630	14.3	5.5	6.7
36992 at	thioredoxin		AB023187	14.2	7	30.1
56889 at	Gual specificity observation 10	NXL	AI653621	14.2	9.8	5.8
70516 24		DUSP10	N36770	14.2	4.1	10.6
79494 at	ופתכווופינוכון לוואואא		AI817736	14.2	6.4	8
5/312 24			T77813	14.2	6.0	17
47782 34			N34516	14.2	10.11	٧
54077 at	hynothetical protein El 120420		R88823	14.2	2	P
16526 at	hypothetical protein FLJ10430		W18181	14.2	60	7
40320 at	Dyburnetical protein MGC5242		AI434025	14.2	13.4	0.00
40210 at	KABIS, member KAS oncogene family	RAB13	X75593	14.1	6.4	500
23210 at	NIAA1268 protein		AA210695	1 7 1	110	0 0
1440 s at			00758X	1	2.1.0	10.5
32827_at	oncogene TC21		703430	141	7.6	2.8
34308_at	H2A histone family, member I		A1305215	14	0.8	5.7
36148 at	٦.	HZAFL	U90551	14	4.9	13.2
32901 s at	nucleophosmin 1	APLP1	U48437	14	10.7	2.1
		NPM1P14	AC005192	14	3.9	1.7
54064_i_at			F000004	,		
72541_at			AA903287	14	2	5.7
57833_s_at	NY-REN-45 antigen		AI052805	14	1.7	1.6
57579_at			AW001803	14	1.1	0
1876 at	Iv-ral simian leukemia viral oncogene homolog A (rag ralatad)		AI580/21	14	4.6	4.6
36872 at	cyclic AMP phosphoprotein 19 kD	KALA	M29893	13.9	4.1	2.2
60019 at			AL120559	13.9	12.3	4.7
87957 r at		LRN	AA947309	13.9	10.6	1.4
49302 at	HBV associated factor		AA513538	13.9	9.9	3.6
64124 at			AI971817	13.9	9.1	5.4
47578 at			AA206408	13.9	3.2	0.5
3			AA160156	13.9	1	0

	ZNF151 Y09723	23	13.8	5.4	4
lymphotoxin alpha	LTA M1644	41	13.8	29	
40339_at gamma-aminobutyric acid (GABA) A receptor, pi	GABRP U95367	67		0.5	
62314_at		94	13.0	2.5	2.0
	AA418490	190		0.5	+
51508_Lat	T92882	32	13.7	7.2	σ
3083∠at	AI871408	801	13.7	6 9	10.2
	AA005023	523	13.7	14.8	4.6
/4565_at Insulin-like growth factor-binding protein 4	IGFBP4 AI440424	124	13.7	75.4	14.
20332_s_at Inypornetical protein MGC5363	AW008462	462	13.7	1	2.5
	A1968055	155	13.7	0.7	0.6
Sualiylate binding	Ā	593	13.7	8.7	
section 3 (acute-phase response factor)	STAT3 L29277		13.6	6.9	2.2
37393 at hairy (Drosophila) homolog	HRY L19314	4	13.6	c	90
at	A1961740	40		0 00	0.0
/ 34_at mucin 4, tracheobronchial	MUC4 M64594	94		7.1	5 6
at	AA846692	392	13.6		0.
	AMPD3 U29926	56	13.6	2.6	0
77134 at Minnous Belle product	AB01451	515	13.5	7.4	
78072 at	AA939344	344	13.5	4.3	
57670 at Inhosphopratein associated with CEMs	AI743607		13.5	1.1	11.
Se liespidolides de	AI860212		13.5	8.4	1.2
56671 at linase endothelial	_1		13.5	12.1	11.7
t at	LIPG N29319		13.5	1.1	1.6
3-hydroxy. 3-methylalitanyl Coentymo A mathema	-		13.5	1.1	3.6
	HMGCS1 AL048840		13.5	2	
37360 at Ivmphocyte antigen 6 complex locus E	∢		13.4	6.4	12.4
9	LY6E U66711		13.4	13.6	8.3
44795 at STAT induced STAT inhibitor 2	A1983632		13.4	8.3	3.1
	AI129818		13.4	1.1	2.8
CCAAT/enhancer h	_		13.4	1.2	3.4
kinecin heavy chain			13.4	3.1	3.4
	KIF2 Y08319	9	13.3	24.6	7.3

Figure 11AA

51024_at			AI400509	13.3	17.3	7.2
51030 at			AA843962	13.3	6.1	2.2
46238_at			A1193110	13.3	1.4	Ó
32150_at	golgi autoantigen, golgin subfamily a, 4	GOLGA4	X82834	13.2	4.8	2.2
36776_at	lymphocyte-activation gene 3	LAG3	X51985	13.2	148.7	69.7
33106_at	nuclear receptor subfamily 1, group H, member 3	NR1H3	U22662	13.2	18.1	18
66903 r_at			AI002222	13.2	2.2	2.6
42803_at	E2F transcription factor 5, p130-binding	E2F5	AI377305	13.2	3.2	2.2
48097_at	transmembrane protein with EGF-like and two follistatin-like domains 1	TMEFF1	AA001144	13.2	8.8	0
46712_at			W63773	13.2	2.4	9.7
32684_at			AF038174	13.1	15.5	2.9
1170_at	colony stimulating factor 1 (macrophage)	CSF1	M37435	13.1	6.9	3.2
36103_at	small inducible cytokine A3 (homologous to mouse Mip-1a)	SCYA3	D90144	13.1	6.1	7.6
62367_at			AI220446	13.1	0.3	2.6
45583_at			AA602585	13.1	6.0	5.9
64189_at	DKFZP564J0863 protein		08009M	13.1	4.1	0
51220_at	small EDRK-rich factor 1A (telomeric)	SERF1A	W67895	13.1	4.7	3.6
53102_s_at	CGI-22 protein		AA627551	13.1	2.6	0
55518_at	tachykinin 3 (neuromedin K, neurokinin beta)	TAC3	AA004764	13.1	4.2	14.6
56080_at			AI703473	13.1	12.8	8.3
37324_at	transferrin receptor (p90, CD71)	TFRC	X01060	13	7.7	1.3
83568_at			R06436	13	9.0	5.1
60504_at			AI859849	13	3.8	4.5
63785_at	Mitochondrial Acyl-CoA Thioesterase		A1074605	13	15.4	3.2
44838_at	hypothetical protein FLJ12752		AI271348	13	4	3.1
65895_at			AL040007	13	17	1.2
41469 at	protease inhibitor 3, skin-derived (SKALP)	PI3	L10343	12.9	0.4	5.4
40061_at	pleiomorphic adenoma gene-like 2	PLAGL2	D83784	12.9	C1	2.9
40137_at	protein tyrosine phosphatase, non-receptor type 1	PTPN1	M31724	12.9	5.3	5.2
36484_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	GALNT3	AI935146	12.9	5.5	8.4
	acetylgalactosaminyltransferase 3 (GalNAc T3)				-	
35992_at	musculin (activated B-cell factor-1)	MSC	AF087036	12.9	1.8	1
37951_at	deleted in liver cancer 1	DLC1	AF035119	12.9	0	2.6
39120_at	metallothionein 1L	MT1L	AA224832	12.9	0.1	0.3

38349_at			AF038564	12.9	10.8	0.5
50745_at			AI143457	12.9	4.2	1
65147_at			AI818579	12.9	0.2	4.1
61489_at			AI718763	12.9	3.7	3.4
65281_f_at			H22954	12.9	0.7	1.2
44853_s_at	CGI-34 protein		AA528059	12.9	10	7.4
73146_at	_	VEGF	1	12.9	5.5	1.6
44376_at	KIAA0582 protein			12.9	5.4	7.3
1573_at	platelet-derived growth factor beta polypeptide (simian sarcoma viral	PDGFB	M12783	12.8		0.5
	(v·sis) oncogene homolog))	
39628_at	RAB9, member RAS oncogene family	RAB9	AI671547	12.8	7.4	3.5
33260_at	son of sevenless (Drosophila) homolog 1	SOS1	L13857	12.8	11.2	5.3
72558_at			AI858718	12.8	1.1	0.7
52850_at	KIAA1151 protein		AA128296	12.8	6.0	4.7
41409 at	basement membrane-induced gene		AF044896	12.7	8.3	С
39857_at	syntaxin 11	STX11	AF044309	12.7	5.6	12.9
32240_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	PSMD5	D31889	12.7	0.8	1.5
37352_at	nuclear antigen Sp100	SP100	M60618	12.7	10	5
57094_at	transmembrane protein 2	TMEM2	AI189381	12.7	1.9	2.1
44920_at			AI914925.	12.7	4.8	7.6
41385_at	differentially expressed in adenocarcinoma of the lung		AB023204	12.6	1.1	1.9
39032_at			AJ222700	12.6	1.1	3.1
38160 at	lymphocyte antigen 75	LY75	AF011333	12.6	13.5	0
32217_at			AF052105	12.6	6.3	7.6
473 g at	signal transducer and activator of transcription 5B	STAT5B	U48730	12.6	4.6	1.9
45721_at	endothelin converting enzyme 1	ECE1	AL039866	12.6	4.3	5.7
63662_at			A1126468	12.6	4.9	4.5
52327_s_at			A1989346	12.6	6.0	5.7
39211_at	hypothetical protein FLJ10374		AF091080	12.5	7.7	5.7
32593_at	KIAA0084 protein		D42043	12.5	6.3	0.5
_ 11			AI028528	12.5	1.3	9.0
76037_at			65998M	12.5	2.5	0
76688_at			AI312606	12.5	0	1.3
/9145_at			W72060	12.5	8.0	8
86629_at			AA614137	12.5	10.6	3.2

Figure 11CC

20435 at	hypothetical protein FLJZ06Z5		AA573749	6.7	5.0	α
39695_at	decay accelerating factor for complement (CD55, Cromer blood group system)	DAF	M31516	9.9		6.2
39710_at	P311 protein		1130531		100	
39749 at	proteasome (prosome, macropain) 26.5 sublinit non ATPage A	NO WOO		0 0	CS.	8./
32697 at	A) monophorphatasa 1	FOMU4		9.9	5.5	0
40803 at		IMPAI	AF042729	9.9	3.8	1
32725 at	PH2 international algorithms		- 1	9.9	3.6	4.5
40901 21	niclest sufceptings	BID	٩١	9.9	4.2	9.3
20707			017989	9.9	1.5	26
32/04 at	serine/threonine protein kinase PRP4 homolog		AB011108	9.9	3.2	8 8
930 at	translocation protein 1	TLOCI	D87127	9.9		90
38119 at	glycophorin C (Gerbich blood group)	GYPC	1	9.9	0	0.00
39134_at	target of myb1 (chicken) homolog	TOM1	٩	99	22	5.7
3/0/8_at	CU32 antigen, zeta polypeptide (TiT3 complex)	CD3Z		9	1.7	0 20
	CGI:111 protein		1	9 9	7.7	2.7.2
90975 i at	_		N22605	0.0		7.7
62371 g at	hypothetical protein FLJ13153		41221377	0.0	0.0	800
59000_at	x 010 protein	× 010	1	0.0	2.5	5.6
44718_at			1	0 0	0.1	4
67141_at			2/0//575/4	0.0	5.7	7.9
43793 at			AIZ0/00/	9.9	1.1	3.7
72458 at			AA262084	9.9	2.9	5.5
49537 at			AI638014	9.9	8.5	1
50371 at	KIAA1321 protein		W18190	9.9	0.8	9.0
			AI743689	9.9	4.1	0
64887 at	Outstive transcription remiliation and an included an included an incl		AA614814	9.9	2.6	3.5
47554 at	paragramman legulation legulation fluctear protein; KIAA1689 protein		AW051603	9.9	9	0.5
81066 1 at			AA226241	9.9	2.8	3.9
53607 at			AI285898	9.9	2.3	3.9
53666 at			C14838	9.9	1.4	9
83553 f at			AA114900	9.9	3.8	6.4
33777 24	thromboscopic Assessment Control of the Control of		AA703100	9.9	9.1	16.2
30777 _at	undingovarie A symmase 1 (platelet, cytochrome P450, subfamily V)	TBXAS1	D34625	9.9	6.5	6.3
51251_at			A1189200	9	C	0 4
806_at	cytokine-inducible kinase	VIAC	1	5 0	7	0.0
		250	- [6.5	9.0	2.5

Figure 11EEE

320/3 at	butyrophilin, subramily 2, member A1	BTN2A1	U90543	6.5	2.5	T
32313_at		TPM2	M12125			
41349 at	presenilin 2 (Alzheimer disease 4)	PSFN2	ı		0 <	
34808_at	KIAA0999 protein		4	0 4	1 -	(
599_at	H2.0 (Drosophila) like homeo box 1	, i	MENTO	0 0	7	3.
36179 at		1107	17/00M	0.0	7.7	
37625 at	Distance de la compare de la c	MAPKAPKZ	012779	6.5	2.4	0
63316 34	DNA binding motif posterio on	IRF4	U52682	6.5	7.6	1
66530 at	מס וווסווו ליווסווו ליווסווו ליווסווו ליווסווו	RBM8B	AL047586	6.5	2	
40000			AI439092	6.5	0.4	9.9
99275 at			AA521311	6.5	10	3
030/3 at			AI351753	6.5	1.5	
40202 at			W93382	6.5	1.2	2.6
75275 at			AI916767	6.5	3.5	1 0
/ 32 / 0_dl	hypoxia-madcible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	HIF1A	Al983856	6.5	1.8	0.0
70210_at			AI798924	r.	1 3	C
70753 g at			AIROGRAN		2:0	,
49132_at			A145007E	5 0	2.7	
45491 s at	myeloid/lymphoid or mixed-lineage leukemia (trithoray (Drosophila)	AAL LTC	0.7600410	0.0	0.0	5.2
		INICEIO	AIGZGD93	6.5	6.2	1.9
49510_at	mitogen-activated protein kinase 8	MAPKR	A1681315	7	000	
68856_r_at					2.3	1.4
74456_r_at			A1970A7A		2.7	
92130_r_at			10111	0 0	0.0	
65794 f at			/011411	0.0	1.8	4.5
55103 at	T.G.1		AL042362	6.5	1.7	0.8
68885 r at			A1831066	6.5	2.3	,
51089 at	KIAA1140 protein		AA594352	6.5	7	3.6
148 at	A POLYMEDACE		AL042799	6.5	4.5	5.4
33326 at	KIAA0118 protein		U88629	6.4	1.4	5.3
920 at			D42087	6.4	2.9	1.8
32563 at	ATPace Na+//x transporting boto 2 cell attach	NKTR	L04288	6.4	0	14.7
56350 at	and, range a anishorang, pera 3 polypeptide	ATP1B3	U51478	6.4	3.6	3.8
15370 21			A1928492	6.4	5.5	1.5
75254 21			AI659019	6.4	5.8	9.6
10204 at			AA643507	6.4	171	23.3

Figure 11FFF

62288_at			,100000			
46537_at			A1330854	6.4		10.2
53907 at	hypothetical protein SBB148		A1190/55	6.4		2.1
57525 at	DKFZP56401863 protein		AA521293	6.4	2.6	3.4
74716 at			AI / 38434	6.4	1.3	3.3
70209 at			AW006759	6.4	0	11.7
13387 c at	towe least out of		AI761629	6.4	1.3	7
٠ J	hypothetical protein PLJ131/1		AW001604	6.4	13.8	66
64106 at	TI Carronate avian avairable		AI984040	6.4		0.7
47655 at	I Lo associated serme-arginine protein 1		AI916676	6.4	0.8	1.1
51249 at	neural polynomialing tract bindia		AI022328	6.4	6.5	8.6
62684 at	Succipate dehydrogenase complex cubraits at		- 1	6.4	2.8	3.2
52335 at	secondary deligate complex, subunit A, Havoprotein (FD)	SDHA	~	6.4	m	5.9
51588 21			AI762208	6.4	2.2	5.1
82806 24			2933319	6.4	0.2	5.7
1205			AI476732	6.4	E 0	
1300 at		TGFBI	M77349	6.4	3.5	9
32034 at	1-box and WD-40 domain protein 1B	FBXW1B	_	6.4		7.0
45/31_at	HSPC003 protein		AA581878	6.4	2	2.7
58954_at	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH.	NDUESR	ר ו	7 0	ייי	7
	(coenzyme Q reductase)			į.		0.0
		MGEA6	U73682	6.3	3.0	
	c-myc promoter-binding protein		X63417	693		2
34951 at	putative chemokine receptor; GTP-binding protein		D10923	0 0	5.00	2.1
41/68_at	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	PRKAR1A	M33336	6.3	1.2	0
		TRAF2	112597	6.9	7.0	
	CCAAT/enhancer binding protein (C/EBP), gamma	CEBPG	1	9 9	7.7	7
38332 at	purinergic receptor P2X, ligand gated ion channel, 4	P2RX4	U83993	633	501	1.7
33370 at	proline-rich Gla (G. carboxyglutamic acid) polypeptide 1	PRRG1	AF009242	6.3		0, 0
34517 at	KAS oncogene family	RAB27A	U57094	6.3	3.5	t o
40191 s at	Stiggroxy: Strictly/glutaryi-Coenzyme A synthase 1 (soluble)	HMGCS1	X66435	6.3		2.0
ı۱~	cathensin W (kmphonsin)		- 1	6.3	4.5	0
41015 at	protein kinase AMP activated alaba 1 acta 1.2.	CTSW		6.3	2.3	4.6
24056 g at	activin A receptor	PRKAA1	۹۱	6.3	0.3	2.7
34030 B at	activiti A receptor	ACVR1B	L10126	6.3	m	C

46/95_at			84431258	8 9	2.3	, 1.1
58131_at			A1806586	6.3		3.11
49875_at			A1733353	0.0	3.5	0.0
52043_at			10171010	5.0		10.0
58327 at	hypothetical protein DKFZp762N2316		T00101	2.0	Ö	
44840 s at			192180	6.3	2	
65364 at			N59198	6.3		7
72400 at			W56309	6.3	9.5	8.1
72051 2 at			AA923345	6.3	8.0	
72031 r at			A1990894	6.3		
02440 at			AI198946	6.3		4.6
54804 r at			T40707	6.3		8.1
53128 at	nypothetical protein FLJ10494		AI678076	6.3	2	3.2
00148 at	nypotnetical protein FLJ20139		AI860687	6.3		
T	liybotnetical protein DNF2p547G183		AI082794	6.3	1	1.1
2510 - 11	100		AW044663	6.3	2	0.5
43319 s at	CGI.107 protein		AA442417	6.3	2.4	1.1
030/0 at			R45447	6.3	2.1	2
01113 at	Hypothetical protein, estradiol-induced		AA442301	6.3	1.9	4.6
47077 -t	C		AA278413	6.3		
₹ †	disrupter of silencing 10		A1125866	6.3		3.5
100	congren, type AIA, alpha 1	COL19A1	D38466	6.3		5.8
40520 g at			AA044197	6.3	6.3	1.6
39112 at	upstream transcription factor 2, c-tos interacting	USF2	Y07661	6.3		5.3
T			W68180	6.3		5.5
Т		STK17B	AB011421	6.2		1.4
T	۲lر	PGM1	- 1	6.2	4.2	1.2
	NII .	PLA2G4C		6.2	1	
Τ	Udilisiation lactor suit nomolog		AF064607	6.2	1.8	0.8
T	Cortistatiii	CORT	N30625	6.2	2.1	
36097 at	immediate and in		AF055023	6.2	3.4	7.9
10 40	uridine obserboodse		M62831	6.2	1.6	15.2
5 6	maintal enhine modiane (N. Chart)	UP	X90858	6.2	5.4	0.2
	To interacting factor (TALE family L	NSMAF	X96586	6.2	6.1	0
30003 at	LO-IIITELACTITIS TACTOR (TALE TAMILY NOMEODOX)	TGIF	X89750	6.2	4.4	9.9
ססטט מו			AI797146	62	40	CV

18021 24	Vinacin house, chain mamber 3					
40051 at	Milesiii ileayy ciidiii ilieliilael 2	KIF2	AI652174	6.2	7.3	2.8
90428 at			AI355272	6.2	6.1	3.4
78954_at			AA420590	62	0	90
68619_at			A1204439	6.2	2.5	0.1-
66092_at			A1951574	10.0	200	1.4
59293_at	poly(A) binding protein, cytoplasmic 1-like		A1962727	0.0	0.00	0 0
68996_f_at			A1681967	0.5	0.0	U.4
58398_at			AA829521	6.2	2.7	1.0
64099_at	hypothetical protein FLJ10700		W81185	2.0	0.4	1.7
44650_at			AI307750	6.2	2.5	200
51962_at	hypothetical protein FLJ12484		W45523	6.2	27	3.0
47087_at			AI310524	6.2	2.5	e e
48300_at			AA713522	6.2	2.4	4.3
63013 at	- 1		AL120446	6.2	7.7	4.2
1361_at	telomeric repeat binding factor (NIMA-interacting) 1	TERF1	U40705	6.2	3.9	26
55525 at			AI972498	6.2	5.5	6 9
37114_at	AT-binding transcription factor 1	ATBF1	L32832			6.9
35086_at	fis485		AB024705	6.1	С	0
39082_at	annexin A6	ANXA6	Y00097	6.1	2.4	0.4
40176_at		RFP	J03407	6.1	3.4	
32111 at		CDYL	AL050164	6.1	0	40
40570_at	forkhead box 01A (rhabdomyosarcoma)	FOX01A	AF032885	6.1	8.1	4.5
32168 s at		DSCR1	U85267	6.1	1.4	0.6
39218_at	zinc finger protein 23 (KOX 16)	ZNF23	AL080123	6.1	c	12
34773 at		TBCA	AF038952	6.1	2.7	
33905_at	methyl-CpG binding domain protein 2	MBD2	AF072242	6.1	9.7	0.5
35625_at	CD97 antigen	CD97	X94630	6.1	4.5	800
36515_at	UDP-:N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase		AJ238764	6.1	1.1	0
35739_at	myotubularin related protein 3	MTMR3	ABOO2369	1 4	0.0	C
37610_at	hypothetical protein FLJ10803		AI765280	9	0,0	
35017_f at	major histocompatibility complex, class I, J (pseudogene)	HLA.J	M80469	9	0 00	
566_at	promyelocytic leukemia	PML	M79462	9	9.0	0.1
76530_at	hypothetical protein FLJ20639		AI749464	1.9	000	0
58201_at	hypothetical protein FLJ20511		AI796121	2	7 %	0

45298 at			000000			
87008			N66638	9	2.8	7.7
04230 41			AI760126	9	α (*)	4.6
63406_at	uncharacterized hematopoietic stem/progenitor cells protein MDS030		AI357582	9	3.6	2.4
65665_at			07000344	+	-	
67989_at			A A B D E B D C	0 0	1.7	1.3
79858 at			A4623636	۱	5.3	1.2
69976 at			A1035351	٥	5.7	3.2
48431_at	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	FUT4	AI970292	9	14.7	13.8
33374_at	complement component 2	2	00200			
44839_s_at		20	LU9/06	٥	8.4	1.7
48167_r_at			44513307	0	7 .	5
91718_at	chromosome 11 open reading frame 1	CIROPEA	WENERS W	0	0.0	23.4
70160_at		1	AAOR3860	0 4	0.7	
69914_at			AA447177	0 4	2.1	1.1
53319_at			AWOOSSE	5 0	3.0	7.7
64476_at			A1047045	٥	1	3.2
63814 at	PRO0149 protein		AL04/045	٥	4	0
50534 at	Small nuclear ribonicleoprotein polypeptide G		AW044607	9	3.2	4.2
61289 at	ATPace Ca++ transporting planning manufacture 1	SNRPG	AA234175	9	0.8	0.5
1	hypothetical protein El 112426	ATP2B1	AI337321	9	1.3	0
	יוז אינוי ביולמן או חיפוון בריז דל אינוי בריז באינוי בריז בריז באינוי בריז באינוי בריז בריז בריז בריז בריז בריז בריז ברי		AI979240	9	6.0	0
64006 2 24			AL120741	9	0.7	0.1
603E2 24	Ilipoilla nividio jusion parmer	LHFP		9	0	13
32704 at	و میشون میشون میشون میشون میشون میشون میشون میشون میشون استون میشون	AA987596	9	1.9	3.4	
35780 at	KIAA1042 statein	DOCK2	D86964	9	2.6	5.6
61278 at			AB028965	9	9	6.4
64330 c at	haryoprietiii (irriportiii) beta 2	KPNB2	AI653355	9	2.7	3.5
33400 5 24			AW002183	9	5.2	99
37089 at	Illingingionaliti neavy constant gamma 3 (G3m marker)	IGHG3	AF067420	5.9	3.8	171
31888 c at			AF052119	5.9	1.1	10.5
40400 z 24	ACADO 7 at third suppressing subtransferable candidate 3	TSSC3	AF001294	5.9	2.6	4.2
10-1-01-1	normologous to yeast mitrogen permease (candidate tumor suppressor)		AF040708	5.9	1.4	2.7
38516_at	sodium channel, voltage-gated, type I, beta polypeptide	SCN1B	L10338	5.9	C	8

П			M91670	5.9	7.8	5	ГÐ
ä	B-cell receptor associated protein BAP29		AI984786	5.9	4		न ्
ij	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD	CSTF3	U15782	5.9			Tm
Ī	NIAAU/ by gene product		AB018312	5.9	7.2		عاد
39008 at ceruio	cerulopiasmin (refroxidase)	CP	M13699	5.9		1	Im
ğ	ne paimitoyitransferase I, muscle	CPT1B		6.3	18.	9	1
1/9/ at cyclin-	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	CDKN2D	U40343	5.9	1:1	6 9	Im
34392 S AL MADI,	MAD1, Merriber RAS oncogene ramily	RAB1	AL050268	5.9	3.7		I
T	NIAAU4/8 gene product		AB007947	5.9	1:1	3.8	Īm
7	bile iamily, member 2	BTG2		5.9	6.0		īm
T	translocase of outer mitochondrial membrane 34		U58970	5.9			Iιο
T			AI984814	5.9			Τ
304/9_dt Inypotin	nypotnetical protein FLJZ0419		278377	5.9		0.8	Ιm
1	000:07		AA031731	5.9			īm
╅	nypomental protein reuzisuz		AI733306	5.9	1.1	1.8	Im
			R73518	5.9	9.6		ा स
. a.			AI279954	5.9			1=
ם ב	ppz. nomolog		AI934584	5.9	1.8		T.C
51642 at			AA777406	5.9			ılm
21043 at			AL036254	5.9	3.9	6.5	Tio
9			AI863033	5.9	11.6		1
46996 s at			AI057283	5.9			1-
65351 r at			R38041	5.9	2.6		I.
47360 at			AA146979	5.9		5.	1
91341 at			AI798960	5.9			T-
46889 at			AI291659	5.9	4.5	3.8	ım
46089 at			N74444	5.9	1.4		100
47856 at			N90525	5.9	2.8		Im
1830 est			AA999846	5.9			τ=
4120E at CTT1 protoin			T91299	5.9	0	8.8	Im
7	/orkonery kindle			5.9	2.9		T-+
\top	retinoblations hinding protein (C/EBP), alpha	CEBPA	- 1	5.9		4.6	1.0
+	dabidraconos (biziz)	RBBP2	S66431	5.9	2.4	7.	
	MADIT UCTIVUT UBCT (AUTUMITOTIC) 1 DETA SUDCOMPIEX, 10 (22KD), PDSW)	NDUFB10	NDUFB10 AA195976	5.9		5.9	<u> </u>
/		-	_				_

Figure 11LLL

			\CCC\ru	5		
38972_at			AE052160			0.9
37424_at HCR (a-helix coiled-coil rod homologue)	gue)		APOSOS	0 0		0.1
Γ	7. 0		AD029343	20.0	3.2	3.5
			W2/949	5.8	1.8)
Τ			AI557322	5.8	0.5	39.3
_			AI192108	5.8	c	3
at chromosome 21 op	ne 18	C210RF18	ר ו	2.2	7 -	
Т		MFAPI	U04209	r o	5.1	7
±		HOAFC	1	0 0	3 6	
				0 0		3.5
GTP-binding protein	overexpressed in skeletal muscle	CEM	1	0.0	X) (0.5
	g transactivator, with Glu/Asp-rich carboxy.	CITED2	11		0.0	25.7
245_at selectin L (lymphocyte adhesion molecule 1	olecule 1)	SFIL	MOSORO	ū	C	-
at			AA586695			7.1.2
growth arrest and D	NA-damage-inducible, gamma	GADD45G	AI952982	r.	αι	
			AI435076		90	٠.٠ ۳
42380_at			AA399389	5.8	0.8	4 6
13 at			H73401	5.8	4.1	9.9
00000 at			AI340002	5.8	1.7	1.2
82504 at			AA602921	5.8	6.5	2.1
62534 at			AI308862	5.8	6.1	3.1
0/ 303 at			AI435586	5.8	4.7	
55306 2+			AI872476	5.8	0.1	0
22330 at			N55264	5.8	2.5	9
43345 at			AI423056	5.8	2.1	0
50210 at			AA429326	5.8	19.9	21.3
27 24			H15157	5.8	4.4	2.6
_			AI694367	5.8	1.7	1.5
CANOA A			T54916	5.8	4.1	35.2
86340 at			AW006123	5.8	7.9	5
mitore appoint			T70214	5.8	2.7	3.8
t adenylate cyclare 3	oreili killase-activated protein kinase 3	MAPKAPK3		5.8	2	5.9
24 at aucilylate cyclase 3	100	ADCY3		5.8	0	6.7
30020_S_at [NH-type splicing regulatory protein	ulatory protein (FUSE binding protein 2)	XISRP	AA628946	2 2	000	

66134_f_at	cofilin 1 (non-muscle)					
54479_at		3	A(50055/	5.8	3.6	12.2
54152 at	eukarvotic translation initiation factor AE hinding protein 1		AA214559	5.8	3.9	5
46304 at	hypothetical protein clone 2746033	EIF4EBP1	AI026669	5.8	5.2	5.8
39378 at	herlin 1 (coiled coil myosia like DOI 2 internal		≤	5.8	8.7	6
37795 at	andenifatase B	BECN1	U17999	5.7	3.3	0
35606 21	historial and a second a second and cond and	ARSB	M32373	5.7	4.3	
20000	institutife decar boxylase	HDC	D16583	5.7	26	3.1
30/_al	eridotrieliai differentiation, sphingolipid G-protein-coupled receptor, 1	EDG1	M31210	5.7		1.2
40408_at	cysteinyl-tRNA synthetase	0	- 1			
41126 at	Solute carrier family 1 (plutamate/neutral amino acid transcatt)	CARS	L06845	5.7	5.7	2
1	member 4	SLC1A4	SLC1A4 AA978353	5.7	7.9	4.7
41399_at	KIAA1111 protein		A COOCOGA			
1452_at	LIM domain only 4		1	2.7	3.1	0.7
34857_at		LM04		5.7	1.5	6
36066 at	KIAA0828 profein		224724	5.7	4.5	0.2
38038 at	limican		≤	5.7	2.4	76
35414 s at	Allacid)	LUM		5.7	C	12.0
30136 21	person (classific syndrollie)	JAG1	U77914	5.7	10	000
50317 24	Oxidative:stress responsive 1	OSR1	AB017642	5.7	3.1	6.7
55750 at	retiriold acid induced 1	RAII	AI926671	57	1 0	
v. j	Hypothetical protein		W44483	57	1.0	3.2
30394 at			T70600	7.0	7.7	
രൂ			A1694520	0.7	3.6	0.5
66745_i_at			440000	5.7	1.9	0.7
60417_r_at			AASOSSS	5.7	0.3	4.5
50377 at			AI081821	5.7	3.3	7
79389 at			AI081607	5.7	1.7	2.7
47144 at	ASB:1 profeio		AI026951	5.7	1.2	0.4
82601 at	B.cell CLL/lymphoma 6 (zinc finger profess 51)		AI018173	5.7	4.1	4.5
42829 at		BCL6		5.7	3.1	α C
85100 at			N58166	5.7	2.8	200
68048 at			AI567916	5.7	3	000
70124 at			AA701259	5.7	0	0.5
R0894 at	histone acetyltransferans		AI770116	5.7	2.6	
43395 s at	Deal (Head) homeles		AA553554	5.7	6.1	4.4
מבייייים ביי	Unida (hisp4u) nomolog, subtamily B, member 5	DNAJBS	DNAJB5 AW006148	7.7	-	

Nir Hacohen, et al.

Inventors:

71040_at			A1926365	14.3		
46.368 at			0000000	0.7	1.4	1.4
51702 at			H80286	5.7	1.5	3.5
31/92 at			68020M	5.7	2.1	
40103 at			R02594	5.7	6.2	
47602 at			AA393223	5.7		100
57968_r_at			AA431469	5.7	2.0	5 4
37214 g at	deoxyribonuclease I-like 1	DNASE111	X90392	5.7	7 5	0.0
1357_at	ubiquitin specific protease 4 (proto-oncogene)	74511	1	7: 3	0.1	27.0
39105_at	vasodilator-stimulated phosphoprotein	1000	1	7.0	4.0	20
53155 at		LOW A		5.7	2.6	5.9
46664 at	anonthosis associated specification and single and anonthosis.		AA608559	5.7	4.4	7.1
37506 at	Historia interacting and the protein containing a CARD		AI148558	5.7	5.1	6.3
37.300 at	money light Light Light		278308	5.6	1.7	1.2
40//3 at		MYL5	L03785	5.6	5.9	
22/10 24	DAPS OTBEST (ANA) II (DINA directed) polypeptide A (220kD)	POLR2A	X63564	5.6	3.1	4.2
5127 of	TANDS GITASE ACTIVATING PROTEIN		AL096752	5.6	7.2	5.2
35137 at	myornesin i (skelemin) (185kU)	MYOM1	06069X	5.6	0.7	2.9
5150 at	hypothetical protein from clone 24/96		AF070596	5.6	4.6	2.4
33231 at	numan immunodeficiency virus type I enhancer-binding protein 1	HIVEP1	X51435	5.6	6.4	12.2
1000 at		REL	X75042	5.6		5 7
9201 at	Kno guanine exchange factor (GEF) 11	ARHGEF11	AB002378	5.6	3.2	
33320_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	SLC11A2	AB004857	5.6		0
35787_at	dynein, cytoplasmic, intermediate polypeptide 2	CIUNU	41986201	5 6		
37177_at	CD58 antigen, (lymphocyte function associated antigen 3)	200	V00636	0 0		
39562_at	CGG triplet repeat binding protein 1	10000	100030	0.0		0.6
40757_at	granzyme A (granzyme 1, cytotoxic T-lymphocyte associated serine	GZMA	M18737	2.0	2.4	0 00
- 1	esterase 3))) ;	?	63.3
46/71 at			W69585	5.6	2.3	000
50840 r at	neurexophilin 4	NXPH4	A1498771	2 2	6.3	2.0
65150_at	CGI-18 protein		A1073484	5.0	70.	3.3
73901_at			AIOPAGE	0.0	Σ.Ο	0
72649_at			00210217	0.0	6.0	1.4
62914_at			A1765590	5.6		1.4
84232 at			A13632/5	5.6	0.0	1.2
69834 r at			A1806926	5.6	1.2	3.9
15-1-20			AI765718	2.0	-	C

42881 24	nypotneticai protein FLJ12492		W81045	5	6	9
71936 at			R88708	5	6	1.6
46960 24			A1148006	5.6	4	2
15337 at			AI743903	5.	C	,
63251 s at			W72338	5.	5	6
91623 at			AA904828	5.0		3
51185 at	PAN2 protein		AI185207	5.		
53302 r at			AI309334	5.6	4	
46727 at			AI741209	5.6	5 4.3	
46808 at			AI146850	5.6	6.0	
53689 at			AL120562	5.6		5
57000 f at	meningioma expressed aptigen 5 (byglyssigless)			5.6		2
46660 at	ein El 110074	MGEAS	_1	5.6		1
46670 at			AA018399	5.6	3.	7
44136 at			AI921097	5.6	5 2.9	
78784 at	Stannin		_1	5.6		
69458 f at		SNN	_1	5.6		
40045 g at	Chromosome 18 open reading frame 1		AI693465	5.6		
56225 at		C180RF1	AF009425	5.6	4.5	
64028 s at			AI744466	5.6	3.3	
49390 at			AI886403	5.6	4.4	
52261 at			AA999858	5.6	5.6	5.6
	O-linked Nacetylphocsamine (GlcNAc) transferse (1188 N		AI970054	5.6	4.7	9
41422 24	acetylglucosamine:polypeptide-N acetylglucosaminyl transferase)	067	077413	5.5	1.1	1.8
38080 24	Thusbuild protein 36 kinase, 90kD, polypeptide 5	RPS6KA5	AF090421	7. 7.	2.2	0
39826 f at	hypothetical protein		AB018276	5,5		
39061 at	bone marrow stromal call artists of		W29115			
1310 at	- 1	BST2	D28137	5.5	σ	6.6
40219 at	HMBA:indivible	PSMB2	D26599	5.5		4.6
40108 at	KIAA0005 gene product		AI796944	5.5	0	
32660 at	KIAA0342 gene product		D13630	5.5	3.2	
377 g at	Sema domain imminoalobilia domaia (12) abata Las		AB002340	5.5		
-0	secreted, (semaphorin) 3C	SEMA3C	SEMA3C AB000220	2.5		

Figure 11PPP

s at	collagen, type I, alpha 2	COL1A2	V00503	5.5	0	
at	Cdc42 effector protein 3		AF094521	5.5	2.1	6
Т	KIAA1128 protein		U90912	5.5	3.5	2.5
<u>.</u>	hypothetical protein FLJ10849		W25874		C	
7	papillary renal cell carcinoma (translocation associated)	PRCC	L		1.5	17
42272 at			AA743565	5.5	1.3	9
58524 at			W03029	5.5	4.1	
24692 s at			AW001883	5.5	6.0	3.2
/4006 at			AI984623	5.5	0.7	
			AA978204	5.5	3.3	2.1
ΞĪ	zinc inger protein 1/3	ZNF173	AW009746	5.5	5.5	14.1
/0/23_at			AI203222	5.5	1.3	
4/409 at			AI452516	5.5	2.9	1.5
+	The supplies of the supplies o		A1688900	5.5	11	7
Ţ	putative INO-DINA-memyitransrerase		AI016585	5.5	5.1	10.4
Τ,			AA993487	5.5	5	2.6
7	catenin (cadnerin-associated protein), alpha 1 (102kD)	CTNNA1	AF102803	5.5	3.7	0.1
23000 at			AA176289	5.5	2.6	0.3
/ 3001 at			AI885677	5.5	0	0.2
_			R22212	5.5	0.8	4.6
_	nypometical protein PRO1068		AA100948	5.5	4.0	3.4
24000 S at			A1660022	5.5	1.2	9.0
00320 at			AI475514	5.5	10.2	32.1
43390 at			AI769269	5.5	7.2	
57770 at			H24422	5.5	1.7	1.6
88025 6 24			AI091581	5.5	2	2.7
50187 of			AI199443	5.5	0.5	2.5
T			H46074	5.5	9.0	6.1
T	doing (Keneral control of arrithmeters 1, yeast) like 1	GCN1L1	AI939557	5.5	0.5	1.2
56856 r at			AI457965	5.5	1.7	0.9
71516 7 at			AA993791		1.4	2.8
69622 24			Z40202	5.5	0.3	2.1
Τ			AI669987	5.5	6.1	4
T	Siliali ilucidal niva activatilig complex, polypeptide 5, 19kD		AI557062	5.5	2.9	5
60061_at	arachidonate 5-lipoxygenase-activating protein	ALOX5AP	A1983204	ις:	7	2 4

hypothetical protein FL111937		SAPAEN	r.	4.2	αυ
ł		20000)
CGI-90 protein		AI800674	5.5	6.2	7.6
		AL050021	5.4	2.5	ō
adenylate kinase 2	AK2	U84371	5.4	2.7	0
H2B histone family, member G	H2BFG	Z80779	5.4	2.5	8.5
ui	GAL	M77140	5.4	8.3	0.4
translocase of inner mitochondrial membrane 17 (yeast) homolog B		AJ005895	5.4	2.2	3.1
DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	AI540318	5.4	6.0	6.2
linger protein 259, pseudogene	ZNF259P	1	5.4	O	0.2
pro-platelet basic protein (includes platelet basic protein, beta-	PPBP	1	5.4	0.4	4.2
nboglobulin, connective tissue-activating peptide III, neutrophili-					
ranscription factor 5, p.130-binding	F2F5		5.4	c	7.0
u	Z	١	5.4	180	I.C.
criptional activator of the c-fos promoter		l	5.4	2.7	6.0
in kinase (cAMP-dependent, catalytic) inhibitor gamma	PKIG	٩	5.4	2.2	9.6
	TNFRSF10B	AF016266	5.4	0.3	3.5
hypothetical protein FLJ10738		W28620	5.4	O	3.6
acetylserotonin O-methyltransferase-like	ASMTL	Y15521	5.4	1.8	2
splicing factor, arginine/serine-rich 4	SFRS4	L14076	5.4	5.3	4.2
hemopoietic cell kinase	HCK	M16592	5.4	0.8	0.6
		A1922968	5.4	0.1	2.4
		AA586814	5.4	5.2	0
		AI741328	5.4	3.8	1.2
angiotensin II, type I receptor associated protein		A1858573	5.4	1.2	0.1
skb1 (S. pombe) homolog	SKB1	AA932371	5.4	1.7	2.5
		AI023295	5.4	7.5	2
NOD2 protein		AA910520	5.4	0.7	1.1
protein kinase Chk2		N24330	5.4	11	1.7
hypothetical protein FLJ12903		A1807668	5.4	2.5	5.1
		AI309016	5.4	3.6	3.2
collagen, type IX, alpha 1	COL9A1	N66408	5.4	2.2	5.2
		AI916887	5.4	1.7	0.1
	DnaJ (Hsp40) homolog, subfamily B, member 6 zinc finger protein 259, pseudogene pro-platelet basic protein (includes platelet basic protein, beta thromboglobulin, connective tissue-activating peptide III, neutrophil: activating peptide:2) E2F transcriptional activator of the c.fos promoter motilin motilin transcriptional activator of the c.fos promoter protein kinase (CAMP-dependent, catalytic) inhibitor gamma tumor necrosis factor receptor superfamily, member 10b hypothetical protein FLJ10738 acetylserotonin O-methyltransferase-like splicing factor, arginine/serine-rich 4 hemopoietic cell kinase NOD2 protein protein kinase Chk2 hypothetical protein FLJ12903 collagen, type IX, alpha 1	Ophii.	DNAJB6 ZNF259P PPBP PPBP MLN TNFRSF10B TNFRSF10B SFRS4 HCK SFRS4 HCK COL9A1	DNAJB6 AI540318 ZNF259P 295118 PPBP M54995 MLN X15393 MLN X15393 MLN X15393 MRNG AB019517 TNFRSF10B AF016266 W28620 ASMTL Y15521 SFRS4 L14076 HCK M16592 AR9286814 AI741328 AI858573 SKB1 AA932371 AI858573 SKB1 AA932371 AI858573 AA910520 N24330 AI807668 AI807668 AI809016 COL9A1 N66408	Ophil- DNAJB6 Al540318 5.4 PPBP M54995 5.4 Ophil- E2F5 U31556 5.4 MLN X15393 5.4 MLN X15393 5.4 PKIG AB019517 5.4 TNFRSF10B AF016266 5.4 ASMTL Y15521 5.4 ASMTL Y15521 5.4 AN922968 5.4 AN922968 5.4 AN932371 5.4 AN932371 5.4 AN932371 5.4 AN932371 5.4 AN932371 5.4 AN932371 5.4 AN932371 5.4 AN932371 5.4 AN932371 5.4 AN93295 5.4 AN93295 5.4 AN93295 5.4 AN93296 5.4 AN93295 5.4 AN93295 5.4 AN93295 5.4 AN93295 5.4 AN93295 5.4 AN93295 5.4 AN93295 5.4 AN932916 5.4 AN9910520 5.4 AN932916 5.4 AN9910520 5.4 AN9910520 5.4 AN9910530 5.4

59341 at			AI311917	5.4	2.4	6.9
47951 at			AA521145	5.4	5.2	5.2
4/8/8 t at			AI656542	5.4	2.8	9
	transporter-like protein		AI768065	5.4	4.2	
ч.			AA707322	5.4	4.9	0.3
8/61/ at	hypothetical protein FLJ13385		AA639580	5.4		1.6
			AI091231	5.4	0.7	1 4
69/15 at			AI743419	5.4	0.5	28
72052 at			N71632	5.4	0.3	4 4
54799_at	glutaminase	GLS	W72090	5.4	0	C
58825 at		PTMA	AI701911	5.4	69	7 3
57042 at	similar to Caenorhabditis elegans protein C42C1.9		W74749	5.4		į c
4905/ g at			AA521489	5.4	11.9	0
5/0/4 s at			AW021642	5.4	1.5	(K
50943 at			W87422	5.4	0.8	5.7
45655 at	tumor antigen SLP-8p		AL045849	5.4	5.7	2.4
46105 at			AA149641	5.4	5.4	C
55009_at			AI359000	5.4	2.2	
			W29045	5.4	0.5	L L
39341_at	thyroid hormone receptor interactor 6	TRIP6	~	5.4	0.0	
37759_at				5.4	2.0	10
39163_at	likely homolog of rat kinase D-interacting substance of 220 kDa; KIAA1 250 protein		W27233	5.4	0.2	6.4
45521 c at	-					
63703 24	DNA polymoras		AI967955	5.4	5.5	5.7
15736 at			AI797479	5.4	3.7	4.8
43/30 at	two-bole channel 1, normong		AL048491	5.4	5.2	5.1
31006 of	Irructose-1, b-bisphosphatase 1	FBP1	U21931	5.4	4	4.9
31550 at	VIAAOSE		AI798834	5.3	1.5	0.4
27700	NIAAUZOO gene product		D87445	5.3	4.6	2.4
37798 at	chromosome 8 open reading frame 2	C80RF2	AB018790	5.3	0.3	2.9
1905 .	NIAAUSO4 protein		AB023181	5.3	3.4	17
1383_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	PPP2R2A	M64929	5.3	7.5	12.4
41170 at	KIAA0663 gene product		AB014563	5.3	2.7	5.0
37575_at			AL050192	5.3	3.6	2.1
					17	1

T	KIAA1046 protein		AB028969	5.3	4.8	3.3
1	modulator recognition factor (M62324	5.3	2.9	7.7
T			AA034067	5.3	1.6	2.1
ar	ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	AI922486	5.3	3.1	4.0
19 .			AW021968	5.3	9.0	0.1
. "			AA128061	5.3	1.7	6.8
81911 at			AW051492	5.3	2	0.4
81/63 t at			AI393033	5.3	2.1	1.2
7			AI674428	5.3	1.4	0.4
s at	catenin (cadherin associated protein), delta 1	CTNND1	AI863000	5.3	4.5	6.6
09401_at	2400001		AI800640	5.3	6.2	23.2
1	nypometicai protein FLJZ0093		W87653	5.3	2.3	3.4
10 0	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		AI989354	5.3	5.6	6.1
T	Typotrietical protein regions		N63911	5.3	2.1	5.8
			AL045717	5.3	1.6	1.2
85939 at			AI694139	5.3	0.4	1.3
31074 at			AA767895	5.3	0.5	0.7
73110 at			AI912203	5.3	1.7	4.9
73011 at			R35404	5.3	1.6	1
75003 at			AI972618	5.3	1.2	2
/3003 at			AI732791	5.3	m	7.4
_			AI872409	5.3	1.9	2
49/30 g at In	nypotnetical protein FLJ11136		AI497781	5.3	2.5	1.1
	nypotnetical protein FLJZU831		AA131537	5.3	6.0	1.2
7	F-box only protein 4	FBX04	AI961240	5.3	1.3	0.5
7	III FLJ10276		AA219406	5.3	1.1	0.1
60705 2+	protein kinase, CAMIP-dependent, regulatory, type II, beta	PRKAR2B	AI792179	5.3	9.7	5
67220 at			R68222	5.3	3.1	1.8
T			AW005511	5.3	m	3
33410 at	lax interaction protein 1		U90913	5.3	3.7	5.3
	Alderlyde genydrogenase 10 (fatty aldenyde dehydrogenase)	ALDH10	U46689	5.3	3.9	5.1
1			AL021707	5.3	3.6	6.2
		MTCP1	Z24459	5.3	2.6	4.3
5 1	Dinashiating settings 1	PTDSS1	D14694	5.3	2.2	5.7
38011_at K	KPB5-mediating protein		AB006572	5.3	2	4.9

Figure 11TTT

152936 at			10000			
55567 at			165/61	5.3	1.5	5.1
18 /0000	G H		AA147933	5.3	5.3	5.2
38084 at		ATP2C1	AJ010953	5.2	9	20
32183_at	splicing factor, arginine/serine-rich 11	SFRS11	M74002	5.2	10	2.7
39407_at	bone morphogenetic protein 1	BMP1	M22488	5.2	0.0	7.0
39742_at	TRAF family member associated NFKB activator	TANK	L		7:1	0 1
31856_at	glycoprotein A repetitions predominant	GARP	1	5.2	700	5.1
31975_at				7 2) -	0.0
33869_at			0100010	2.5	0.0	2.1
39342_at	methionine-tRNA synthetase	MADO		3.5	3.2	3.8
830 at	Tax1 (human Ticell leukemia virus tyne I) binding protein 1		ı	2.6	J	0
1105 s at	T cell receptor beta locus	TANIBRA	-	5.2	0.8	3.6
39950 at	acid sphingomyvelipase like phosphodiophogo	- KB(0)	-	5.2	1.3	11.7
984 g at			Y08136	5.2	0	6.0
37200 24	חוסופווו עווופאפ ד	MAPK12	X79483	5.2	5.9	8.8
1110 ct		GYS1		5.2	2	С
1119 at	replication protein A2 (32kU)	RPA2	105249		0.5	0
38384_at	phosphoribosylglycinamide formyltransferase,	GART	l^	50	7.0	0
	phosphoribosylglycinamide synthetase,				7.7	7.0
	phosphoribosylaminoimidazole synthetase					•
38397_at	polymerase (DNA-directed), delta 4	POI D4	1109196	5 2	-	1
38437_at	MLN51 protein	1000	X80100		100	٦
277 at	myeloid cell leukemia sequence 1 (BCI 2.related)	1.01	000199		7.p	1.7
56371 at		MCLI	L08246		3.9	10
48873 24	Cana 33/Min. 6		AA534298	5.2	m	0
53777 at			AI571452	5.2	3.4	25.2
74423 at	itypotiletical protein FLJZZ693		AI672353	5.2	3.8	2.2
00000			AI793024	5.2	2.2	2.6
50000 ot			T64664	5.2	0.1	0.3
20000 at			AI097194	5.2	3.3	3.2
00000	lurig type-i celi membrane-associated glycoprotein		AA149854	5.2	3.5	6.4
80829 at			AA210905	5.2	4	7
59566_at			AA705681		- 2	0 0
4854/_at	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	PLEKHA1	AA875839		1.9	3.5
84960_at			A1004417	0.4	0.5	C
45272_at			AAABBEO	200	2 2	710
		_			i	107.

70053_r_at			AI734928	5.2	9.0	2.2
70170_f_at			AI251913	5.2	2.5	1.8
50205_at	leptin receptor	LEPR	N46838	5.2	5.1	15
80421_s_at	solute carrier family 21 (organic anion transporter), member 12	SLC21A12	AI347130	5.2	3.1	0
43535_at			N37020	5.2	2.2	0
87493 at			AL042667	5.2	0.4	0
47430_at			T65857	5.2	0	Ö
66512_at			AI970258	5.2	1.6	2
45624_at	core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3		AI967968	5.2	6.9	4
	galactosyltransferase					
62306_at	hypothetical protein		197347	5.2	2.3	2.8
55915_r_at	hypothetical protein LOC54149		AI922520	5.2	13.7	15.9
46612 at	KIAA1624 protein		R39794	5.2	10.2	1.6
64740_at			AA470369	5.2	3.5	2.2
55800_at	hypothetical protein AL133206		W72766	5.2	2.2	0
61299_at	chaperonin containing TCP1, subunit 6A (zeta 1)	CCT6A	R43952	5.2	2.8	1.6
55650_at			W22914	5.2	1.7	2.5
51599_at			2945576	5.2	2.2	6.4
31816_at	glucosidase, alpha; acid (Pompe disease, glycogen storage disease	GAA	X55079	5.2	1.3	5.9
40955_at	prostate turnor over expressed gene 1	PTOV1	U79287	5.2	2.6	4.6
41540 at	protein phosphatase 1, regulatory subunit 7	PPP1R7	250749	5.2	2.9	5.2
34811_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c	ATP5G3	U09813	5.2	3.2	6.2
36601 at	Vincialia Vincialia	ION.	M33308	20	4.6	5.1
37002 at	biliverdin reductase B (flavin reductase (NADPH))	BLVRB	D32143	5.2	3.8	5.3
48750 at			AI983115	5.2	4.6	4.9
44638_at	insulin-degrading enzyme	IDE	AA573292	5.2	2.6	4.2
59136_at			AA779895	5.2	5.1	5.2
48811_at	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase		AW007594	5.2	4	5
54912_at	translocase of inner mitochondrial membrane 13 (yeast) homolog B	TIMM13B	AL035821	5.2	3.4	5.4
51123 at			H11724	5.2	5	4.9
52012_at			AI659020	5.2	3.5	5.3

Figure 11VVV

53120_at	hypothetical protein FLJ20442		AIGRIGIE	5.2	67	0 /
	caspase 9, apoptosis related cysteine protease	CASP9	160521			100
40491_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21	DDX21		5 1	1 -	4.7
32735_at	KIAA0931 protein		AB023148	, r	<u> </u>	2.3
34719_at	glutaminase	0		1 1	10	
39320_at	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta.	CASPI	.1	11.0	0 9) -
	convertase)			1		1.1
35227_at	retinoblastoma-binding protein 8	RBBP8	U72066	5 1	σ	7.3
34378_at	adipose differentiation-related protein	ADFP	X97324	2 1		
35845_at	SEC24 (S. cerevisiae) related gene family, member B	SEC24B	[⁴	1.4	1.0	100
36888_at	KIAA0841 protein		L	25	ά	t C
38027_at	fibulin 1	FBI N1	X53742	5.1	0 0	0 0
32792 at	GCIP-interacting protein p29		AI 031432	5 1	0.0	0.0
38369_at	myeloid differentiation primary response gene (88)	MYD88	1170451	1.0	3.6	4 C.
38824_at	Tat-interacting protein (30kD)		AE030102	3.1	חַ	18.4
37082 at	KIAA0426 gene product		AF039103	2.1	2.8	12.6
54747 at	andosultine alaha		- 1	5.1	9.0	2.3
SE027 - 24	בויסספתוווופ פוטוומ	ENSA	- 1	5.1	5.2	0
03027			AA532470	5.1	2.1	2.1
04961_1_at	collagen, type III, alpha I (Enlers-Danlos syndrome type IV, autosomal dominant)	COL3A1	T54146	5.1	8.6	5.6
42564_at			W84667	-	C	
78014_at			AA271E12	7.7	6.3	4.0
47832 at			M3/1313	1.0	7.7	0.7
43363 c at			AA100654	5.1	0	1
10000 S	т.		AI978590	5.1	1.9	10.4
30763_at	NIMA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2		AA779863	5.1	9	3.4
.4			AI984505	5.1	α	10
84167_at			AI742722	٦,	2.0	1.7
88155_at	H2B histone family, member B	H2BFB	AI125923	5 1		100
-4			W87470	5.1	1 4	000
.4			AI989784	5.1	~	A
58901 at			AW021543	5.1		4.4
61/45 r at			N76044	5.1	2.7	α
4439/_at			H11252	5.1	4.3	4 4
52072_at	hypothetical protein FLJ10718		AA873182	5.1	0.8	4.1

Figure 11WWW

	aucilyiate killase 3 alpha like		N32441	5.1	33	40
5861/at			AA149312	5.1	3.4	60
	histidyi-tRNA synthetase	HARS	AW022495	5.1	4.3	ς.
64847 at			AA394155		4 4	0.7
54410_at			N70443	5 1	100	1.0
80825_at			A150011E	1 -	7.70	
40279_at	KIAA0121 gene product		050011	0.7	9.0	
1630 s at	spleen tyrosine kinase	AAS	L	0.1	3.4	3.7
33833 at	Spectrin ainha non-enthrocytic 1 (alpha fadrin)	010		5.1	3.9	4.9
32594 at	Chaperonin containing TOP1 cultural 4 (Aprile)	SPIANI	J05243	5.1	3.8	5.7
18110 34	hypothetical cratein E 111021	CCT4	AF026291	5.1	2.5	1.7
51170 of	hypothetical protein FLJ112/1		N91279	5.1	3.3	4.6
211/3 at	oreleding Attimitied guanine nucleotide exchange protein 2		AI741843	5.1	2.9	7.9
65171 at	classical milities growing lactor, peta-induced, 68KD	TGFBI		5.1	2.2	5.1
610E2 at	CIONE TED4/39		N36909	5.1	4.5	5.2
01033 dt			AA773816	5.1	5.1	. 5
49569 at	in FLJ20281		AI690893	5.1	4.2	4.5
bbb03_at	baculoviral IAP repeat-containing 6	BIRC6	AA886981	5.1	29	5.4
45293 at	hypothetical protein from EUROIMAGE 363668		AA631902	5.1	4 4	
56418_at	uncharacterized hematopoietic stem/progenitor cells protein MDS027		N25128	5.1	3.7	5.8
45224_at			0.003000			
57714_at			70053007	1.0	3.2	3.5
36908 at	mannose recentor C type 1		AA429113	5.1	3.6	5.1
55695 at	~1 2	MRC1		5.1	4.2	4.6
38134 at	plainmorphic adaptions and 1	GCSH		5.1	4.5	4.2
31898 at	KIDAD212 gans product	PLAG1	U65002	5	0.7	1.4
321/2 at	sering /thronging kings 2 /C+20	кіаа0212	- [5	3.7	2.3
10/0 + 2+	serine with evillie kinase 3 (SteZu, yeast nomolog)	STK3		5	4.1	3.6
32232 24	theric oxide synthase 2A (Inducible, hepatocytes)	NOSZA		2	0.4	2.7
32653 at	(18) 1, member B (torsin B)	TORIB	AF007872	ß	6.9	13
32002 at	MIAAU1/U gene product		AL041663	5	C	
343/3 at	upstream regulatory element binding protein 1		297054	5		
1070 at	힐.	GSTM5	L02321	S		4 8
10/2 K at	GATA-Unaing protein Z	GATA2		S	1.5	6.3
30004 at	iliajor vault protein	MVP	X79882	S	11.8	6.0
391/0_at			AL049957	Ľ	1 4	

82798_g_at	chromosome 6 open reading frame 32	CEORE32	AW016644	Ľ		2 6
48488_at				7 4	5 6	C.2
89829_at			00361017	n u	5 0	0
66361 at			A13120	ñ	0.0	0.0
73713 24	DAD mambar of DAS accepted femilialism		AA009699	2	4.3	0.8
53030 at	AND, HEILIDEL OF AND OFFICE PARTIES. LIKE ZA	RABL2A	AI051621	5	0.4	2.5
33020 at			AI929168	5	1.1	3.6
624/2 at			H49102	5	1.5	2.3
83036 at			AI271559	2	0.5	m
82/68 g at			AA913354	2	0.8	2.5
83224 r at			AI053582	5	1.6	0.5
55108 s_at			AI915696	5	2.9	1.6
/9105 at			AA830599	5	5.6	2.2
09388 at			AI299040	2	0	2.6
49516 at			AA531016	5	9.9	3.5
61354 at			AA218990	5	1.3	2
70495 at			AI453095	5	4.2	28
5/608 at			AA523335	5	1.7	C
46169 at			AI745624	5	4.5	12.3
46514_at			R38647	2	2.9	C
53321 r at			AL043875	5	3.5	5 1
51991 at			AI884621	2	1	0.5
45204 s at			AI378647	2	10.2	5.2
45/8/ at			N29695	5	2.3	5.4
5555/ r at			AI825880	5	2.2	2.4
20339 at	nypotnetical protein FLJ13222		R52747	5	2.7	8
13120 at	ginydropyrimidinase-iike 3	DPYSL3	AI983251	5	7.2	0
402// at			AI031551	2	10.2	1.6
20000 at	radzo, member RAS oncogene tamily	RAB23	AI742498	2	1.4	1.6
22493 at			AA187437	2	0	0.5
40/24 at	(erisin	TNS	AL046979	2	3.9	0
54167 at			2963428	5	1.7	
20001 at			3162292	5	1.8	1.5
35001 at	procollagen-lysine, Z-oxoglutarate 5-dloxygenase 3	PLOD3	AF046889	വ	2.1	5.9
40000 dt	corricorropin releasing normone	CRH	V00571	5	4.7	3.8
48059_at			R61448	2	4.4	3.5

I						
39340_at	hexosaminidase A (alpha polypeptide)	HEXA	M16424	5	1.5	5.1
65737_r_at			AI701293	5	2.7	5.7
58780_s_at	hypothetical protein FLJ10357		R42449	5	2.6	4.6
	CGI-69 protein		AI354351	2	3.5	5.2
	anaphase promoting complex subunit 7		AA131793	2	2.4	5.2
34427 g at	Ω	HLALS	U22963	4.9	3.7	6.0
38892_at			D87077	6.4	2.5	1.2
Г	homolog of yeast SPB1		AJ005892	6.4	1.3	0.7
36270_at	CD86 antigen (CD28 antigen ligand 2, B7.2 antigen)	98GO	1	4.9	13.2	3.9
35720 at	KIAA0893 protein		AB020700	4.9	2.2	10.8
ᇕ	gamma-aminobutyric acid (GABA) B receptor, 1	GABBR1	AL031983	4.9	6.0	10.3
	JAK binding protein		AB000734	4.9	9	7.7
	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS A/Ro)	SSAZ	J04137	4.9	2.3	1.4
35363_at	DEAD/H (Asp.Glu-Ala Asp/His) box polypeptide 17 (72kD)	DDX17	AL080113	4.9	2.7	0
	ras association (RaIGDS/AF·6) domain containing protein JC265		AL049538	4.9	2.9	3
40347_at			AA913812	4.9	3.5	0.7
at	CD6 antigen	9CO	U34624	4.9	2.5	12.2
40712_at	a disintegrin and metalloproteinase domain 8	ADAM8	D26579	4.9	7.2	1.2
75743_at			AA668789	4.9	3.4	1.6
78468_at			F26341	4.9	1	2.7
90341_at			H04388	4.9	4.3	0.2
91905_s_at			AI609998	4.9	0.7	1.3
47215_r_at			AA129058	4.9	5.9	8.4
49237_at	RNA binding motif protein, X chromosome	RBMX	AI971694	4.9	2.5	12.8
63242_i_at			AI809894	4.9	2	4.7
54658_at	hypothetical protein FLJ10955		AI961496	4.9	3.3	1.5
44731_at			A1807804	4.9	3.6	2.2
84588_at			AI691077	4.9	2.9	4.3
56965_at	HSPC056 protein		N51105	4.9	6.4	1
74935_at	hypothetical protein FLJ11274		W04760	4.9	0.3	2.6
43690_at			AA019641	4.9	0.2	0.4
75820_r_at			AI679201	4.9	1.6	2.5
65936_at			AA034414	4.9	3.3	4.7
69763_r_at			A1865825	4.9	6.0	3.8

441/0 at			H53031	4.9	0.8	2.8
72092 T at			AA677864	6.4	3.4	7.5
r at			T91504	4.9	9.0	99
at	papillomavirus regulatory factor PRF.1		N25612	4.9	2.5	
sat	J.S.P.Y⊞Ke	TSPYL	AI972301	4.9	1.5	1.3
51941 at			AA442900	4.9	2.5	1.5
61063 at			AI248920	4.9	1.3	0.2
45612 at			AI744560	4.9	3.7	5.9
40000 at			AA479835	4.9	0.8	6.0
T			AW003215	4.9	1.8	2.6
T	⊏ [AA524056	4.9	1.2	2.8
T	nypotnetical protein FLJ113U/		AI820049	4.9	2	1.6
T			AA524361	4.9	4.8	3.6
39313_dl	KAB-OD protein		AI458521	4.9	3.5	2
03319 41			AI075909	4.9	1.1	3.4
F.	- 1		R42423	4.9	2.9	α
	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	SMARCA5	N36842	4.9		4.2
ä	KIAA0602 protein		AB011174	0 V	7.0	0 0
	hypothetical protein		AF070638		7.7	1.0
at	ribosomal protein L3	E Ida	1		0.0	0.0
	ralA binding protein 1	RAI RP1				7
56546_at	KIAA1545 protein	1	L12342	1. V. C	7	4.3
53884_at			AA21200F	2 4	5.9	5.8
43306 at			AA312905	4.9	3.9	4.7
43038 r at	43038 r at KIAA1363 profein		AA126841	4.9	2.3	5.6
43053 g at			AI/69531	6.4	9.0	5.1
1	DKEZPA34E1735 protein		AW025012	4.9	3.2	4.6
1	24		AW005775	4.9	3.5	2
+	hypothatical protein Ft 190000		AI810687	4.9	2.7	5.3
T	hypothetical protein FLJ23239		W67828	4.9	3.8	4.4
T	Typodietical protein ness		N21131	4.9	4.9	4.8
	DID and GNO L		AL048421	4.9	3.8	4.8
	DID and CINC Hornology 1, basic leucine zipper transcription factor 1	BACH1	AB002803	4.8	1.3	2
1711_at	tumor protein p53-binding protein, 1	TP53RP1	1109477	0.0	2.1	,

Figure 11AAAA

32940 at	Alport syndrome, mental retardation, midface hypoplasia and	AMMECR1	AMMECRI AJ007014	4.8	1.1	8
	elliptocytosis chromosomal region, gene 1					
39302 at	desmocollin 2	DSC2	X56807	4.8	0.5	2.2
33894 at	neuroepithelial cell transforming gene 1	NET1	AJ010046	4.8	1.7	0.5
35145 at	MAX binding protein	TNM	X96401	4.8	5	Ô
39604_at	pleckstrin homology, Sec7 and coiled/coil domains, binding protein	PSCDBP	AF068836	8.4	2.4	2.2
36971 at	KIAA0257 protein		D87446	4.8	5.4	2
35675 at	vinexin beta (SH3-containing adaptor molecule-1)		AF037261	4.8	2	8.7
35303 at	insulin induced gene 1	INSIG1	928960	4.8	2.6	0
35838_at	clones 23667 and 23775 zinc finger protein		090919	4.8	2.4	2.4
32530_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	YWHAQ	X56468	4.8	2.9	7.4
37358_at	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	UBE2E1	AI039880	8.4	1.7	4.6
231_at	transglutaminase 2 (C polypeptide, protein glutamine gamma. glutamyltransferase)	TGM2	M55153	8.4	2.5	0
39182_at	epithelial membrane protein 3	EMP3	U87947	4.8	3.8	2
75627_at			AA703201	4.8	4	1
52929 at			AL044396	4.8	1.5	4.6
50829_at			AA706818	4.8	10.8	10.5
64448_at	DKFZP727G051 protein		AA203321	4.8	0.8	1.6
89166_at			AI953998	4.8	4.6	0.7
67240_at			AI377910	4.8	9.0	0.4
51628_at			AA009692	4.8	2.8	0
85526_at			R64696	4.8	3.2	0
85530_at			AI732798	4.8	0.5	1.4
63817_at	DKFZP434B203 protein		AA099904	4.8	2.6	6.3
58926_r_at	hypothetical protein		A1979070	4.8	1.1	3.3
73656_r_at			AI719644	4.8	1.2	6.1
64152_at			AA703523	4.8	0	0.4
59698_at			H11817	4.8	0.1	9.2
76989_at			41333655	4.8	0	0.3
48635_r_at			T95654	4.8	2.1	2.6
69001_at			AA831691	4.8	2.4	2.1

Figure 11BBBB

50134_at			R66534	4.8	1.5	5.8
73439 at	hypothetical protein MGC3156		AA349855	4.8	2	2.8
63373_at			AA194033	4.8	4.8	2.2
73574_at			AI290214	4.8	3.7	8.1
64577 at			H60064	4.8	2.1	2.9
44066 s_at	G protein-coupled receptor kinase-interactor 1	GIT1	AI887641	4.8	2.8	5.5
53546_at			AI168683	4.8	3.7	6.7
62165_at	x 006 protein		W72231	4.8	3.2	5.9
45580_s_at			A1983200	4.8	3.6	1.8
53680_at			AI130786	4.8	0	1.3
51813_at			AI797095	4.8	7.1	1.8
46237_at			AW001342	4.8	2.5	6.7
58682_at	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	DDXBP1	AI348378	4.8	6.2	0
52347_at	CGI-60 protein		A1985204	4.8	0.3	1.4
54989_at			H43374	4.8	4.9	1.2
51697_r_at			AA649308	4.8	m	4
55601_at			AI742770	4.8	2.9	0
47608_at			AI697401	4.8	1.1	1.2
47330_at			W81697	4.8	1.5	9.3
70054_i_at			199829	4.8	1.7	3.5
73569_r_at			AI708856	4.8	6.0	2.7
75232_at			N31820	4.8	1.1	1.3
80059_at			H79244	4.8	1.1	3.4
84212_i_at			AI203819	4.8	0	2.6
38716_at	calcium/calmodulin-dependent protein kinase kinase 2, beta	CAMKK2	_	4.8	0	2.4
41603_at	transducin (beta)-like 3	TBL3	00500	4.8	3.8	5
39866_at	ubiquitin specific protease 22	USP22	AB028986	4.8	2.6	5.9
40113_at	GS3955 protein		D87119	4.8	3.1	4.1
40824_at	RAN binding protein 16	RANBP16	AB018288	4.8	2.5	5.3
38943_at	holocytochrome c synthase (cytochrome c heme lyase)	HCCS	U36787	4.8	2.9	4.4
38733_at	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break reioining: Ku autoantipen, 80kD)	XRCC5	M30938	4.8	1	4.3
33198_at	binder of Arl Two		AA206524	4.8	2.3	6.8
56520 at	Inudix (nucleoside diphosphate linked moiety X) type motif 5	NUDTS	AI188576	4.8	3.3	4.3
45307 at			A1921204	4.8	1.6	5.9

50244 at	Inucleotide binding protein 2 (E.coli MinD like)	NUBP2	NUBP2 AA552351	4.8	5.6	6.4
45878 at			W21966	4.8	3.9	4.6
39971 at	lymphoblastic leukemia derived sequence 1	LYL1	M22637	4.8	3.5	4.8
38612 at	tetraspan 3		M69023	4.7	3.5	6.0
38630 at			AL080192	4.7	4.6	1.8
39486 s at	KIAA1237 protein		W28968	4.7	1.1	9.0
1713_s_at	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDk4)	CDKNZA	U26727	4.7	0	5.6
39410 at	development and differentiation enhancing factor 2	DDEF2	AB007860	4.7	0.2	6.1
40202 at		BTEB1	D31716	4.7	1.5	3.5
40064_at		ALS2CR3	ALS2CR3 AB011121	4.7	8.0	1.5
40470 at	oxoglutarate dehydrogenase (lipoamide)	НОВО	D10523	4.7	3.6	0.3
32820 at		CNOT4	U71267	4.7	4	10.4
39310 at		BDKRB2	X86163	4.7	0.2	4.6
610 at	adrenergic, beta 2., receptor, surface	ADRB2	M15169	4.7	6:0	2
33492_at			AI624840	4.7	1.8	7.1
35285_at	solute carrier family 4, sodium bicarbonate cotransporter, member 4	SLC4A4	AF007216	4.7	0.1	1.8
40310_at	toll-like receptor 2	TLR2	AF051152	4.7	3.5	0
35190 at	KIAA0469 gene product	KIAA0469	AL031447	4.7	1.3	2
37977_at	KIAA1528 protein		AI138834	4.7	2.4	0.4
39141_at	ATP-binding cassette, sub-family F (GCN20), member 1	ABCF1	AF027302	4.7	4.1	0
467_at	osteoclast stimulating factor 1	OSTF1	U63717	4.7	2.5	0
42270_at			W24320	4.7	1.5	6.1
56991_at			A1927199	4.7	1.2	6.5
57016_at	hypothetical protein FLJ11264		A1692513	4.7	6.4	10
52287_at	long-chain fatty acid coenzyme A ligase 5		AA514342	4.7	0.8	0
	_		A1634548	4.7	0	0.7
81262_at			AI280818	4.7	9.0	0.2
89955_at			AW020975	4.7	1	0
66849_at			AI160370	4.7	1.4	1.8
58452_at	sperm associated antigen 9	SPAG9	`	4.7	2.4	11.1
75150_at			A1631846	4.7	3.8	1.1
83391 at			AI638800	4.7	1.1	2.8

Figure 11DDDD

62765 r at	62765_r_at hypothetical protein FLJ22995		D20046	4.7	10.6	2 0
62652 at			AI962194	4.7	3.1	2.7
50608 r at	putative brain nuclearly targeted protein		AI792919	4.7	1.3	, r.
67063 at			AL048402	4.7	3.1	9 -
68160 at			AA436007	4.7	4.7	3.1
87787 at			AI874267	4.7	4.2	0
87877 at			T83663	4.7	1.6	0.5
56911 r 24			T69727	4.7	4.4	82
86833 7 34			N66563	4.7	1.5	2.3
44202			н68862	4.7	3.1	7.3
72672 at			AA417797	4.7	3.8	6.1
52201 24			AI765157	4.7	1.8	0.7
70816 at			AA894564	4.7	5	4.3
82301 21			AA630392	4.7	2.3	C
14500 at			AA160048	4.7	0.1	0 1
72514 at			AA604268	4.7	3.1	2.4
EA307 0+			N42884	4.7	- 2	
7450/ at			AI762856	4.7	4.8	4.
50174 at			AL043934	4.7	0.8	C
77680 23	FIN30 200 11		N36861	4.7	2.1	L T
75780 - at	r LIVZS gene product		AW002527	4.7	7	6.3
49583 at			N93263	4.7	3.4	
53670 24			AA027059	4.7	2.2	1 7
52855 at			AA664156	4.7	17.4	9 1
43752 at			AI885781	4.7	11.3	14.6
39443 c at	outochrome c oxidase subunit Wh		AA191495	4.7	1.4	0.5
т"	DKEZPEKKO1646 protein	COX5B	M19961	4.7	2.3	5.7
Τ	lymphocyte, specific protein 1		AL050084	4.7	2.3	3.8
56906 at		LSP1	M33552	4.7	1.1	8.8
45254 at	translocase of inner mitochondrial manufactures.		AA193416	4.7	4.1	4.6
	CG1-99 protein	TIMM10	W02499	4.7	4.6	4.9
Π			AI342336	4.7	2.7	6.4
44705 at	hymothetical protein		AA789332	4.7	2.9	2.6
47907 at	Typotitetical protein		AA133356	4.7	3.9	4.9
			AI094180	4.7	2.0	7.7

Figure 11EEEE

42031_at	40001	HSPA8	A1986374	4.7	6.0	ع
			AI201843	4.7	4.2	
45492_at			AWOOSSE			1
44823 s at	11		200700	7.7	٥	4
43929 at			AA5214/6	4.7	4.4	4
55970 24			AA225263	4.7	4.6	4.4
17875 at			AI701480	4.7	2.3	3,
47.07.0 at			W15284	4.7	1.9	3.6
40/09 at	nypotnetical protein MGC4368		AL121013	4.7	r.	9
824 at	glutathione-S-transferase like; glutathione transferase omega		U90313	4.6	6 5	5
41695 at	KIAAU414 protein		AB007874	4.6		4 6
39906 r at	ADP ribosylation fa	ARFGAP1	AA402332	4 6	-	10
31345 at	protease		AB002134		27	7 4
31916 at	Killer cell lectin-like receptor subfamily A, member 1	KLRA1	AF047445		13	5.5
4042/ at	COA1 / (Veast) homolog, cytochrome c oxidase assembly protein	COX17	AA149486	4.6	6	0
327.38_at	NAUH dehydrogenase (ubiquinone) Fe·S protein 2 (49kD) (NADH. coenzyme Q reductase)	NDUFS2	AF050640	4.6	1.3	
38904_at	v src avian sarcoma (Schmidt-Ruppin A.2) viral oncogene homolog	SRC	AF077754	4.6	1.9	12.7
33760_at	peroxisomal biogenesis factor 14	DEY14	70017646	,		
35166_at	Down syndrome critical region gene 3		AD01/340	4.0	3.4	0.2
40612_at	KIAA1117 protein	CHUSCHS	00/343	4.6	7.1	5.7
427 f at	Interferon alpha 10		AB023040	4.6	9.9	3.6
35613 at	4	IFNA10	V00551	4.6	0.5	25.4
37493 at			AL042599	4.6	2.9	27.9
1860 at	- 1		H04668	4.6	4.7	3.3
36880 24	En frament of late Lite Attention	TP53BP2	U58334	4.6	9.9	0.5
36053 at	MAN Constitution (Set, flight affinity), receptor for; gamma polypeptide	FCER1G	M33195	4.6	1.2	1.8
37711 at	MANDS because against decapentablegic, Urosophila) homolog 4	MADH4	U44378	4.6	3.1	3.4
01111_at	enhancer factor 2C)	MEF2C	857212	4.6	0.7	8.7
56131_at			70037114	,		
64966_at			A114083/	4.6	1.8	2.4
65518_at	RNA polymerase I transcription factor RRN3		Albb8641	4.6	5.2	6.1
75179 at	17		N22/30	4.6	3.9	1.6
	(ionnologous to yeast UBC4/5)	UBE2D3	R81146	4.6	4.3	2.1
90289_at			AI827330	4.6		

Figure 11FFFF

73715_at			41126206	12 /	-	
66690_at			Нарада	1 2		12.3
61224 at			171017	j (0.0	1.0
44060 at	selenoprotein W. 1	1000	1/1014	4.0	0	1.5
79626 at		SEPW1	AA625451	4.6	1.9	17.2
1020 91	22 Saint (22)		AA962105	4.6	2.3	0
62010 at	Spricing ractor (CC1.3)		AI400626	4.6	m	1.3
02010 at			AI202885	4.6	2	2.2
83402 at			AA700080	4.6	3.4	i c
84383 at			AI949708	4.6	2.2	62
6548U at			AA166751	4.6	4.5	1 7
4/4/1 at			AA916868	4.6	40	o c
44/49 at			T66226	46	26	1.5
87408_at			AI221305	4 6	0.10	2.5
43151_at			T87150	200	0.00	0,0
69446_at			4 4 6 5 5 0 0	7	2	3.7
77935 at			000000	0	0.4	2.7
87284 at			A1939620	4.6	2.5	3.9
42047			AA044789	4.6	3.8	9.0
51074 at			AA042952	4.6	1.3	4.3
010/4 g at	_		N49836	4.6	4.1	0.4
45550 at	periin		AL046918	4.6	2	C
72133 at			W90634	4.6	2.1	0
75525 at	KIAAU336 gene product		R34331	4.6	6.7	212
82032 at			AI823999	4.6	22	3.5
44643 at	Т		AI633734	4.6		2
42630 r at	hypothetical prote		H88129	4.6	280	000
61/69 at	neparan sultate (glucosamine) 3.0-sulfotransferase 3A1	HS3ST3A1	N71828	4.6	3.3	2.2
40112 r at			AI700523	4.6	2	C
33204 at	nypotnetical protein SBBI6/		W79937	4.6	0.5	
12250 at	squamous cell carcinoma antigen recognized by T cell		W81246	4.6	1.3	
4/309 at			AA887112	4.6	ō	00
40211 at	nypotnetical protein dJ1141E15.2		A1190033	4.6	2.6	1 6
00//0 at			AA179496	4.6	0	0
19302 at			AI653767	4.6	18.2	19.8
43233 at			AA033783	4.6	3.3	0
40914 at			H46965	4.6	0.5	2.5

36444 s at	36444 s. at small inducible cytokine A5 (RANTES)	SCYA5 /	AF088219	4.6	3.7	4.5
41749_at	ES1 (zebrafish) protein, human homolog of	1	U53003		8	4.1
41727_at	KIAA1007 protein	4	AB023224	4.6	2.9	5.2
41562_at	murine leukemia viral (bmi-1) oncogene homolog	BMI1	L13689	4.6	3.5	4.3
32562_at	endoglin (Osler-Rendu-Weber syndrome 1)	ENG	X72012	4.6	4.7	9
38041_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyloalactosaminyltransferase 1 (GalNAc-T1)	GALNT1	U41514	4.6	3.3	3.5
38789 at		TKT	L12711	4.6	3.3	4.9
48810_at	hypothetical protein DKFZp761H221		AI547243	4.6	3.7	6.5
43824_at			AI952129	4.6	2.5	5.3
44632_at		1	AA007697	4.6	2.4	4.7
45758_at		,	AA034095	4.6	m	5.9
65620_at	hypothetical protein FLJ14005		W52855	4.6	4.4	4.7
50036_at			Af189011	4.6	3.9	4.4
53935_at			W74486	4.6	2.4	4
55571_at			W58459	4.6	1.5	3.1
37119_at	vesicle associated membrane protein 4	VAMP4 /	AL035296	4.5	2	0.9
34530_at			W73822	4.5	7.6	1.2
33019_at	Parkinson disease (autosomal recessive, juvenile) 2, parkin	PARK2	AB009973	4.5	2.3	10.5
33283_at	arrestin, beta 2	ARRB2 /	AF106941	4.5	0.8	0
31524 f at	H2B histone family, member K	H2BFK	280782	4.5	1.4	7.4
33665_s_at	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	CSF2RA	M73832	4.5	2.3	0.4
34312_at	nuclear receptor coactivator 2	NCOAZ	AI040324	4.5	m	7.6
33773_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10		U13948	4.5	0	2.6
33504_at	neurexophilin 2	NXPH2 ,	AF043467	4.5	1.4	0.8
37828_at	hypothetical protein FLJ11220		AL050064	4.5	1.2	4.4
36703_at	small inducible cytokine subfamily A (Cys.Cys), member 25	SCYA25	U86358	4.5	-	2.9
36452_at	synaptopodin	,	AB028952	4.5	1.6	3.6
35826_at	suppressor of Ty (S.cerevisiae) 5 homolog	SUPT5H	AF040253	4.5	3.1	3.6
	KIAA0027 protein		D25217	4.5	1	1.3
37941_at		MYBPC2	X73113	4.5	1.3	6.7
38355_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome	DBY	AF000984	4.5	2.3	0.7
56367_at			AI630997	4.5	1.8	1.1

Figure 11HHHH

65139_at	hypothetical protein FLJ12150	AIS	AI925240	4.5	8.6	8.0
76305_at		AA	AA764974	4.5	1.4	0.5
76356_at		AA	AA203497	4.5	1.6	1.6
59043_at		AIS	AI243147	4.5	0	0.4
82499_at		AIS.	AI925051	4.5	1.1	0
56803_at	wingless type MMTV integration site family, member 5A	WNT5A AIS	A1968085	4.5	1.3	0
67164_at		AI	AI367020	4.5	2.1	0.1
65478_at		AI.	AI744031	4.5	3.9	1.2
43273_at		Ale	AI655806	4.5	0.8	1.4
68245_at		Í	H48278	4.5	2.5	1.7
79480_i_at	- 1	Ż	N49201	4.5	1.7	1.7
56269_at	hypothetical protein FLJ12701	A	AI338045	4.5	2.5	1.4
49469_at		AIS	AI871490	4.5	1.4	1.4
73771 at		AIG	AI632232	4.5	2.5	3.7
57270 f at	glutaminase	GLS AIS	A1968420	4.5	4.8	0.3
86475_f_at		A	AI337926	4.5	3.1	3.1
63849 at	karyopherin beta 2b, transportin	NA!	AI885873	4.5	0	9.0
86015_at		Ale	AI652445	4.5	9.0	0.4
87673_at		AIG	AI982610	4.5	9.0	0.2
84407_r_at		AIC	332906	4.5	9.0	
85125 g at		AIC	AI074707	4.5	2	3.6
53978_at		AW	AW024692	4.5	1.2	11.3
45918_at		Z	N53560	4.5	1.6	3.9
43356_s_at	D-type cyclin-intera	Als	A1970622	4.5	1.4	0
62261_s_at	LIM domains containing 1	LIMD1 AIS	933287	4.5	3.7	1.7
45661_at		Z	N90348	4.5	5.5	6.7
60188_at		AA	AA629050	4.5	8.1	3.1
65892_at	fatty acid binding protein 1, liver	FABP1 AA	AA001405	4.5	2.7	0
53997_at	seven transmembrane domain orphan receptor	AA	AA622413	4.5	1.7	0.7
54521 g at		All	A1084224	4.5	4.3	1.4
46234_at	CGI-148 protein	AA	043242	4.5	4	4.9
54067_at		Ali	AI982669	4.5	0.3	0
		Al	A1770067	4.5	3.3	0.7
62971_at	hypothetical protein FLJ12428	I AI	AI799804	4.5	2.9	2.3
61005_at		AA	AA009648	4.5	3	4.1

Figure 11IIII

57423 at			86055744	7 2	4	0
87232 at			AA487296		5 -	0 4
33308_at	glucuronidase, beta	GUSB	M15182	4.5	8.0	4.8
32317_s_at	suifotransferase family, cytosolic, 1A, phenol-preferring, member 2	SULTIA2	U34804	4.5	3.1	4.1
39135_at	KIAA0767 protein		AB018310	4.5	3.7	4.3
47714_at			AA018412	4.5	2.4	2.7
33689_s_at	D.dopachrome tautomerase	TOO	AF012434	4.5	1.8	4.7
55301_at			AI634118	4.5	2.6	4.3
57497_at			AA419263	4.5	3.9	4.1
58468_at			C17704	4.5	4.5	4.3
58647_at	glutathione S-transferase M1	GSTM1	AA203289	4.5	æ	3.2
46594_at	hypothetical protein FLJ20186		AW014780	4.5	4.3	4.6
44079_at	general transcription	GTF3A	AA166851	4.5	3.9	4.9
43485_s_at	hypothetical protein FLJ21343		A1633875	4.5	2.9	3
47104_at			A1760368	4.5	3.4	4
47561_at			AA877614	4.5	3.5	5.7
39385_at	alanyl (membrane) aminopeptidase (aminopeptidase N,	ANPEP	M22324	77	3.5	0.1
	aminopeptidase M, microsomal aminopeptidase, CD13, p150)					
36347_f_at	H2B histone family, member D	H2BFD	AA873858	4.4	1.4	6.4
40407_at	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	KPNA2	U28386	4.4	2	2
31342_at	UDP-N-acetyl-alpha-D-galactosamine.polypeptide N-	GALNT2	X85019	4.4	1.3	3.9
	acetylgalactosaminyltransferase 2 (GalNAc-T2))	<u> </u>
32635_at	transcriptional intermediary factor 1 gamma		AB029036	4.4	3.7	6.1
32693_at	KIAA1040 protein		AB028963	4.4	0.7	13.5
33219_at	KIAA1097 protein		AB029020	4.4	3.7	1 7
41770 at	monoamine oxidase A	MAOA	AA420624	4.4	0	Ō
34655_at	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	MPP2	AI951832	4.4	0.2	10.4
38982_at	TRF2-interacting telomeric RAP1 protein		W28865	4.4	1 6	4.3
35213_at	WW domain binding protein 4 (formin binding protein 21)	WBP4	AF071185	4.4	1.9	2.6
41584_at	nudix (nucleoside diphosphate linked moiety X) type motif 3	NUDT3	AF062529	4.4	6.0	6.4
35007_at			AC004940	4.4	0.5	0.8
37403_at	annexin A1	ANXAI	X05908	4.4	2.6	4.1
37088_at	serine/threonine kinase 13 (aurora/IPL1-like)	STK13	AF059681	4.4	2.6	3.9
56940 g at			AI963304	4.4	3.6	4.3

Figure 11JJJJ

46116 at			AA044743	4.4	1.5	1.8
56456 at	nypothetical protein dJ1181N3.1		AI632926	4.4	2.2	9.0
81567_at			AI190905	4.4	17	00
			AI290653	4.4	23	4
76717_at			AI375865	4.4	5	3.3
66616_at			AA285069	4.4	2.7	9
64991 at	- 1		AI762686	4.4	O	C
64346 r at	nuclear factor (erythroid-derived 2)-like 2	NFE2L2	AW023229	4.4	2.7	00
82372_at			AA907150	4.4	6.0	60
84/65 at			AI446030	4.4	7.1	1.9
49312_at	CGI-102 protein		AA747303	4.4	3.2	7.4
63398_at	similar to Bos taurus P14 protein		AA130220	4.4	6.9	212
67890 at			AI613399	4.4	3.2	1.3
8/942 at			AA936705	4.4	27	1 6
45280_at	hypothetical protein DKFZp566G1424		AA703316	4.4	i	
47565_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog)	MLL	W55861	4.4	1.4	2.9
70379_at			A1744361		-	
44328 at	hypothetical protein MGC5487		AA905113	4 4	410	200
62495 f. at			AI433785	4.4	17.4	1 00
43367_at	hypothetical protein FLJ20730		AI979164	4 4	- 2	70.7
-9		HEYL	AL040197	4.4	3.2	5 1
രൂ.	hypothetical protein FLJ11269		AI741524	4.4	1.9	6.3
56384 1 at			R17914	4.4	1.3	0.5
48696 at			H48142	4.4	0	0
30204 41			AA703335	4.4	1	2.9
63969 at	ribosomai protein 515a	RPS15A	AW003898	4.4	2.9	0
7247E - at			AI031837	4.4	0	0.8
72000 -1 91			AA063087	4.4	0.2	1.2
75926 at			A1638648	4.4	1.9	3
406/0 at			AA536137	4.4	9.0	2.1
60134 at			AL038866	4.4	1.3	0.3
22 24			H61529	4.4	3.1	3.6
14302 at			AA028209	4.4	1	2.6
41928 at			AA029647	4.4	3.2	1.6

Figure 11KKKK

inventors.	Mil Haconen, er

MAR-binding protein; Golgi-associated, gamma-adaptin ear containing, NFIB U70862 4.3 0.9 ARP-binding protein; Golgi-associated, gamma-adaptin ear containing, AC002400 4.3 0.9 ARP-binding protein; Golgi-associated glycopiolen I (binds to nuclear special AT-rich sequence binding protein I (binds to nuclear special AT-rich sequence binding protein I (binds to nuclear special AT-rich sequence binding protein I (binds to nuclear special AT-rich sequence binding protein I (binds to nuclear special AT-rich sequence binding protein I (binds to nuclear special AT-rich sequence binding protein I (binds to nuclear special AT-rich sequence binding protein I (binds to nuclear special AT-rich sequence binding protein I (binds to nuclear special AT-rich sequence binding protein I (binds to nuclear special AT-rich sequence (BY-DDT) Synthase; alpha1,4 AA-Rich State	463 2 634	and a social containing protein 2	GAB2	AB011143	43	1.0	
ARPE Indiang protein Comparing adaptin ear containing	20075 at		1	U70862	4.2	7.0	
2	39975_at	NIAM1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2	1 -	4C002400	4.3	0.0	0.4
Separation ATTICLE sequence binding protein 1 (binds to nuclear start special ATTICLE sequence binding protein 1 (binds to nuclear start seafold-associating DNAs) AFTICLE Sequence binding protein 1 (binds to nuclear start seafold-associating DNAs) AFTICLE SEQUENCE SE	10332_at	7-60 protein					
State Disciploening DIAM 2) Diametra Secretaria DIAM 2) Di	16899_at	special AT-rich sequence binding protein 1 (binds to nuclear	_1_	AF109134 M97287	4.3	4.2	5.3
State Stat	7188 at	phosphogogloving confirm UNA's))	0
Light Ligh	1000	prosprincipy (wate carboxykinase 2 (mitochondrial)	PCK2	X92720	4 3	2 2	
Second point 1 2 3 3 3 3 3 3 3 3 3	0209 at	dystroglycan I (dystrophin-associated glycoprotein 1)	DAG1	119711	0.0	2.6	
## ## ## ## ## ## ## ## ## ## ## ## ##	8/96 at	complement component 1, q subcomponent, beta polypeptide	CIOB	X03084	4.5	2.0	1.9
at uncharacterized hematopoietic stem/progenitor cells protein MDS031 W499628 4.3 4.5 7.3 at eukaryotic translation initiation factor 2C, 1 EIF2CI AA806364 4.3 3.1 0.5 at cysteinyi-tRNA synthetase CARS AA908890 4.3 2.7 0.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) CARS CAB93130 4.3 0.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 at tryptophanyl tryptophanyl tryptophanyl tryptophanyl tryptophanyl tryptophanyl tryptophanyl tryptophanyl tryptophanyl tryptophanyl tryptophanyl tryptophany	003/_at	globotriaosylceramide/CD/7 synthase; Gb3/CD77 synthase; alpha1,4. galactosyltransferase; 4-N-acetylglucosaminyltransferase	1	4A769110	5.4	1.4	0.4
at cysteinyl:tRNA synthetiase 4 3 4 5 5 at cysteinyl:tRNA synthetiase 4 3 4 5 5 at cysteinyl:tRNA synthetiase 4 3 4 5 5 at cysteinyl:tRNA synthetiase 4 3 4 5 5 at cysteinyl:tRNA synthetiase 4 3 4 5 5 at cysteinyl:tRNA synthetiase 4 3 4 5 at cysteinyl:tRNA synthetiase 4 3 5 5 at cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) CRSP6 CO5931 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl tRNA synthetiase 2 (mitochondrial) WARS2 R40635 4 3 5 at tryptophanyl trypt	5927_at						
AMST8480 4.3 1.3 1.3	1181_at	uncharacterized hematopoietic stem/progenitor cells protein MDS033		W49628	4.3	4.5	7.8
at evkaryotic translation initiation factor 2C, 1 at evkaryotic translation initiation factor 2C, 1 at evkaryotic translation initiation factor 2C, 1 Bat cysteinyl-tRNA synthetase S_at cysteinyl-tRNA synthetase S_at cysteinyl-tRNA synthetase S_at cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) at tryptophanyl tRNA synthetase 2 (mitochondrial) at tryptophanyl tRNA synthetase 2 (mit			<u> </u>	W044698	4.3	0	0
at eukaryotic translation initiation factor 2C, 1 EIF2C1 AA806364 4.3 2.7 2.2 2.4 2.3 2.1 2.4 2.	414_at			0.00			
at cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cysteinyl.tRNA synthetase cyteinyl.try cysteinyl.tRNA synthetase cysteinyl.try cysteinyl.tRNA synthetase cyteinyl.try cyteinyl.try cysteinyl.tRNA synthetase cynitochondria cyteinyl.try	3260_at		1	W8/8480	4.3	1.3	3
State Cysteinyl-tRNA synthetase	639_at		7	VA806364	4.3	2	4.5
g at CARS A4908890 4.3 2.7 at AA534436 4.3 0.9 s. at AN032972 4.3 0.9 at AW434032 4.3 0.9 at AA434032 4.3 0.9 at AA434032 4.3 0.9 at AI027334 4.3 0.9 at AI653006 4.3 0.9 at AI653006 4.3 1.5 2.5 at Cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) CRSP6 C05931 4.3 1.5 2.7 4 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 2 at hypothetical protein FLJ10415 WARS2 R40635 4.3 1.5 at glt glutaminase A13 1.5 2 A13 A13 1.5 2 A13 A13 1.5 A13 A13 1.5	1954_at		1	41971316	4.3	3.1	0.4
at AAB54436 4.3 0.9 1 s_at AI032972 4.3 0.9 1 at AW04040 4.3 0.9 0.9 at AA434032 4.3 0.9 0.9 at AA434032 4.3 0.9 4 at AI627334 4.3 0.9 4 at Cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) CRSP6 CRSP6 4.3 0.9 2.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R05931 4.3 1.5 2 at hypothetical protein FLJ0415 WARS2 R05931 4.3 1.5 4 at hypothetical protein FLJ0415 WARS2 R05931 4.3 1.5 4 f_at glt glutaminase A7524061 4.3 1.5 2.7 4 f_at glt glutaminase A7524061 4.3 1.5 2.7 4	278 g at		- 1	A908890	4.3	2.7	1.8
s_att Al022972 4.3 0 at Aw004040 4.3 0.9 at Al468014 4.3 0.9 at AA434032 4.3 2.5 0 at Al627334 4.3 0.9 4 at Al653006 4.3 1.3 2 at cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) CRSP6 CO5931 4.3 1.5 2 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R405305 4.3 1.6 0 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40535 4.3 1.6 4 at hypothetical protein FLJ10415 Af524061 4.3 1.7 4 at glt glutaminase Af524061 4.3 1.5 2 f_at glt glutaminase Af524061 4.3 1.5 2	068_at			A534436	4.3	6.0	1.9
at AW004040 4.3 0.9 at Al468014 4.3 0.9 at AA434032 4.3 2.5 0.0 at AA434037 4.3 2.5 0.0 at Al65306 4.3 1.3 2. at cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) CRSP6 CO5931 4.3 1.5 2. at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.5 0.0 at hypothetical protein FLJ10415 WARS2 R40635 4.3 1.7 4.3 f_at glutaminase AA524061 4.3 1.7 0.0	554 s_at			1032972	4.3	0	0
at Add88014 4.3 0 at AAA34032 4.3 2.5 at R10307 4.3 0.9 at AI653006 4.3 1.3 r AI65807 4.3 1.5 at cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) CRSP6 C05931 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 2.7 at hypothetical protein FLJ10415 WARS2 R40635 4.3 1.7 f_at glutaminase AA524061 4.3 1.7	293_at		A .	W004040	4.3	6.0	0
at AA434032 4.3 2.5 at R10307 4.3 0.9 r_at Al65306 4.3 1.3 at Al65306 4.3 1.5 at cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) CRSP6 C05931 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.7 at hypothetical protein FLJ10415 WARS2 R40635 4.3 1.7 f_at glutaminase Gls Al768354 4.3 1.7	1699_at			11468014	4.3	0	0
at R10307 4.3 0 at Al627334 4.3 0.9 r_at Al65806 4.3 1.3 at Al222295 4.3 1.5 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 2.7 at hypothetical protein FLJ10415 WARS2 R40635 4.3 1.7 f_at glutaminase Gl.S. Al768354 4.3 1.7	708_at		A	A434032	4.3	2.5	0.4
at Al62/334 4.3 0.9 r_at Al65/3006 4.3 1.3 at Al65/897 4.3 1.5 at cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) CRSP6 C05931 4.3 2.7 at hypothetical protein FLJ10415 WARS2 R40635 4.3 1.7 f_at gutaminase GISI Al76836 4.3 1.5	195 at			R10307	4.3	0	4.1
r_at Al653006 4.3 1.3 at Al656897 4.3 1.5 -at cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) CRSP6 C05931 4.3 2.7 at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 2.7 at hypothetical protein FLJ10415 A3 1.7	496_at		7	11627334	4.3	6.0	2.5
at Al656897 4.3 1.5 _at cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) CRSP6 C05931 4.3 2.7 _at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 2.7 _at hypothetical protein FLJ10415 A3 1.7 _f_at glutaminase 4.3 1.5	306 r at		4	1653006	4.3	1.3	3.3
at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 2.7 at hypothetical protein FLJ10415 (GIS) (GIS) AA524061 4.3 2.7	302_at		4	1656897		1.5	2.2
at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.7 f at glutaminase AA524061 4.3 1.5	319_at	1 -	_1	1222295	4.3	1.6	0.3
at tryptophanyl tRNA synthetase 2 (mitochondrial) WARS2 R40635 4.3 1.7 at hypothetical protein FLJ10415 AA524061 4.3 1.5 f_at glutaminase 6.1 St. Al768354 4.3 3.5		(//KD)		C05931	4.3	2.7	4.8
1 Sputierical protein FLJ10415 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1	539 at		丄	R40635	4.3	1 7	
d Biudiminase	٠,۱,٠	Digital	A	A524061	43		
	404 al	giutaminase	ı	1768357	0 7	5.0	

Figure 11MMMM

10000			AI926365	5.7	1.2	-
51792_at			H80286	5.7	1.5	
46153 at			W07089	5.7	2.1	
47602 at			R02594	5.7	6.9	
57968 r at			AA393223	5.7	100	0
37214 g at	deoxyriboniclease Libe 1		AA431469	5.7	1 a c	9.4
1357 at	ubiquitin specific	DNASE1L1	X90392	5.7	7.6	0 0
39105 at		USP4	1	5.7	3.0	0.0
53155 at	State Priosprioprotein	VASP		5.7	2.6	oli
46664 at	aboutosis.associated speck like associated		AA608559	5.7	0.7	ייני
37506_at	Huntingtin-interacting protein A		A1148558	5.7	5.1	7.1
40773_at	myosin, light polyneptide 5, regulatory			5.6	1 7	
40791_at	polymerase (RNA) II (DNA directed) polymerase (RNA) II (DNA directed) polymerase	MYL5		5.6	5.9	
33418 at		POLR2A	X63564	5.6	3.1	200
35137_at	myomesin 1 (skelemin) (185kD)		AL096752	5.6	7.2	5.7
35198_at	hypothetical protein from clone 24796	MYOM1	06069X	5.6	0 7	3.6
35251_at	human immunodeficiency virus type I enhance hindi		AF070596	5.6	46	6.7
1856_at	V-rel avian reticuloendotheliosis viral opcomes hand	HIVEP1	X51435	5.6	6.4	10.0
39281_at	Rho guanine exchange factor (GEE) 11	REL	X75042	5.6	4 1	16.6
35320 at	Solute carrier family 11 (proton countries	ARHGEF11	AB002378	5.6	3.2	
	transporters), member 2	SLC11A2	AB004857			2
35787_at	dynein, cytoplasmic, intermediate polypentide 2					,
37177_at	CD58 antigen, (lymphocyte function associated aptiggents)	DNC12	AI986201	5.6	5.6	
39562_at	CGG triplet repeat binding protein 1	CD58	Y00636	5.6	6.5	90
40757_at		CGGBP1	AF094481	5.6	2.4	
16771 24	esterase 3)	GZMA	M18737	5.6	1.3	23.9
50000			WEGERE			
5150 of	neurexopniin 4	NXPHA	1779011	0.0	2.3	2.8
00100 at	Udi-18 protein	1	1/01010	5.6	2	3.3
/3901_at			AIU/3484	5.6	1.8	C
72649_at			AI984965	5.6	6.0	1 4
62914_at			AI765590	5.6	0.7	1 4
84232_at			AI363275	5.6	6.0	101
69834_r_at			AI806926	5.6	1.2	3.0

42881 at			W81045	5.6	3.6	
			R88708	5.6		
46960 at			A1148006	5.6	A	
			AI743903	5.6		C
63251 s at			W72338	5.6		
			AA904828	5.6		
51185 at PAN2 protein	protein		AI185207	5.6		
+			Al309334	5.6	4	33
46727 at			AI741209	5.6	4.	101
46808 at			AI146850	5.6		
53689 at			AL120562	5.6		
Ŀ	meningioma expressed antigen 5 (byglygganga)		_	5.6	2.2	
1	in FI 110074	MGEA5	_	5.6		
Г	hypothetical protein FI 120038		AA018399	5.6		
Г	١		AI921097	5.6		60
Π			W68512	5.6	2.8	4 1
ŧ		NNS	W72938	5.6		0.4
١.,	chromosome 18 onen reading frame 1		AI693465	5.6	2.1	15.9
1		C180RF1	AF009425	5.6		
64028 s at			AI744466	5.6	3.3	4.6
49390_at			AI886403	5.6	4.4	5.9
52261_at			AA999858	5.6	5.6	5.6
s at	O-linked N-acetylglucosamine (GlcNAc) transferance (LIDB N		AI970054	5.6	4.7	6.4
acetylgli	acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	190	U77413	5.5	1.1	1.8
T	TAK 1-hinding protein 3: KIAAA233	RPS6KA5	AF090421	5.5	3.3	0
1.	hynothetical protein		AB018276		000	ò
1	hone marrow stromal cell anticon 2		W29115		80	1.0
Γ	me macropain) cubinais has a	BST2	D28137	5.5	9.7	9
	HMBA inducible	PSMB2	D26599	5.5	7	4.6
	KIAA0005 gene product		AI796944	5.5	C	0.0
Γ	KIAA0342 gene product		D13630	5.5	3.2	0.0
377 g at sema do	Sema domain, immunoplobulin domain (Ig), short basis demain		AB002340	5.5	3.6	3.2
	secreted (semiophoria) 20	SEMASCI	SEMA3C AB000220	7.	0	

\top	30203		2.5	1.2
Т	AF09452	1	2	0.0
	090912		5	2.5
	W25874		5	
22772 at papilialy lettal carcinoma (translocation-associated)	PRCC X99720		5 1.5	17
58524 at	AA743565		5	9
54400 s at	W03029		.5	C
74006 at	AW001883		.5	3.2
66774 at	AI984623	3 5.	.5	
74975 f at Tring finger protein 173	-	5.	3.3	2.1
שווים ווויפרוו דיווים	ZNF173 AW009746	16 5.	5.5	14.1
47489 at	AI203222		5 1.3	O
75201 f at	AI452516		.5 2.9	1.5
55280 at Distative NE DNA mathyltonafeas	A1688900	0 5.	.5	7
	AI016585		.5	10.4
÷	-	.7 5.	.5	2.6
59608 at	CTNNA1 AF102803		.5	0.1
73601 at	AA176289		.5 2.6	0.3
63950 at	AI88567	7	.5	0.2
43838 s at hypothetical protein DDO1069	R22212		.5	4.6
manal managed for	AA100948		5.5 0.4	3.4
68328 at	A1660022		.5	0.6
45390 at	AI475514			32.1
42965 at	AI769269		.5 7.2	0
57470 at	H24422		5 1.7	1.6
88025 s at	A109158		5	2.7
50187 at	Al199443		5 0.5	2.5
at IGCN1 (general control of amino acid sustitution)	\dashv		9.0	6
Po in in in in in in in in in in in in in	GCN1L1 A1939557	7	.5	1.2
66856 r at	AI457965			6.0
71516 r at	AA993791		5.5	2.8
69622 at	240202		5 0.3	2.1
small nuclear RNA	A1669987			4
Γ		5.		r.
Coccessor Caracinate OnipovyBellase activating protein	ALOX5AP A1983204		5	5.4

44693 at hypothics 44693 at hypothics 52107 g at CGI-90 39748 at adenyles 40788 at adenyles 31522 f at H2B his 35879 at galanin 33713 at transloc 41234 at DnaJ (+ 31633 g at zinc fin 39209 r_at pro-plat hypothetical protein FLJ1937 CGI-90 protein		1 2005014	2 1	2.	3	
	-90 protein		2000	•	0 1	C
 			2000014		7.7	5.0
1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-			AIBUUD/4		6.2	7.6
~ - - 			_	5.4	2.5	0
 		AK2		5.4	2.7	C
	HZB histone family, member G	H2BFG		5.4	25	α
	ının	GAL	L		Si a	0.0
	translocase of inner mitochondrial membrane 17 (yeast) homolog B		<u> </u>		2.2	3.1
	DnaJ (Hsp40) homolog, subfamily B member 6	00. 440	_ !_			
	finder protein 250 projudezasa	DIANBO	`	5.4	6.0	6.2
E E		ZNF259P	Z95118	5.4	0	0.0
	pro-platelet basic protein (includes platelet basic protein, beta- thromboglobulin, connective tissue-activating peptide III, neutrophil- activating neptide, 2)	РРВР	M54995	5.4	0.4	4.2
	E2F transcription factor 5, p130-binding	1100	-			
	uil.	E723		5.4	0	0.7
П		MLN	X15393	5.4	1.8	5
	transcriptional activator of the c-tos promoter		M94630	5.4	2.7	60
	protein Kinase (CAMP dependent, catalytic) inhibitor gamma	PKIG	AB019517	5.4	2.2	9 6
Т	turnor necrosis factor receptor superfamily, member 10b	TNFRSF10B	AF016266	5.4	0.3	3.5
_	nypotnetical protein FLJ10/38		W28620	5.4	0	3.6
Т	acetylserotonin O-metnyitransterase-like	ASMTL		5.4	1.8	2
T	splicing factor, arginine/serine-rich 4	SFRS4	L14076	5.4	5.3	4.2
7043 s at nem	nemopoletic cell kinase	HCK	M16592	5.4	0.8	0.6
91700 at			AI922968	5.4	0.1	2.4
55158 at			AA586814	5.4	5.2	0
T	Otonoin I than I the second of		AI741328	5.4	3.8	1.2
T	aligiotensin ii, type i receptor associated protein		AI858573	5.4	1.2	0.1
T	L (S. POLIDE) HOLHOLOR	SKB1	AA932371	5.4	1.7	2.5
T			AI023295	5.4	7.5	0
T	NOUZ protein		AA910520	5.4	0.7	
T	protein kinase CnkZ		N24330	5.4	-	1.7
01400 at	ilypoilietical protein FLJ12903		A1807668	5.4	2.5	5.1
1			AI309016	5.4	3.6	3.2
	collegal, type IA, alplia 1	COL9A1	N66408	5.4	2.2	5.2
01447_at			AI916887	5.4	1.7	0.1

			AI311917	5.4	2.4	6 9
0,1			AA521145	5.4	5.2	50
4/8/8_t_at	KIAA0117 protein		AI656542	5.4	α C	3.5
43488 at	transporter-like protein		AI768065	5.4	4.2	
			AA707322	. r	7.7	7 0
87617_at	hypothetical protein FLJ13385		AA639580	1 2	7.7	50
68909_at			AI001231	4.0	1.7	1.6
69715_at			01742410	4.0	0.0	1.4
72052 at			A1743419	5.4	0.5	2.8
54799 at	glutaminase		N/1632	5.4	0.3	4.4
58825 at	prothymosin alpha (gene segmence 30)	OLS OLS	- 1	5.4	0	0
57042 at	similar to Caenorhabditis alorgen profits 04201.0	PIMA	Al701911	5.4	6.9	7.3
49057 g at	similar to daction labour is elegans protein 04201.9		W74749	5.4	1.6	0
57077 s at			AA521489	5.4	11.9	0
50073 24			AW021642	5.4	1.5	m
45655 at			W87422	5.4	0.8	5.7
45055 at	turnor antigen SLP 8p		AL045849	5.4	5.7	2.4
40103 at			AA149641		5.4	i
55009 at			AI359000	5.4	20	0
	- 1		W29045		0.5	r O r
39341 at		TRIP6	AJ001902	5.4	000	
3//59_at	.≌1		U51240	5.4	2.0	1 0
39163_at	likely homolog of rat kinase D-interacting substance of 220 kDa;		W27233	5.4	6.0	y. 4
	KIAA1250 protein			 -	,	r.
45521_s_at			A1967955	2.7	4	-
63793_at			AI797479	5 7	0.0	2.7
45/36_at	two-pore channel 1, homolog		AI 048491	2.0	7.0	0.4
36495_at	fructose-1,6-bisphosphatase 1	FBP1	1121931	1 2	2.0	3.1
31996_at	brefeldin A inhibited guanine nucleotide exchange protein 2		A1798834	200	-	y. 4. 0
41634 at	KIAA0256 gene product		D87445		200	4.0
37798_at	chromosome 8 open reading frame 2	CRORF2	AB018790		0.0	2.4
41134_at	KIAA0964 protein	3	AB023181	0.0	0.0	2.9
1383_at	protein phosphatase 2 (formerly 2A), regulatory subunit R (PR 52)	Acacada	Medono		4.5	1./
		777711	67670INI	 	ç.,	12.4
41170 at	KIAA0663 gene product		AB014563	5.3	2.7	CC CC
37575_at			AL050192	5 23	3.5	0.00

38778 at	KIAA1046 protein					
38278 24	modulotor socialis factorial		AB028969	5.3	4.8	3.3
50051 at	modulator recognition factor I		M62324	5.3	2.9	77
20004 41	C		AA034067	5.3	- 2	2.1
45639 at	ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	١.,	5.3	3.10	7.7
49298 at			AW021968	5.3	0.6	5 0
2000/ at			AA128061	5.3	1.7	100
61911 at			AW051492	5.3	2	9
8/35g 2+			AI393033	5.3	2.1	- 1
61840 g at	Tiredpool aigotto		AI674428	5.3	1.4	0.4
50451 24	catenini (cadillerini associated protein), delta 1	CTNND1	AI863000	5.3	4.5	6
45323 at	hypothetical protoin El 120003		AI800640	5.3	6.2	23.2
85691 at	יון איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן		W87653	5.3	2.3	3.4
45247 at	hypothetical protein El 111069		AI989354	5.3	5.6	6.1
91891 at			N63911	5.3	2.1	5.8
85939 at			AL045717	5.3	1.6	1.2
86004 at			AI694139	5.3	0.4	1 3
71077			AA767895	5.3	0.5	7.0
73112 at			AI912203	5.3	1.7	4 9
73811 24			R35404	5.3	1.6	
75063 24			AI972618	5.3	1.2	0
87431 at			AI732791	5.3	m	74
49736 g at	hypothetical protein		AI872409	5.3	1.9	10
13067	himpothetical proc		AI497781	5.3	2.5	-
45504 at	ilyputietical protein FLJZU831		AA131537	5.3	60	117
43405 s at	hypothatical protein 4	FBX04	ш	5.3	1.3	0.5
70228 r at	protein kingso of MO document		AA219406	5.3	1.1	0
69705 at	Protein Amase, CAMIT-UEDEINGENT, regulatory, type II, beta	PRKAR2B		5.3	9.7	
67220 at			R68222	5.3	3.1	
30/16 24	Tay information managed to		AW005511	5.3	m	7
40400 24	aldebide debide 1		U90913	5.3	3.7	L C
35336 at	KIAAAAAS 2000 J. J. J. J. J. (Tatty aldenyde dehydrogenase)	ALDH10		5.3	3.9	0,1
35688 4 21	Tours Test		AL021707	5.3	36	5.0
37320 at	mature r-cell profit	MTCP1	224459	5.3	2.6	4.3
30011 ot	priodulatinyiseriile synthase I	PTDSS1	D14694	5.3	2.2	5.7
- 1	Rr 85-mediating protein		AB006572	5.3	2	4 9

Figure 11TTT

52936_at			165761	5.3	1.5	5.1
55567_at			AA147933	5.3	5.3	5.2
38684_at	ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	AJ010953	5.2	9	2.2
32183_at	splicing factor, arginine/serine-rich 11	SFRS11	M74002	5.2	1.9	0.0
39407_at	bone morphogenetic protein 1	BMP1	M22488	5.2	2.4	5
39742_at	TRAF family member-associated NFKB activator	TANK	U59863	5.2	4	3.1
31856_at	glycoprotein A repetitions predominant	GARP	Z24680	5.2	3.9	5.3
31975_at			X55503	5.2	1.5	1.9
33869_at			AL080218	5.2	3.2	3.8
39342_at	methionine-tRNA synthetase	MARS	X94754	5.2	1.9	C
830_at	Tax1 (human T cell leukemia virus type I) binding protein I	TAX1BP2	U25801	5.2	0.8	3.6
1105_s_at	T cell receptor beta locus	TRB@	M12886	5.2	1.3	11.7
39950_at	acid sphingomyelinase-like phosphodiesterase		Y08136	5.2	0	6.0
984_g_at		MAPK12	X79483		5.9	8.8
37299_at		GYS1	J04501		2	0
1119_at	replication protein A2 (32kD)	RPA2	J05249	5.2	0.5	9.0
38384_at	phosphoribosylglycinamide formyltransferase,	GART	X54199		2.7	0.1
	phosphoribosylaminoimidazole synthetase					
38397_at	polymerase (DNA-directed), delta 4	POLD4	009196	5.2	1	C
38437_at	MLN51 protein		X80199	5.2	2.6	1.7
277_at	myeloid cell leukemia sequence 1 (BCL2 related)	MCL1	L08246	5.2	3.9	10
56371_at			AA534298	5.2	3	0
48873_at	Gene 33/Mig-6		AI571452	5.2	3.4	25.2
53777_at	hypothetical protein FLJ22693		AI672353	5.2	3.8	2.2
74423_at			AI793024	5.2	2.2	2.6
82222_at			T64664	5.2	0.1	0.3
50080 at			AI097194	5.2	3.3	3.2
51715 at	lung type-I cell membrane-associated glycoprotein		AA149854	5.2	3.5	6.4
80829_at			AA210905	5.2	4	3.4
59566_at			AA705681		1.5	4.5
48547_at	pleckstrin homology domain containing, family A (phosphoinositide hinding specific) member 1	PLEKHA1	AA875839	5.2	1.9	3.5
84960 at			71777014	2	4	C
2000			1140010	3.6	0.0	0.6
452/2_at			AA058569	5.2	5.6	2.4

70053_r_at			AI734928	5.2	0.6	2.2
101/0-1 at			AI251913	5.2	2.5	1 0
80421 5 at	Split receptor	LEPR	N46838	5.2	5.1	15
13535 at	solute carrier railing 41 (organic anion transporter), member 12	SLC21A12	AI347130	5.2	3.1	C
87703 at			N37020	5.2	2.2	0
47430 at			AL042667	5.2	0.4	0
66512 at			T65857	5.2	0	0
15624 at	Manager and Manage		AI970258	5.2	1.6	2
43024_al	core i ODF-galactose: N-acetylgalactosamine-alpha-R beta 1,3. galactosyltransferase		AI967968	5.2	6.9	4
62306_at	hypothetical prote		T07247	C	0	
55915_r_at	hypothetical protein LOC54149		197347	2.6	2.3	2.8
46612_at	KIAA1624 protein		U26226IA	5.2	13.7	15.9
64740 at			R39794	5.2	10.2	1.6
55800 at	hypothetical protein Al 133206		AA470369		3.5	2.2
61299 at	chaperonin containing TCP1 cubinit 60 (2010 1)		W72766		2.2	0
55650 24	מישקט מייים מייים וייים אין די אחחווון חא (לפומ ד)	CCT6A	R43952	5.2	2.8	1.6
1500 at			W22914	5.2	1.7	2.5
2101C			2945576	5.2	22	6.0
51610_at	glucosidase, alpna; acid (Pompe disease, glycogen storage disease type II)	GAA	X55079	5.2	1.3	5.9
40955_at	prostate tumor over expressed gene 1	PTOVI	1170007	C		
41540_at	protein phosphatase 1, regulatory subunit 7	PPP1B7	750740	2.6	4.6	4.6
34811_at	ATP synthase, H+ transporting, mitochondrial F0 complay subunit c	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	230/43	2.5	2.9	5.2
	(subunit 9) isoform 3	5500	009813	5.2	3.2	6.2
36601_at	vinculin	iON	M33308	5.2	9 7	
	biliverdin reductase B (flavin reductase (NADPH))	BI VRB	D32143	7.0	0,1	10.1
48750 at	class I cytokine receptor		A1983115	2.0	0.0	5.0
44638_at	insulin-degrading enzyme	IDE	AA573292	2.5	0.7	4 4
59136_at			AA779895	7.5	2.0	4.2
48811_at	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase		AW007594	5.2	7.0	5.2
54912_at	translocase of inner mitochondrial membrane 13 (yeast) homolog B	TIMM13B	AL035821	5.2	3.4	5.4
51123 at						
52012 at			H11/24	5.2	5	4.9
			AI659020	5.2	3.5	5.3

Figure 11VVV

53120_at	hypothetical protein FLJ20442		AI681916	5.2	4.3	4.8
487 g at	caspase 9, apoptosis related cysteine protease	CASP9	U60521	5.1	4.2	2.4
40491_at	DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 21	DDX21	W84531	5.1	1.3	2.3
32735_at	KIAA0931 protein		AB023148	5.1	1	0.7
34719_at	glutaminase	STS	AB020645	5.1	0	0
39320_at	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	CASP1	U13697	5.1	6.9	1.1
35227_at	retinoblastoma binding protein 8	RBBP8	U72066	5.1	6.0	5.3
34378_at	adipose differentiation related protein	ADFP	X97324	5.11	13.3	0.1
35845_at	SEC24 (S. cerevisiae) related gene family, member B	SEC24B	AJ131245	5.1	1.2	3.4
36888_at	KIAA0841 protein		AB020648	5.1	0.8	6.9
38027_at	fibulin 1	FBLN1	X53742	5.1	6.0	0.5
32792_at	GCIP interacting protein p29		AL031432	5.1	3.2	4.1
38369_at	myeloid differentiation primary response gene (88)	MYD88	U70451	5.1	15	18.4
38824_at	Tat-interacting protein (30kD)		AF039103	5.1	5.8	12.6
37082_at	KIAA0426 gene product		AB007886	5.1	9.0	2.3
54747_at	endosulfine alpha	ENSA	AA167734	5.1	5.2	0
65027_r_at			AA532470	5.1	2.1	2.1
84981_r_at	collagen, type III, alpha 1 (Ehlers-Danios syndrome type IV, autosomal dominant)	COL3A1	154146	5.1	8.6	5.6
42564_at			W84667	5.1	2.9	4.6
78014_at			AA371513	5.1	2.7	0.7
47832_at			AA100654	5.1	0	
43363_s_at			AI978590	5.1	1.9	10.4
50763_at	KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2		AA779863	5.1	9	3.4
42631_at			AI984505	5.1	1.8	2.1
84167_at			AI742722	5.1	2.7	0.4
88155_at	H2B histone family, member B	н2вғв	AI125923	5.1	0	9.0
48374_at			W87470	5.1	1.4	9.1
74131_at			AI989784	5.1	2	4
			AW021543	5.1	0	4.4
61745_r_at			N76044	5.1	2.7	∞
44397 at			H11252	5.1	4.3	4.4
52072_at	hypothetical protein FLJ10718		AA873182	5.1	0.8	4.1

Figure 11WWW

149054 21	adenylate Vinare 3 alpha lika					
50617 ot			N32441	5.1	3.1	0.4
2001/ 40	f.		AA149312	5.1	3.4	0.3
74823_t_at	nistidyl-tRNA synthetase	HARS	AW022495	7	7.3	- 0
64847_at				1 -	2	0.1
54410_at			NZOAAS	1.0	4 1	3.4
80825 at			14/0443	2.1	7.7	0
40279 at	KIAA0121 gene product		A1590115	5.1	9.0	0
1000 at	Minoritz Beile product		D50911	5.1	3.4	3.7
1030 S at	spieen tyrosine Kinase	SYK	Z29630	5.1	3.9	4 9
33833 at	Spectrin, alpha, non-erythrocytic 1 (alpha fodrin)	SPTANI	J05243	5.1	a c	7.7
32594_at	chaperonin containing TCP1, subunit 4 (delta)	CCT4]	5	2.5	7.
48110_at	hypothetical protein FLJ11271		1.	5	2 2	7.7
51179_at			AI741843	5 1	0.0	7
68339_at	transforming growth factor, beta-induced, 68kD	TGFBI	A1624028	5.1	22	. r
651/1_at	clone FLB4739		6069EN	7	7 2	100
61853_at			AA773816	2	7	2.5
49569_at	hypothetical protein FLJ20281		A1690893	1 -	1.0	7.0
(65603 at	baculoviral IAP repeat containing 6	20010	20000	1,0	4.2	4.5
45293 at	hynothetical protein from ELIBOIMANCE 2626.60	מואכס	AA886981	5.1	2.9	5.4
56418 24	The first of box of the condition of the		AA631902	5.1	4.4	4
of too	unchal acterized fierhalopoletic stem/progenitor cells protein MDS027		N25128	5.1	3.7	5.8
45224_at			0.000000	l		
57714_at			44400113	7.0	3.2	3.5
36908 at	mannose recentor. Citype 1			5.1	3.6	5.1
55695 21		MKC1	- 1	5.1	4.2	4.6
38137 24	Specific cleavage system protein in (arminometriy) carrier)	GCSH		5.1	4.5	4.2
31808 24	Vicionistry and adelional gene 1	PLAG1		2	0.7	1.4
22142 at	MANAZIZ Belle product	kiaa0212	D86967	5	3.7	23
32142 at	serine/threonine kinase 3 (Ste20, yeast homolog)	STK3		5	4.1	3.6
1946 T at	nitric oxide synthase ZA (inducible, hepatocytes)	NOS2A		5	40	2.0
32233 at	torsin family 1, member B (torsin B)	TOR1B	AF007872	LC.	0 9	13
	KIAA01/0 gene product		AI 041663	, L	0.0	21
	upstream regulatory element binding protein 1		797054	0		10
	glutathione S-transferase M5	GSTME	102301		7.7)
1072 g_at	GATA binding protein 2	CATAG	1772010	n i	1.1	4.8
38064 at	major vault protein	20100	-	מו	1.5	6.3
39170 at		1414	7006/	ה	11.8	0.9
			AI 049957	ŭ	17.	7

Title: Response of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

	1	- 1				
82798 g at	chromosome 6 open reading frame 32	C60RF32	AW016644	5	0	2.5
48488_at	hypothetical protein		AI889499	2	0	0
89829_at	hypothetical protein FLJ10521		AI913628	5	9.0	9.0
66361_at			AA009699	5	4.3	0.8
73713_at	RAB, member of RAS oncogene family-like 2A	RABL2A	AI051621	5	0.4	2.5
53828_at			AI929168	5	1.1	3.6
62472_at			H49102	2	1.5	2.3
83036_at			AI271559	5	0.5	3
82768 g_at			AA913354	5	0.8	2.5
83224_r_at			AI053582	5	1.6	0.5
66108_s_at			AI915696	2	2.9	1.6
79105_at			AA830599	2	5.6	2.2
69388_at			A1299040	5	ō	2.6
49516_at			AA531016	5	9.9	3.5
61354_at			AA218990	2	1.3	1.5
70495_at			AI453095	2	4.2	2.8
57608_at			AA523335	5	1.7	0
46169_at			AI745624	Ŋ	4.5	12.3
46514_at			R38647	5	2.9	0
53321_r_at			AL043875	5	3.5	5.1
51991 at			AI884621	2	1	0.5
45204 s at			AI378647	5	10.2	5.2
45787_at	cyclin L ania-6a		N29695	5	2.3	5.4
53657_r_at	non-kinase Cdc42 ef		AI825880	2	2.2	2.4
58339_at	hypothetical protein FLJ13222		R52747	S	2.7	3
73128_at	dihydropyrimidinase-like 3	DPYSL3	AI983251	S	7.2	0
46277_at			AI031551	2	10.2	1.6
58688_at	RAB23, member RAS oncogene family	RAB23	AI742498	2	1.4	1.6
55495_at			AA187437	5	0	0.5
46724_at	tensin	INS	_	2	3.9	0
52252 i_at			2963428	2	1.7	1
54167_at			3162292	5	1.8	1.5
39801_at	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	PLOD3	AF046889	S.	2.1	5.9
40382_at	corticotropin releasing hormone	CRH	V00571	22	4.7	3.8
48059_at			R61448	5	4.4	3.5

58780 c at		1	4740TM	2	1.5	ĹC.
7X/X			AI701293	2	2.7	ı.c
20,00	_		R42449	ır	26	3.7
45255 at	CGI-69 protein		AI354351) LC	0,10	5 4
45808_at	anaphase promoting complex subunit 7		AA131793	יע	000	7.0
34427 g at	major histocompat	U IV	1		7.7	2.6
38892_at	KIAA0240 protein	100			3.7	0.0
33437 at	homolog of yeast SPB1		1001001		6.2	1.5
36270 at	CD86 antipen (CD28 antipen ligand 2, R7.2 antipen)	2000	١,	4.9	1.3	0.7
35720 at	מינים ביו	വജമ	- 1	4.9	13.2	3.9
31590 9 34	1		AB020700	4.9	2.2	10.8
71502 pt	IAK hinding prote	GABBR1	AL031983	4.9	6.0	10.3
41332 at	Sizes and an analysis of the sizes of the si		AB000734	4.9	9	7.7
32535,41	Sjugren syndrome antigen AZ (b0kD, ribonucleoprotein autoantigen SS) A/Ro)	SSAZ	J04137	4.9	2.3	1.4
35363_at	DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 17 (72kD)	DDX17	AL080113	0 7	2.7	
36550_at	ras association (RalGDS/AF-6) domain containing protein JC265		AL049538	4.9	000	
4034 / at			AA913812	0 7	2 2 2	
40668 s at	_	CD6	1_	0.7	0.0 R	10.7
40712 at	a disintegrin and metalloproteinase domain 8	ADAM8		0.4	0.7	16.6
75743 at			44668789		7.0	1.6
78468_at			20/00/07	v. 4.	3.4	1.6
90341 at			1,04200	y. 4		2.7
			H04388	4.9	4.3	0.2
47215 r at			A1609998	4.9	0.7	1.3
49237 at	PMA hinding motif		_1	4.9	2.9	8.4
63277 34	T	RBMX	_1	4.9	2.5	12.8
57658 24	hypothotical aratain El 1100EF		AI809894	4.9	2	4.7
44731 at	וואסטוופווימן און דרטווטאליי		A1961496	4.9	3.3	1.5
87588 24			AI807804	4.9	3.6	2.2
56065 at	HCDCORE Strategie		AI691077	4.9	2.9	4.3
77035 24			N51105	4.9	6.4	
13690 at	hypothetical protein reduit/4		W04760	4.9	0.3	2.6
75820 r at			AA019641	4.9	0.2	0.4
65036 24			AI679201	4.9	1.6	2.5
0753 at			AA034414	4.9	3.3	4.7
69/63 r at						

72002 t at			H53031	4.9	0.8	2.8
07/16 2 04			AA677864	4.9	3.4	7.5
Т			T91504	4.9	9.0	6.6
1	papiliornavirus regulatory factor PRF-1		N25612	4.9	2.5	
s at	LOPY-IIKe	TSPYL	AI972301	4.9	1.5	
01002 at			AA442900	4.9	2.5	1.5
01003 at			AI248920	4.9	1.3	0.2
45012 at			AI744560	4.9	3.7	5.9
55086 at			AA479835	4.9	0.8	6.0
Τ	hypothatical profess El 190319		AW003215	4.9	1.8	2.6
			AA524056	4.9	1.2	2.8
Τ	hypothetical protein (Latrau)		AI820049	4.9	2	1.6
T	DAB Sh protoin		AA524361	4.9	4.8	3.6
1	ווייסות מסימעני		AI458521	4.9	3.5	2
84063 1 24			AI075909	4.9	1.1	3.4
7	CMI /SNE zalotad		R42423	4.9	2.9	8.1
	chromatin, subfamily a, member 5	SMARCAS	N36842	4.9	3.2	4.2
T	KIAA0602 protein		AB011174	4 9	7.0	7.0
at	hypothetical protein		AF070638	0 4	2.7	7
1	ribosomal protein L3	RPI 3	AI 022326	50	0.00	0.0
Т	ralA binding protein 1	RALBP1	L42542	4 9		4.3
at	KIAA1545 protein		H17730	4 9	5.9	2 4
53884_at			AA312905	4.9	6.8	4 7
43300 at	VIAA1363 2004014		AA126841	4.9	2.3	5.6
\top	אומיס ליניים אין אין אין אין אין אין אין אין אין אין		AI769531	4.9	9.0	5.1
┰	OKEZDASAE173E azatoja		AW025012	4.9	3.2	4.6
7	יייייייייייייייייייייייייייייייייייייי		AW005775	4.9	3.5	5
1	hypothetical protein Fl 123239		AI810687	4.9		5.3
Τ	hypothetical protein HES6		W6/828			4.4
Π			N21131	4.9	4.9	4.8
	BTB and CNC homology 1 basic lenging zigner transcription 4		AL048421	4.9	3.8	4.8
	Support the support of the support o	BACH1	AB002803	4 8:	1.3	2
1/11_at	tumor protein p53-binding protein, 1	TP53BP1	U09477	4.8	3.1	1 7

Figure 11AAAA

ellipto	elliptocytosis chromosomal region, gene I	AMMECR1	AJ007014	8 .8	1.1	8
desmo	l i	DSC2	X56807	8	2	
neuroe	neuroepithelial cell transforming gene 1	NET1	AJ010046	0.4		2.7
MAX b	MAX binding protein	LNW	X96401	4 8	, ,	
plecks	pleckstrin homology, Sec7 and coiled/coil domains, binding protein	PSCDBP	14	8.4	2.4	2.2
KIAA0	KIAA0257 protein		087446	o v		
vinexir	vinexin beta (SH3-containing adaptor molecule-1)		AF037261		4.0	7 0
insulin	insulin induced gene 1	INSIGI	1196876	0.4	2 6	0.7
clones	clones 23667 and 23775 zinc finger protein		090919	2 4	2.7	0 0
tyrosin proteir	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	YWHAQ	X56468	4.8	2.9	7.4
ubidu	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	UBE2E1	AI039880	4.8	1.7	4.6
transg glutam	transglutaminase 2 (C polypeptide, protein glutamine gamma- glutamyltransferase)	TGM2	M55153	4.8	2.5	0
epithe	epithelial membrane protein 3	EMP3	U87947	4.8	8	4
			AA703201	4.8	4	1
-			AL044396	4.8	1.5	46
0/1/10	- 1		AA706818	4.8	10.8	
UNFZF	UKFZF/Z/GUS1 protein		AA203321	4.8	0.8	
			AI953998	4.8	4.6	0.7
1			AI377910	4.8	9.0	0.4
			AA009692	4.8	2.8	0
1			R64696	4.8	3.2	0
DVC7D	DKE784348303 = 201-1-		AI732798	4.8	0.5	1.4
Τ			AA099904	4.8	2.6	6.3
73656 " at Inypotin	nypometical protein		A1979070	4.8	1.1	33
			AI719644	4.8	1.2	6.1
\downarrow			AA703523	4.8	0	0.4
1			H11817	4.8	0.1	9.2
			A1333655	4.8	0	0.3
40033 Lat			T95654	4.8	2.1	2.6
		-				

Figure 11BBBB

73439 at 63373 at			K66534	Δ Σ	1.5	2.0
63373 at	hypothetical protein MGC3156		AA349855	4.8	2	2.8
			AA194033	4.8	4.8	2.2
73574_at			AI290214	4.8	3.7	8.1
64577_at			H60064	4.8	2.1	2.9
44066_s_at	G protein-coupled receptor kinase-interactor 1	GIT1	AI887641	4.8	2.8	5.5
53546_at			AI168683	4.8	3.7	6.7
62165_at	x 006 protein		W72231	4.8	3.2	5.9
45580_s_at			A1983200	4.8	3.6	1.8
53680_at			AI130786	4.8	0	1.3
51813_at			AI797095	4.8	7.1	1.8
46237_at			AW001342	4.8	2.5	6.7
58682_at	DEAD/H (Asp.Glu-Ala-Asp/His) box binding protein 1	DDXBP1	AI348378	4.8	6.2	Ō
52347_at	CGI-60 protein		AI985204	4.8	0.3	1.4
54989_at			H43374	4.8	4.9	1.2
51697_r_at			AA649308	4.8	m	4
55601_at			AI742770	4.8	2.9	0
47608_at			AI697401	4.8	1.1	1.2
47330 at			W81697	4.8	1.5	9.3
70054_i_at			199829	4.8	1.7	3.5
73569_r_at			AI708856	4.8	6.0	2.7
75232_at			N31820	4.8	1.1	1.3
80059_at			H79244	4.8	1.1	3.4
84212_i_at			AI203819	4.8	0	2.6
38716_at	밁	CAMKK2	AB018330	4.8	0	2.4
41603_at	_	TBL3	00500	4.8	3.8	5
39866_at	ubiquitin specific protease 22	USP22	AB028986	4.8	2.6	5.9
40113_at	GS3955 protein		D87119	4.8	3.1	4.1
40824 at		RANBP16	AB018288	4.8	2.5	5.3
38943_at	holocytochrome c synthase (cytochrome c heme-lyase)	HCCS		8.4	2.9	4.4
38733_at	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)	XRCC5		8.8	1	4.3
33198_at	binder of Arl Two		AA206524	4.8	2.3	6.8
56520_at	Inudix (nucleoside diphosphate linked moiety X)-type motif 5	NUDTS	AI188576	8.4	3.3	4.3
45307_at			AI921204	4.8	1.6	5.9

	Process Street E (E.Coll MILID IIAG)	NUBP2	AA552351	4.8	5.6	6.0
45878 at			W21966		3.6	4.6
399/1_at	lymphoblastic leukemia derived sequence 1	LYL1	M22637	4 8	3.5	
38612_at	tetraspan 3		M69023	4.7	2.5	1 0
38630_at			AI 080192	7 7	0.0	
39486_s_at	KIAA1237 protein		W28968	1 7	4.0	2.1
1713_s_at	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CDKN2A	1	4.7	0	5.6
39410_at	development and differentiation enhancing factor 2	DDEF2	AB007860	7 7	C	10
40202_at	basic transcription element binding protein 1	BTEB1	1	4.7	1.0	0.1
40064_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3	ALS2CR3	⋖	4.7	0.8	1.5
40470_at	oxoglutarate dehydrogenase (lipoamide)	OGDH	010523	7 /	9 6	
2820_at	CCR4-NOT transcription complex, subunit 4	CNOTA		,,,	0.0	0.3
9310 at	bradykinin receptor B2	BDKRR2		1.1	1 0	10.4
610_at	adrenergic, beta-2., receptor, surface	ADRB2	1_	4.7	0.0	0.4
33492 at	- !		AI624840	4.7	α-	7 7
35285_at	solute carrier family 4, sodium bicarbonate cotransporter, member 4	SLC4A4	AF007216	4.7	0.1	1.8
40310_at	toll-like receptor 2	CA 1T	AF051150	1		
	KIAA0469 gene product	KIAA0469		1,4	3.5	
37977_at	KIAA1528 protein		1_	1, 1	0.1	7
39141_at	ATP-binding cassette, sub-family F (GCN20), member 1	ABCET	AE027202	4.7	2.4	0.4
467_at	l g	OSTE	163717	4.7	4.1	0
42270_at		1 200	003/1/	4.7	2.5	0
56991_at			W24320	4.7	1.5	6.1
57016 at	hypothetical protein FL111264		A1927199	4.7	1.2	6.5
52287 at	Hong-chain fatty acid coenzyme A linase E		AI692513	4.7	6.4	10
76152 c at	ים בסבוולאווופ ע ווצמאב		AA514342	4.7	0.8	0
ı] k			A1634548	4.7	0	0.7
89955 34			AI280818	4.7	0.6	0.2
66840 24			AW020975	4.7		C
58452 at			AI160370	4.7	1.4	-
75150 at	speriil associated antigen 9	SPAG9	AL079765	4.7	2.4	111.1
1 JI JU at			AI631846	4.7	3.8	1.1
3331_a(0000001	,		

Figure 11DDDD

hypoprietical protein		300001 13 1177	20	120046	4.7	10.6	2.9
Putative brain nuclearly, targeted protein	52765_r_at	hypothetical protein FLJZZ999	VIOLV	20107	4.7	3.1	4.8
t putative brain nuclearly targeted protein MA36007 47 44 47 47 47 47 47	52652 at		217	02010	7.7	13	5
AAU ORGANIZATION AAU ORG	0608_r_at	putative brain nuclearly targeted protein	AIV	61676	1.7	2 - 5	9.5
AMA36007 4.7 4.7 4.7 4.7 4.7 4.7 4.7 4.7 4.7 4.	7639 at		ALO	48402	4.7	1 7	
Al874267 4.7 44 44 45 45 45 45 45 4	7963 at		AA4	36007	4.7	4./	3.1
183663 4.7 14 14 14 14 14 14 14 1	0160 24		AI8	74267	4.7	4.2	5
t FLN29 gene product			18	3663	4.7	1.6	0.5
Ne6563 4.7 1			91	9727	4.7		8.2
H68862 47 H68862 47 State H6884564 4.7 State H6884564 H688	0		9N	96563	4.7	1.5	2.3
AAA17797 4.7	00911 r at		H	38862		3.1	7.3
Alignate Alignate Alignate Alignate Alignate	1003 r at		AA4	117797	4.7	3.8	6.1
AA894564 4.7 AA650392 4.7 AA650392 4.7 AA650392 4.7 AA6604268 4.7 AA664268 4.7 AA664268 4.7 AA6643934 4.7 AA6643934 4.7 AA6643934 4.7 AA6643934 4.7 AA664156 AA7 AA789332 AA789332 AA7 AA789332 AA7889332 AA7889332	14202 at		AI7	65157		1.8	0.7
AA630392 4.7	20/5 at		AA8	394564	4.7	5	4.3
AA160048 4.7 AA604268 4.7 AA604268 4.7 AA604268 4.7 AI762856 4.7 AI76	22204 at		AAE	30392	4.7	2.3	0
AA604268 4.7 AA604268 4.7 AIC62856 4.7 AIC62856 4.7 AIC62856 4.7 AIC62856 4.7 AIC62851 4.7 AIC62851 4.7 AIC62851 4.7 AIC62852 4.7 AIC62853 4.7 AIC62853 4.7 AIC60846 protein	0010 at		AA1	160048	4.7	0.1	1.9
at FLN29 gene product	4500 ot		AAE	504268	4.7	3.1	2.4
at FLN29 gene product	4300 at		Ž	12884	4.7	1.2	0.3
ALO43934	4207 at		AI7	,62856	4.7	4.8	1.4
FLN29 gene product	6610 at		ALC	043934	4.7	0.8	0
st FLN29 gene product 4.7 at N93263 4.7 n AA027059 4.7 at AA664156 4.7 n AA664156 4.7 at Cytochrome c oxidase subunit Vb AA191495 4.7 n COX5B M19961 4.7 NMPhocyte-specific protein LSP1 M33552 4.7 translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 W02499 4.7 cGI-99 protein AA134236 4.7 hypothetical protein AA133356 4.7 hypothetical protein AA133356 4.7 AA194180 4.7	0174 at		Z	36861	4.7	2.1	5.5
N93263 4.7	7680 r at	El NO9 gene product	AW	002527		7	6.3
AA027059 4.7 AA664156	15/82 c at		Z	93263	4.7	3.4	0
at cytochrome c oxidase subunit Vb AAB5781 4.7 1 at cytochrome c oxidase subunit Vb AA191495 4.7 DKFZP56601646 protein LSP1 M33552 4.7 Iymphocyte specific protein 1 LSP1 M33552 4.7 Itanslocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 W02499 4.7 CGI-99 protein AA1833356 4.7 Inypothetical protein AA1833356 4.7 ABA1833356 4.7 ABA183356 4.7 ABA183356 4.7	0603 34		AA	027059		2.2	1.7
AIB85781 4.7 1	3670 at		AA	664156		17.4	9.1
AA191495 4.7	20070 at		AIS	385781	4.7	11.3	14.6
sat cytochrome c oxidase subunit Vb COX5B M19961 4.7 at DKFZP56601646 protein LSP1 AL050084 4.7 at Improcyte-specific protein AA193416 4.7 at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 W02499 4.7 at CGI-99 protein AA23336 4.7 at hypothetical protein AA133356 4.7 at hypothetical protein AA133356 4.7	13752 at		AA	191495	4.7	1.4	0.5
at DKFZP56601646 protein AL050084 4.7 at Imphocyte-specific protein 1 LSP1 M33552 4.7 at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 W02499 4.7 at CGI-99 protein AA789332 4.7 at hypothetical protein AA789332 4.7 At hypothetical protein AA133356 4.7	20/02 at	Т		19961	4.7	2.3	5.7
at lymphocyte-specific protein 1 LSP1 M33552 4.7 at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 W02499 4.7 at CGI-99 protein AA789336 4.7 at hypothetical protein AA133356 4.7 AA1342336 4.7	11335 at		AL	050084	4.7	2.3	3.8
at Franciscose of inner mitochondrial membrane 10 (yeast) homolog TIMM10 W02499 4.7 at CGI-99 protein Al342336 4.7 at AA789332 4.7 at hypothetical protein AA133356 4.7 AA1342335 4.7	36793 at	1	_	33552	4.7	1.1	8.8
at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 W02499 4.7 at CGI-99 protein AA789332 4.7 at hypothetical protein AA133356 4.7 AA1342335 4.7	56906 at		AA	193416	4.7	4.1	4.6
at CGI-99 protein A1342336 4.7 at at hypothetical protein AA133356 4.7 AA133356 4.7 AA133356 4.7	15254 at			02499	4.7	4.6	4.9
at hypothetical protein 4.7 AA133356 4.7 AA133356 4.7 AA1094180 4.7	18860 at		A	342336	4.7	2.7	6.4
at hypothetical protein 4.7 AA133356 4.7 AI094180 4.7	50855 at		AA	789332	4.7	2.9	2.6
A1094180 4.7	14705 at		AA	133356	4.7	3.9	4.9
	7007		A	094180	4.7	2.2	4.5

44833 s at	44833 s at Theat shock 70kD protein 8	HSPA8	A1986374	4.7	6.0	6.7
42831_at			AI201843	4.7	4.2	4.7
45492 at			AW002385	4.7	5	4.7
44823_s_at			AA521476	4.7	4.4	4.8
43929_at			AA225263	4.7	4.6	4.4
55940_at			AI701480	4.7	2.3	3.4
47875_at			W15284	4.7	1.9	3.6
48769_at	hypothetical protein MGC4368		AL121013	4.7	3	6.1
824_at	glutathione.S-transferase like; glutathione transferase omega		U90313	4.6	6.5	0
41695_at	KIAA0414 protein		AB007874	4.6	2.2	4.6
39906_r_at	ADP-ribosylation factor GTPase activating protein 1	ARFGAP1	AA402332	4.6		2.7
31345_at	airway trypsin-like protease		AB002134	4.6	2.7	15.7
31916_at	killer cell lectin-like receptor subfamily A, member 1	KLRA1	AF047445	4.6	1.3	5.6
40427_at	COX17 (yeast) homolog, cytochrome c oxidase assembly protein	COX17	AA149486	4.6	2	6.0
32738_at	NADH dehydrogenase (ubiquinone) Fe.S protein 2 (49kD) (NADH. coenzyme O reductase)	NDUFS2	AF050640	4.6	1.3	0
38904_at	v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog	SRC	AF077754	4.6	1.9	12.7
33760_at	peroxisomal biogenesis factor 14	PEX14	AB017546	4.6	3.4	0.2
35166 at	Down syndrome critical region gene 3	DSCR3	D87343	4.6	7.1	5.7
40612_at			AB029040	4.6	9.9	3.6
427_f_at	interferon, alpha 10	IFNA10	V00551	4.6	0.5	25.4
35613_at			AL042599	4.6	2.9	27.9
37493_at			H04668	4.6	4.7	3.3
1860_at	turnor protein p53-binding protein, 2	TP53BP2	U58334	4.6	9.9	0.5
36889_at		FCER1G	M33195	4.6	1.2	1.8
36953_at		MADH4	U44378	4.6	3.1	3.4
37711_at	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	S57212	4.6	0.7	8.7
56131 at			A1146837	4.6	1.8	2.4
64966_at			AI668641	4.6	5.2	6.1
65518_at	RNA polymerase I transcription factor RRN3		N22730	4.6	3.9	1.6
75179_at	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	UBE2D3	R81146	4.6	4.3	2.1
90289_at			AI827330	4.6	4	0

Figure 11FFFF

173715 at			AI126206	4.6	1.9	12.3
66690 at			Н92909	4.6	0.5	0.1
61224 at			171614	4.6	0	1.5
44060 at	selenoprotein W, 1	SEPW1	AA625451	4.6	1.9	17.2
79626_at			AA962105	4.6	2.3	0
46457_at	splicing factor (CC1.3)		AI400626	4.6	3	1.3
62818 at			AI202885	4.6	2	2.2
83402_at			AA700080	4.6	3.4	3
84383 at			AI949708	4.6	2.2	6.2
65480_at			AA166751	4.6	4.5	1.7
47471_at			AA916868	4.6	0.4	6.0
44749_at		-	T66226	4.6	2.6	1.1
87408_at			AI221305	4.6	0.3	3.5
43151_at			T87150	4.6	0.3	3.7
69446_at			AA862900	4.6	4.5	2.7
77935_at			A1939620	4.6	2.5	3.9
87284_at			AA044789	4.6	3.8	9.0
42947_at			AA042952	4.6	1.3	4.3
51074 g at			N49836	4.6	4.1	0.4
45336_at	peflin		AL046918	4.6	2	0
72133_at			W90634	4.6	2.1	0.3
75525_at	KIAA0336 gene product		R34331	4.6	6.7	2.1
82032_at			AI823999	4.6	5.2	3.5
44643_at			A1633734	4.6	0	0
42630_r_at	hypothetical protein FLJ13220		H88129	4.6	2.8	2.9
81769_at	heparan sulfate (glucosamine) 3-0-sulfotransferase 3A1	HS3ST3A1	N71828	4.6	3.3	2.2
46112_r_at			AI700523	4.6	2	0
55264_at	hypothetical protein SBBI67		W79937	4.6	0.5	0
62477_at	squamous cell carcinoma antigen recognized by T cell		W81246	4.6	1.3	0
47359_at			AA887112	4.6	0	6.0
46211_at	hypothetical protein dJ1141E15.2		AI190033	4.6	2.6	1.6
80778_at			AA179496	4.6	0	0.1
55362_at			AI653767	4.6	18.2	19.8
43295_at			AA033783	4.6	3.3	0
45914_at			H46965	4.6	0.5	2.5

Figure 11GGGG

36444 s at	36444 s at Ismall inducible cytokine A5 (RANTES)	SCYAS	AF088219	4.6	3.7	4.5
41749 at	ES1 (zebrafish) protein, human homolog of	C210RF33		4.6	m	4.1
41727 at	KIAA1007 protein		AB023224	4.6	2.9	5.2
41562 at	murine leukemia viral (bmi-1) oncogene homolog	BMI1	L13689	4.6	3.5	4.3
32562 at		ENG	X72012	4.6	4.7	9
38041 at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	GALNT1	U41514	4.6	3.3	3.5
l	acetylgalactosaminyltransferase 1 (GalNAc-T1)					
38789 at	transketolase (Wernicke-Korsakoff syndrome)	TKT	L12711	4.6	3.3	4.9
48810 at	hypothetical protein DKFZp761H221		AI547243	4.6	3.7	6.5
43824 at			AI952129	4.6	2.5	5.3
44632 at			AA007697	4.6	2.4	4.7
45758 at			AA034095	4.6	3	5.9
65620 at	hypothetical protein FLJ14005		W52855	4.6	4.4	4.7
50036 at			AI189011	4.6	3.9	4.4
53935_at			W74486	4.6	2.4	4
55571_at			W58459	4.6	1.5	3.1
37119 at	vesicle associated membrane protein 4	VAMP4	AL035296	4.5	2	6.0
34530_at			W73822	4.5	7.6	1.2
33019 at	Parkinson disease (autosomal recessive, juvenile) 2, parkin	PARKZ	AB009973	4.5	2.3	10.5
33283 at	arrestin, beta 2	ARRB2	AF106941	4.5	8.0	0
31524 f at	H2B histone family, member K	н2вғк	Z8028Z	4.5	1.4	7.4
33665_s_at		CSF2RA	M73832	4.5	2.3	0.4
34312 at	nuclear receptor coactivator 2	NCOAZ	AI040324	4.5	8	7.6
33773_at	myeloid/Jymphold or mixed-lineage leukemia (trithorax (Drosophila)		U13948	4.5	0	2.6
33504 at	neurexophilin 2	NXPH2	AF043467	4.5	1.4	0.8
37828 at	hypothetical protein FLJ11220			4.5	1.2	4.4
36703 at	small inducible cytokine subfamily A (Cys.Cys), member 25	SCYA25	_	4.5	1	2.9
36452_at	synaptopodin		AB028952	4.5	1.6	3.6
35826_at	suppressor of Ty (S.cerevisiae) 5 homolog	SUPT5H	AF040253	4.5	3.1	3.6
36897_at	KIAA0027 protein		D25217	4.5	1	1.3
37941_at	myosin-binding protein C, fast-type	MYBPC2	X73113	4.5	1.3	6.7
38355_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome	DBY		4.5	2.3	0.7
56367 at			A1630997	4.5	1.8	1.1

Figure 11HHHH

65139 at	hypothetical protein FLJ12150		AI925240	4.5	9.8	0.8
			AA764974	4.5	1.4	0.5
76356 at			AA203497	4.5	1.6	1.6
59043 at			AI243147	4.5	0	0.4
82499 at			AI925051	4.5	1.1	0
56803 at	wingless-type MMTV integration site family, member 5A	WNT5A	AI968085	4.5	1.3	O
67164 at			AI367020	4.5	2.1	0.1
65478 at		_	AI744031	4.5	3.9	1.2
43273 at			AI655806	4.5	0.8	1.4
68245 at			H48278	4.5	2.5	1.7
79480 i at			N49201	4.5	1.7	1.7
56269 at	hypothetical protein FLJ12701		AI338045	4.5	2.5	1.4
49469 at			AI871490	4.5	1.4	1.4
73771 at			AI632232	4.5	2.5	3.7
	glutaminase	GLS	AI968420	4.5	4.8	0.3
86475 f at			AI337926	4.5	3.1	3.1
63849 at	karvopherin beta 2b, transportin		AI885873	4.5	0	9.0
86015 at			AI652445	4.5	9.0	0.4
87673 at			AI982610	4.5	9.0	0.2
84407 r at			AI032906	4.5	9.0	1
85125 g at			AI074707	4.5	5	3.6
53978 at			AW024692	4.5	1.2	11.3
45918 at			N53560	4.5	1.6	3.9
43356 s at	D-type cyclin-interacting protein 1		AI970622	4.5	1.4	0
62261 s at	LIM domains cont	LIMDI	A1933287	4.5	3.7	1.7
45661 at			N90348	4.5	5.5	6.7
60188 at			AA629050	4.5	8.1	3.1
65892 at	fatty acid binding protein 1, liver	FABP1	AA001405	4.5	2.7	0
53997 at			AA622413	4.5	1.7	0.7
54521 g at			AI084224	4.5	4.3	1.4
46234 at	CGI-148 protein		AA043242	4.5	4	4.9
54067_at			AI982669	4.5	0.3	0
48633_at	KIAA1254 protein		A1770067	4.5	3.3	0.7
62971 at	hypothetical protein FLJ12428		AI799804	4.5	2.9	2.3
61005 at			AA009648	4.5	3	4.1

57423 at		AA433928	4.5	0.5	0.8
		AA487296	4.5	1.2	5.3
33308 at	glucuronidase, beta	GUSB M15182	4.5	0.8	4.8
32317 s at	•	SULT1A2 U34804	4.5	3.1	4.1
39135 at	KIAA0767 protein	AB018310	4.5	3.7	4.3
47714 at		AA018412	4.5	2.4	2.7
33689 s at	D-dopachrome tautomerase	DDT AF012434	4.5	1.8	4.7
55301 at		AI634118	4.5	2.6	4.3
57497 at		AA419263	4.5	3.9	4.1
58468 at		C17704	4.5	4.5	4.3
58647 at	glutathione S-transferase M1	GSTM1 AA203289	4.5	3	3.2
	hypothetical protein FLJ20186	AW014780	4.5	4.3	4.6
44079 at	general transcription factor IIIA	GTF3A AA166851	4.5	3.9	4.9
43485 s at	_	AI633875	4.5	2.9	3
47104 at		AI760368	4.5	3.4	4
47561 at		AA877614	4.5	3.5	5.7
	۱ ـ	ANPEP M22324	4.4	3.5	0.1
	aminopeptidase M, microsomal aminopeptidase, CD13, p150)				
36347 f at	· -	H2BFD AA873858	4.4	1.4	6.4
40407 at	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	KPNA2 U28386	4.4	2	2
31342_at		GALNT2 X85019	4.4	1.3	3.9
	acetylgalactosaminyltransferase 2 (GalNAc·T2)			-	
32635_at	transcriptional intermediary factor 1 gamma	AB029036	4.4	3.7	6.1
32693_at	KIAA1040 protein	AB028963	4.4	0.7	13.5
33219_at	KIAA1097 protein	AB029020	4.4	3.7	1.7
41770 at	monoamine oxidase A	MAOA AA420624	4.4	0	0
34655_at	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	MPP2 A1951832	4.4	0.2	10.4
38982 at	TRF2-interacting telomeric RAP1 protein	W28865	4.4	1.6	4.3
35213 at	WW domain binding protein 4 (formin binding protein 21)	WBP4 AF071185	4.4	1.9	2.6
41584_at	nudix (nucleoside diphosphate linked moiety X) type motif 3	NUDT3 AF062529	4.4	0.9	6.4
35007_at		٧	4.4	0.5	0.8
37403_at	annexin A1	ANXA1 X05908	4.4	2.6	4.1
37088 at	serine/threonine kinase 13 (aurora/IPL1-like)	STK13 AF059681	4.4	2.6	3.9
56940 g at		A1963304	4.4	3.6	4.3

Figure 11JJJJ

0,	FO 100		AA044743	4.4	1.5	1.8
48118 at	USI-37 DIOUGII		A1632926		2.0	0 6
56456 at	hypothetical protein dollowing.1		A1190905	4 4	1.7	6.0
177750 at			AI290653	4.4	2.3	4.1
76717 at			AI375865	4.4	0.5	3.3
			AA285069	4.4	2.7	9
64991 at			AI762686	4.4	0	0
64346 r at	nuclear factor (erythroid-derived 2)-like 2	NFE2L2	AW023229	4.4	2.7	2.9
82372 at			AA907150	4.4	6.0	0.9
84765 at			AI446030	4.4	7.1	1.9
49312 at	CGI-102 protein		AA747303	4.4	3.2	7.4
63398 at	similar to Bos taurus P14 protein		AA130220	4.4	6.9	2.1
67890 at			AI613399	4.4	3.2	1.3
87942 at			AA936705	4.4	2.7	1.6
45280 at	hypothetical protein DKFZp566G1424		AA703316	4.4	1.5	1.1
47565_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila)	WLL	W55861	4.4	1.4	2.9
70379 at	(Moronia)		AI744361	4.4	1.2	0.7
44328 at	hypothetical protein MGC5487		AA905113	4.4	2	6.1
62495 f at			A1433785	4.4	17.4	28.1
43367 at	hypothetical protein FLJ20730		AI979164	4.4		0.4
43489 at	hairy/enhancer-of-split related with YRPW motif-like	HEYL	AL040197	4.4	3.5	5.1
43931 at	hypothetical protein FLJ11269		AI741524	4.4	1.9	6.3
56384 i at			R17914	4.4	1.3	0.5
48696 at			H48142	4.4	0	0
56264 at				4.4		2.9
89969 at	ribosomal protein S15a	RPS15A	~	4.4	2.9	0
83888 r at			AI031837	4.4	0	0.8
72475 r at			AA063087	4.4	0.5	1.2
72928 at			A1638648	4.4	1.9	3
45876 at			AA536137	4.4	9.0	2.1
60537_at			AL038866	4.4	1.3	0.3
60124 at			H61529	4.4	3.1	3.6
74302 at			AA028209	4.4	1	2.6
41928 at			AA029647	4.4	3.2	1.6

/8/96_i_at	Integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	ITGAE	AI735664	4.4	2	2.9
42048_at			AA897644	4.4	2.5	37.2
48992_at			AA435933	4.4		6.4
77840_f_at			AI720888	4.4	8.1	16.6
			AF052185	4.4	3.3	4.3
33601_at			AF052145	4.4	2.2	3.1
41213_at	peroxiredoxin 1	PRDX1	X67951	4.4	2	5.1
34764_at	leucyl-tRNA synthetase, mitochondrial		D21851	4.4	1.4	3.8
33916_at	imidazoline receptor candidate		AB023192	4.4	3.8	3.6
41498_at	KIAA0911 protein		AB020718	4.4	2.4	3.6
34368_at	histone deacetylase 2	HDAC2	U31814	4.4	2	4.7
38479_at	acidic protein rich in leucines		407969	4.4	2.9	5.1
37967_at	lymphocyte antigen 117	LY117	AF000424	4.4	1.8	4.4
65144_at			AA625373	4.4	4.7	4.9
43406_s_at	ZAP3 protein		AA890650	4.4	3.1	4.5
44297_at			AA613167	4.4	4	4.3
48094_at			AA531025	4.4	3.8	4.1
ω,			AL040188	4.4	4	4.6
			AI888055	4.4	8.0	4.9
"II"			AA524968	4.4	3.9	4.4
57261 f at	ribosomal protein, large, P0	RPLPO	AA588862	4.4	4.1	7.9
31985_at			AL049228	4.3	2.7	7.2
41694_at		BN51T	M17754	4.3	1.6	5.8
41703_r_at	A kinase (PRKA) anchor protein 7	AKAP7	AF047715	4.3	0.7	5.2
39412_at	zinc finger protein 173	ZNF173	U09825	4.3	2	16.9
34544 at	zinc finger protein 267	ZNF267	X78925	4.3	2.9	3.9
1448_at	some, macropain) subun	PSMA3	D00762	4.3	4	5.6
35449_at	Killer cell lectin-like receptor subfamily B, member 1	KLRB1		4.3	8.0	4.5
38899 s at	38899_s_at hypothetical protein FLJ20693		U95822	4.3	5.7	3.1
32819_at	H2B histone fam	H2BFS	AJ223352	4.3	1.2	3.5
ij	kinectin 1 (kinesi	KTN1	D13629	4.3	1.1	0
32904_at		PRF1	M28393	4.3	1.2	0.8
33900 at	follistatin-like 3 (secreted glycoprotein)	FSTL3	U76702	4.3	0	5.7
34006 s at	34006_s_at mitogen-activated protein kinase 8	MAPK8	L26318	4.3	0.7	9.0

Figure 11LLLL

35253_at	GRB2-associated binding protein 2	GAB2	AB011143	4.3	1.0	
463 g at	nuclear factor I/B	NFIB	<u> </u>		7.1	
39975_at	KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing,		Æ	4.3	0.0	4.0
0000	ARE-Diriging protein Z					-)
40332 at	/-bU protein		AF109134	7 3	0 1	1
36899_at	special AT-rich sequence binding protein 1 (binds to nuclear	SATRI	M97287	5.5	7.4	5.3
	matrix/scaffold-associating DNA's)	ק ק	102/6W	4.	8.4	6.6
37188_at	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	PCKO	002008	(
36989_at	dystroglycan 1 (dystrophin-associated plycoprotein 1)	CAS	\perp	2.4	5.2	0
38796_at	complement component 1. a subcomponent heta patraentide	CAGI	- 1	4.3	1.7	1.9
56837 at	globotriaosylceramide/CD77 synthase. Gh3/CD77 synthase.	2708	- 1	4.3	3.9	0
1	galactosyltransferase; 4-N-acetylglucosaminyltransferase		AA769110	4 w	1.4	0.4
56927_at			00000			
91181 at	Uncharacterized hematopolistic stem/programitor colla-		W49628	4.3	4.5	7.8
	The state of the s		AW044698	4.3	0	0
57414 at						
58260 at			AA8/8480	4.3	1.3	3
87639 at	elikaryotic translation initiation factor of		AA806364	4.3	2	4.5
89954 at	Costeinvl.tRNA evothetese	EIF2C1	- 1	4.3	3.1	0.4
49278 o at		CARS	- 1	4.3	2.7	1.8
85068 at			AA534436	4.3	6.0	1 9
80554 s at			AI032972	4.3	0	C
85293 31			AW004040	4.3	6.0	C
90699 21			AI468014	4.3	0	C
43708 at			AA434032	4.3	2.5	0.4
68195 at			R10307	4.3	0	4.1
68496 at			AI627334	4.3	6.0	25
86306 1 21			A1653006	4.3	1.3	i m
70302 24			AI656897	4.3	1.5	20
56310 at			AI222295	4.3	1.6	0
30317_at	coractor required for Sp1 transcriptional activation, subunit 6 (77kD)	CRSP6	C05931	4.3	2.7	4.8
49539_at	tryptophanyl tRNA synthetase 2 (mitochondrial)	WARS2	R40635	7	7	
440//_at	hypothetical protein FLJ10415		AA524061	4 4	7.7	
65484_f_at	glutaminase	0		2 6	7.7	٦
		3		7	7	

Figure 11MMMM

Titte: Response of Dendritic Cells to a... Inventors: Nir Hacohen, *et al.*

56299_at			AI004324	4.3	1.5	0
43246_at			N66550	4.3	ō	1.3
61207_at			N54899	4.3	3.4	9.7
79246_at		4	AW008270	4.3	1.2	0
63800_at		1	AA195158	4.3	2.9	3.3
55443_at		1	AA631027	4.3	1.7	4.2
65846_at			A1268230	4.3	1.8	0
55431_at	KIAA0986 protein		AI218624	4.3	0.4	1.3
64466_at	RNA binding motif protein 7	RBM7	A1990688	4.3	2.5	3.7
55361_at			AI821565	4.3	6.5	8.3
84659_at			A1658664	4.3	0.8	4.4
912_s_at	phospholipase A2, group IB (pancreas)	PLA2G1B	M21056	4.3	0.2	2.3
38935_at			X72790	4.3	2.3	14.1
87358_i_at			AA226717	4.3	2.9	0.7
89544_r_at			171320	4.3	1.7	1.3
32116_at	expressed in activated T/LAK lymphocytes		AB002405	4.3	1.1	5.3
40848 g at	40848 g at JKIAA0750 gene product		AB018293	4.3	4.2	4
35199_at	KIAA0982 protein	1	AB023199	4.3	2.7	4.4
33920_at	diaphanous (Drosophila, homolog) 1	DIAPHI	AF051782	4.3	3.2	3.8
36185_at	alanyi-tRNA synthetase	AARS	D32050	4.3	1.3	3.7
38424_at	KIAA0747 protein	1	AB018290	4.3	2.9	4
210_at	phospholipase C, beta 2	PLCB2	M95678	4.3	3.7	3.6
64269_at		1	AW023766	4.3	9	8.5
59411_at		(AA130954	4.3	1.4	2.5
51983 at			C00851	4.3	4.3	3.8
53906_at	differentially expressed in FDCP (mouse homolog) 6	DEF6	AA523303	4.3	4.3	4.3
59761 r at			AA648933	4.3	4.2	3.9
44127_at		<i>'</i>	AA604375	4.3	2.8	9.9
46236_at	gap junction protein, beta 2, 26kD (connexin 26)	7865	AA442698	4.3	0.7	5.3
46572_at			A1924230	4.3	2.3	4.2
65930_at	30S ribosomal protein S7 homolog		N78337	4.3	2.5	4.4
54158 at			AI453531	4.3	2.8	4.6
45115_at			AA909042	4.3	4.2	4.5
54969_at			AI829724	4.3	3.5	4
42700 i at			T86284	4.2	60	0.5

Figure 11NNNN

35078_at	intercellular adhesion molecule 4, Landsteiner-Wiener blood group	ICAM4	x93093	4.2	6.0	2.8
1532 g at			2021			
39386 at	gene predicted from cDNA with a complete coding consecu		cscoco	4.2	2.2	1.9
31880 24				4.2	1.7	5.5
22052 24	meiali-A	MLANA		4.2	0.3	12.6
32033 dt	k	CCNT2	AF048731	4.2	60	96
1638_at	ets variant gene 6 (TEL oncogene)	ETV6	U11732	4.2	9	1.6
2050_s_at	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	RAC1	<u> </u>	4.2	1.9	1.2
40874_at	endothelial differentiation-related factor 1	FOF	A 1005250	C		
35480_at	Daspartate oxidase		1	4.6	8.1	
38571_at	FGFR1 oncogene partner	Sign		7.4	0.5	5.8
41189 at	tumor necrosis factor recentor superfamily, member 12 /translagation	T COULTE		4.2	5.4	0
	chain association membrane protein)	NILINI	Y09392	4.2	2.3	0.5
338_at		ATF6	AF005887	4.2		
40555_at		PIGF			1 4	1.0
40813_at	solute carrier family 5 (inositol transporters), member 3	SICSAR	1	100	10	0.2
35245_at	coagulation factor V (proaccelerin, labile factor)	35.00A3		2.4	0.0	0
39684_at	membrane protein, palmitoviated 3 (MAGIIK n55 subfamily member	20074	ı	7	0	0.4
	3)	ν Γ	03//0/	4.2	0.5	8.6
36486_at	KIAA0805 protein		0000000			
36171_at	activated RNA polymerase II transcription cofactor 4		AB010340	4.2		1.9
38005 at	ransporter similar to C		A1521453			2.7
58842 at	tein El 110702		AJ005866	4.2	0.5	0.5
5/971 24	Entransport of Information 1		AI084071	4.2	3.1	0.3
53747 at	o ingline in oi igo, receptor, transporter, alpha	FCGRT	AW024627	4.2	2	1.4
	Polyton A ovidan Daring		AA422178	4.2	2.8	3.2
78725 24	acyticoetizytte A Oxtodse 3, pristanoyi	ACOX3	A1992213	4.2	4.5	0
61067 7 24	3/11/04/11 10		AI290467	4.2	3.4	C
42720 -1			AA470798	4.2	3.7	6.4
42/39 at			190760		2.3	11
442010 01			Z38762	4.2	1.2	4.7
75761 at	сагрохурершазе ім	CPM	1	4.2	2.5	2
62602 at			AA808948	4.2	5	0.4
02002 at			AA418402	4.2	3.5	0
0214/_at	Inypotnetical protein FLJ11155		A1265860	4.2	0.5	1 V

	T90064	4.2	2.4	1.9
- 11	AI870859	4.2	0.4	1.1
hydroxysteroid (17-beta) dehydrogenase 7	HSD17B7 AA811920	4.2	1.6	0
	AA780679	4.2	2.2	2.2
	AA151678	4.2	-	0.2
nypothetical protein MGC4827	AI655261	4.2	6.0	2.1
	AI088029	4.2	0.3	0
hypothetical protein FLJ10339	177538	4.2	0.8	0
		4.2	1.6	1.7
ANK-binding kinase 1	TBK1 N20936	4.2	2.2	1
	AI864659	4.2	1.1	22
Į	AA197062	4.2	1.6	13
hypothetical protein FLJ10826	AI817242	4.2	2.8	0
	R54026	4.2	4.4	5.1
	AI830095	4.2	0.7	0.4
	AA209471	4.2	3.6	5.6
	A1936575	4.2	2.6	2.7
restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	RSN AW008377	4.2	4.3	0.2
	H79046	4.2	21	7 3
RAB9-like protein	N21460	4.2	8 9	7
	AA532743	4.2	1 6	3.6
	AI525818	4.2		0
- 1	AI142861	4.2	0.1	4.7
hypothetical protein FLJ10707	AI052745	4.2	1.8	0.1
- 1	AA180163	4.2	4.2	9.3
nyaluronan synthase 3	HAS3 AI338972	4.2	2.9	5.7
	AA286940	4.2	4.9	5.5
	W25528	4.2	1.9	2.2
	T54906	4.2	3.5	4.2
	AA203328	4.2	4.4	7.2
	T88970	4.2	1.3	4.6
	3155163	4.2	1.6	5.2
	AI075770	4.2	2.2	1.9
	0000000	,		

Figure 11PPPP

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ventors:	Nir	Hacohen,	et	а

79773 at			A1685649	4.2	1 4	7 0
87057 i_at			R07361		1.3	1.5
32237_at	KIAA0265 protein		D87454	4.2	2.8	4
1675_at	RAS p21 protein activator (GTPase activating protein) 1	RASA1	M23379	4.2	2.1	3.8
38483_at	hypothetical protein		AJ011916	4.2	1.5	6.5
	dynein, axonemal, light polypeptide 4	DNAL4	AL008583	4.2	1	6.8
56968_at	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)	MEF2D	AL118605	4.2	2.7	3.7
53848_at			A1422099	4.2	3.7	5.4
57066_at	hypothetical protein		AI023043	4.2	2.1	9
51713_at			AI660536	4.2	3.8	4.2
¥	chromosome 20open reading frame 3	C200RF3	H09341	4.2	2.7	5.8
45285 at	proteasome (prosome, macropain) subunit, alpha type, 7	PSMA7	AA877820	4.2	3.4	5.1
	caspase recruitment domain protein 9		AI307612	4.2	3.6	4.2
50293_at			AI823782	4.2	4.5	4.9
49071_at			AI541411	4.2	1.4	4.2
51188_at			AA454038	4.2	3.6	4.2
61366_at	hypothetical protein MGC3731		AA700395	4.2	2	2.4
52908_at	hypothetical protein FLJ21324		AA865619	4.2	3.9	4.1
			AA287801	4.2	m	3.3
±	hypothetical protein FLJ13576		AW023011	4.2	3.2	4.3
39551_at	KIAA1696 protein		29986N	4.1	2.6	2.2
31909_at	KIAA0754 protein		AB018297	4.1	2.3	2.3
2066_at	BCL2-associated X protein	BAX	L22474	4.1	4.6	9.6
32643_at	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	GBE1	L07956	4.1	4.8	0.4
40779_at	smg GDS-ASSOCIATED PROTEIN		U59919	4.1	2.4	
41147_at			AF038186	4.1	15.4	3.6
35944_at	ring finger protein 1	RINGI	AL031228	4.1	2.5	0.2
436_at		11.5	X04688	4.1	1.1	m
33439 at	transcription factor 8 (represses interleukin 2 expression)	TCF8	D15050	4.1	2	8.6
39627_at		EEA1	L40157	4.1	0	9.0
40615_at		EIF3S1	AA780049	4.1	5.9	9.0
1728_at	murine leukemia viral (bmi-1) oncogene homolog	BMII	L13689	4.1	0.4	4.4
36833_at	Bruton agammaglobulinemia tyrosine kinase	BTK	U78027	4.1	7.2	1.1

- 1	heat shock transcription factor 4	HSF4	D87673	4.1	7	6.6
37001_at	calpain 2, (m/II) large subunit	CAPNZ	M23254	4.1	4.8	2.6
37669 s at	ATPase, Na+/K+ transporting, beta 1 polypeptide	ATP1B1	016799	4.1	2.5	1.4
37640_at	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	HPRT1	M31642	4.1	5.7	0.1
37980_at	CBF1 interacting corepressor		U03644	4.1	9.1	į ∞
38301_at	adenosine kinase	ADK	U50196	4.1	1.1	7.9
63309_at	CGI-15 protein		AI241474	4.1	0.4	4.9
58414 <u>a</u> t	KIAA1350 protein		AI276062	4.1	2	0.9
46472 at			AI765222	4.1	1.6	3.4
43022_at	hypothetical protein FLJ22351		AA196189	4.1	2.1	4.6
50751_at			AA181800	4.1	1.6	1.2
76909_at			AI243872	4.1	m	0
77058_at			AA044778	4.1	7.5	2.8
85607_at			AI681283	4.1	3.7	0
44188_at			AI864170	4.1	2.5	0.4
91895 f_at			AI335251	4.1	6.3	3.2
78947_at			AI033572	4.1	0.8	1.2
76920_at			AA745592	4.1	3.6	4.6
79408_at			A1128226	4.1	2.1	6.0
79900_at			A1803624	4.1	0.3	1.9
80150 r_at	copine VII	CPNEZ	A1278055	4.1	m	2.8
81568 r_at			AI356410	4.1	0	28.4
٦			AA621047	4.1	3.8	4.3
82421_i_at			AI554417	4.1	6.2	8.8
1185_at	interleukin 3 receptor, alpha (low affinity)	IL3RA	D49410	4.1	3.4	0.8
64298 r_at	arrestin, beta 2	ARRB2	AW002000	4.1	0.8	0
59054_at			AA489100	4.1	6.6	4.8
87801_at			AA604144	4.1	2.4	5.4
43566_at			AI674899	4.1	1.3	4.1
79414_at			A1435069	4.1	2.1	9.0
56226_at		EIF2C2	A1146465	4.1	2.4	0
32243 g at	_	CRYAB	AL038340	4.1	2.1	5.2
67455_at	ets variant gene 2	ETV2	AI188430	4.1	1.2	2.8
59605_at			AA528070	4.1	1.2	1

Figure 11RRRR

RARREST
16 (monocarboxylic acid transporters), member 3

Figure 11SSSS

70878_at			AI189108	4.1	3.7	1.8
77905_r_at			A1287423	4.1	0.5	0
41103 at	bromodomain and PHD finger containing, 1	BRPF1	M91585	4.1	3.1	3.7
288_s_at	lamin B receptor	LBR	L25931	4.1	1.5	2.5
31896_at	neuroblastoma-amplified protein		AL050281	4.1	1.5	2.7
36443_at	dynein, axonemal, heavy polypeptide 9	DNAH9	X99947	4.1	4.1	3.7
32253_at	arginine-glutamic acid dipeptide (RE) repeats	RERE		4.1	1.9	3.4
38956_at	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase		AF052111	4.1	3.1	3.9
41342_at	RAN binding protein 1	RANBP1	D38076	4.1	3.8	4.7
38671_at	KIAA0620 protein		AB014520	4.1	4.3	5.3
41535_at	deleted in oral cancer (mouse, homolog) 1		AF006484	4.1	1.5	4.8
35331_at	catenin (cadherin-associated protein), alpha-like 1	CTNNAL1	79076U	4.1	3.3	4.1
37010 at	general transcription factor IIA, 2 (12kD subunit)	GTF2A2	AI203737	4.1	3.7	4.3
37029_at	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	ATP50	X83218	4.1	2.2	4.6
	(oligomycin sensitivity conferring protein)					-
48833_at	HSPC040 protein		AI749098	4.1	3.2	4.1
50282_at	hypothetical protein FLJ10975		AA522810	4.1	2.4	4.2
66623_r_at			AA971467	4.1	3.9	2.6
44078_at			W95017	4.1	5.1	5.5
58200_at			AI818585	4.1	e	m
57045_f_at	ribosomal protein L23	RPL23	AW015905	4.1	2.5	4.3
51223_at	phosphoinositide-3-kinase, catalytic, beta polypeptide	PIK3CB	AI916796	4.1	1.8	3.7
64036_at	hypothetical protein FLJ10716		AI968206	4.1	2.2	3.5
45284_at	butyrate induced transcript 1		AF169958	4.1	2.9	3.8
48106_at	hypothetical protein FLJ20489		H14241	4.1	3.6	3.9
45335_at	CGI-28 protein		AI037884	4.1	2.7	4.4
46242_at			AA215796	4.1	2.8	4.1
87839_at			AA860301	4.1	4.1	3.6
52841_at			AA731740	4.1	4	4
46247_at	succinate CoA ligase, GDP-forming, alpha subunit	SUCLG1	AA826261	4.1	3.3	5.5
54948_at			AI684747	4.1	3.5	3.9
52856_at	potential nuclear protein C5ORF5; GAP-like protein		AA430306	4.1	8.0	4.6
48731_at			AI948491	4.1	1.6	4.4
33004 g at	33004 g at NCK adaptor protein 2	NCK2	AI275502	4	0.5	0.3

41447_at	KIAA0990 protein	KIAA0990	AB023207	4	0.8	0.7
37484 at	integrin, alpha 1	ITGA1	X68742	4	2.3	3.4
1786_at	c-mer proto-oncogene tyrosine kinase	MERTK	U08023	4	1.4	2.6
40719 at	adenosine A2b receptor pseudogene	ADORA2BP	AL022398	4	2.9	2.3
39419_at	sperm associated antigen 9	SPAG9	AB011088	4	1.6	5.1
34933_at	paired box gene 9	PAX9	AJ238381	4	0	2.1
41860 at			AF070559	4	2.5	1.3
648_at	arginine vasopressin receptor 1B	AVPR1B	L37112	4	2.7	6.0
38201_at	branched chain aminotransferase 1, cytosolic	BCAT1	U21551	4	1.2	1.2
38512_r_at		ELAVL3	D26158	7	1.5	5.1
40616 at	antigen ∪) eukarvotic translation initiation factor 3. subunit 1 (alpha. 35kD)	EIF3S1	037670	4	0.7	6.3
33267 at			AF035315	4	1.5	3.9
32747 at	aldehyde dehydrogenase 2, mitochondrial	ALDH2	X05409	4	4.5	0.1
37383_f_at	major histocompatibility complex, class I, B	HLA.B	X58536	4	2.7	4.3
32324_at	tyrosine 3.monooxygenase/tryptophan 5.monooxygenase activation	YWHAB	X57346	4	1.7	6.0
35965 at	heat shock 70kD protein 6 (HSP70B')	HSPAE	X51757	4	C	4 6
34782 at	jumonii (mouse) homolog	- WC	AL021938	4	4.3	1.4
37350 at	proteasome (prosome, macropain) 26S subunit, non ATPase, 10	PSMD10	AL031177	4	2.7	1.8
34823_at	dipeptidy/peptidase IV (CD26, adenosine deaminase complexing	DPP4	X60708	4	0.4	9.0
1274 s at	cell division cycle 34	CDC34	L22005	4	3.4	1.4
37328 at		PLEK	X07743	4	2.8	1.9
37373_at	UDP-glucose pyrophosphorylase 2	UGP2	U27460	4	1.6	0.2
38341_at	staufen (Drosophila, RNA-binding protein) homolog 2	STAU2	AL079286	4	2.5	6.2
75498_at			AA868356	4	1.2	3.2
91377 g at	hypothetical protein FLJ11132		AA707653	4	3.2	0
56854_f_at			AI742034	4	0.4	0.2
90417_at	ribosomal protein S6 kinase, 90kD, polypeptide 5	RPS6KA5	AI382181	4	0	0
74763_at	cold shock domain protein A	CSDA	AI081577	4	0.5	1
76133_at			AI654230	4	1.6	0.7
76046_at			AA702810	4	2.4	0.1
82368_at	olfactory receptor, family 7, subfamily E, member 12 pseudogene	OR7E12P	AI809176	4	1.4	3.2
53732 at			AA055909	4	1.4	0.7

Figure 11UUUU

48854_i_at		AW025683	4	2.1	4.5
77232_at		AI683999	4	0	0.2
70635_f_at		AI799862	4	2.1	2.5
89005 r_at		AI923675	4	2.6	2.2
77231_at		Al761622	4	3.1	7
91579_at		AI939511	4	2.1	1.2
83904_at		AI985614	4	2	4.3
92166_at		AI190864	4	2.2	2.8
63270_at		AA027103	4	0	2.6
63074_at		AA570454	4	3.7	4.7
90054_r_at		R02815	4	0.3	2.3
85864_at		AW023438	4	0.5	0.3
72783_at		AI655284	4		2.3
45723_at	transmembrane protein vezatin; hypothetical protein DKFZp761C241	AI805297	4	2.2	0
62972 at	KiAA1376 protein	W56118	4	2	17.8
55549_s_at	Kruppel-type zinc finger protein	AI783578	4	1.2	4.6
43949_at		AI290991	4	2	0.5
45446_at		R53916	4	1.2	
73460_i_at		H52268	4	0.2	0.8
65571_at		AI768785	4	1.6	0
56880_at		R12560	4	1	
62396_r_at		AI291705	4	3.1	3.4
71617_at	hypothetical protein FLJ23112	AI937612	4	9.5	
43355 s. at		77007N	4	2.6	1.5
62876_at		AI393573	4	0	0
46316_at	hqp0256 protein	A1494647	4	9.0	0
57739_at	hypothetical protein FLJ20195	AI949010	4	3.5	8.7
61641_at		AA479481	4	1.5	3.8
79034_at		AA907783	4	2.5	6.0
50148 r_at		A1963083	7	2	0.1
64834_at		AA447325	7	0.1	5.3
59574_at		AI807378	7	E.1	4.8
44675_at	xylosyltransferase	AA043495	7	0	0
64564_at		R96525	4	1.6	2.2

Figure 11VVVV

45174_at			44453197			
46378_at			AA010557			v) (
43818_at	calcineurin-binding protein calsarcin-1		VW0700700	1		
65887_at	transducer of ERBB2, 2	COOT	1	1		7.0
41957_i_at		7001	.1.	4		
44809 at	hypothetical protein FL J10803		732007	4		
55055 at			AWUU8368	4		0.3
55383 at			/89ZZN	4	5.9	
19501 at			AA454036	4	2.4	2.5
199091 dl	nucreoporin po4		AL040287	4	1.7	0.4
42242 al			AA978128	4	1.4	2.5
/5/12_at			AW007237	4	0.4	
80430 r at	- 1		R09516	4	0.1	9
32874_at	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3		4		
41430_at	WD repeat domain 7	WDR7	AB011113		C +	000
33857_at	p47		1_			
39741_at	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A	a H U V H	L	1		
	thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta			1	>	4.9
	subunit			-		-1.
2058_s_at	integrin, beta 5	ITGB5	M35011	A	2	3 6
39794_at	ubiquitin specific protease 8	USP8	1	4		
40129 at	protein kinase, DNA-activated, catalytic polypeptide	PRKDC	U47077	4		
40//0 t_at	heterogeneous nuclear ribonucleoprotein D.like	HNRPDL	AB017019	4		
318/3 at	Rho GTPase activating protein 4	ARHGAP4	1	4		
35170_at	<u> </u>	MAN2C1	AF044414	4		
33031_dt		POLR2H	N37689	4	1.7	3.5
34371 at		PPP4R1	U79267	4	0.1	
34020 at		NUDTI	D16581	4	3.1	8
34020 41	~I	POLR21	AL037557	4	2.9	4.6
33369 at	٦.		D50532	4	4	
30102 at		VDAC3	AF038962	4	E.O	5 1
30104 at	ubiquinol-cytochrome c reductase hinge protein	UQCRH	AA526497	4	2.4	
3/30/_at	guanine nucleotide binding protein (G protein), alpha inhibiting activity nolvnentide ?	GNAI2	X04828	4	1.6	
	- I and of local					_

37982_at Independence (Coencyme A declean somerase (3.2 trans-enoyl Coencyme A declean somerase) CTSC AIZ46687 4 3 <	1885_at	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	ERCC3	M31899	4	2.4	4.3
DVI_SCADE Ne6640		dodecenoyi Coenzyme A delta isomerase (3,2 trans-enoyi Coenzyme A isomerase)	DCI	225821	4	e e	3.5
Page Page		cathepsin C	USLO	41246687	-	-	
Name				N66640	1 <	1.1	3.5
Page Page		dishevelled 2 (homologous to Drosophila dsh)	DVL2	AW016304	t <	6.3	4.6
Integration Page		ribonuclease, RNase A family, k6	RNASFE	AWOZEANS		2.7	4.1
W74642		fatty acid hydroxylase		R54585	1	3.4	3.7
AAB13014		hypothetical protein FLJ10535		W74642	1		
Algority 4 2.6 Algority 4 2.2 Alatosis 3.9 1.4 Alatosis 3.9 1.4 Interior Arotasis 3.9 1.4 LHCGR M63108 3.9 1.1 LHCGR M63108 3.9 0.2 LHCGR M63108 3.9 2.5 LHCGR M63108 3.9 2.2 RANGAPI 3.9 0.2 Angora 3.9 0.2 Angora 3.9 0.8 Angora 3.9 4.4 Angora 3.9 4.4 Angora 3.9 4.2 Angora 4.2 Angora 3.9 0.1<		KIAA1150 protein		AAR13014	1	2.4	3.3
AISTO481		inorganic pyrophosphatase		AI806119	7	7.0	3.6
hypothetical protein DKF2p762166 Al341534 4 2.5 CD74 antigen (invariant polypeptide of major histocompatibility CD74 Al341534 4 2.2 CD74 antigen (invariant polypeptide of major histocompatibility CD74 Al241628 4 2.2 complex, class II antigen associated) ANXA3 M20560 3.9 0 annexin A3 Integrin, A3 ANXA3 AZ0560 3.9 1.1 integrin, alpha 10 LHCGR M63108 3.9 1.1 buteinizing hormone/choriogonadotropin receptor LHCGR M63108 3.9 1.1 basic transcription factor 3, like 1 LHCGR M63108 3.9 2.2 Ran GFPase activating protein 1 RANGAD ALACAD 3.9 2.5 Ran GFPase activating protein 1 RANGAD ALACAD 3.9 2.5 Aminor histocompatibility antigen HA.1 CTH S52028 3.9 0.1 DKFZP434D193 protein CTH S52028 3.9 0.1 DKFZP434D193 protein CKA1005 ARACAD <	_	hypothetical protein FLJ10968		1000113	4	8.1	
CD74 antigen (invariant polypeptide of major histocompatibility antigen (invariant polypeptide of major histocompatibility antigen munor bioding protein 2 CD74 antigen (invariant polypeptide of major histocompatibility antigen HA-1 CT42918 4 2.2 ANXA3 M20560 3.9 0.0 Integrin, alpha 10	_	hypothetical protein DKFZp7621166		A18/0481	4		4.2
CD74 antigen (invariant polypeptide of major histocompatibility CD74 antigen (invariant polypeptide of major histocompatibility) CD74 antigen (invariant polypeptide of major histocompatibility) CD74 ANXA3 M20560 3.9 O O O O O O O O O O O O O O O O O O O	_			AI341234	4	2.2	4.5
ANXA3 ANXA	_	CD7/ antigon (invariant polymontials of		AI445628	4	2.2	2.7
annexin A3 ANXA3 M20560 3.9 0 immunoglobulin mu binding protein 2 integrin, alpha 10 114754 3.9 1.4 integrin, alpha 10 LITGA10 AF074015 3.9 1.1 Lucin Ling portion and control of cont		complex, class II antigen associated)	CD74	N22918	4	3.2	3.7
integrin, alpha 10 IGHMBP2 L14754 3.9 1.4 luteinizing hormone/choriogonadotropin receptor LHCGR M63108 3.9 1.1 basic transcription factor 3, like 1 LHCGR M63108 3.9 3.2 heterogeneous nuclear ribonucleoprotein C (C1/C2) HNRPC M16342 3.9 2.2 Ran G Pase activating protein 1 RANGAP1 X82260 3.9 2.5 zinc finger protein 230 ZNF230 U95044 3.9 2.5 minor histocompatibility antigen HA-1 ZNF230 U95044 3.9 0.1 cystathionase (cystathionine gamma-lyase) CTH S52028 3.9 0.1 DKFZP434D193 protein CTH S52028 3.9 4.4 general transcription factor IIB GTF2B M7566 3.9 4.4 crystallin, beta 44 CRYSTAIN SCRD1 U84894 3.9 4.4 crystallin, beta 44 CRYSTAIN SCRD1 U8487 3.9 0.1 crystallin, beta 47 SCRYD1 U8487 3.9	_	annexin A3	ANXA	MODERO	3.0		
integrin, alpha 10 lutelinizing hormone/choriogonadotropin receptor lutelinizing hormone/choriogonadotropin receptor lutelinizing hormone/choriogonadotropin receptor lutelinizing hormone/choriogonadotropin receptor LHCGR M63108 3.9 1.1 BTF3L1 M90354 3.9 3.2 BARF3L1 M90354 3.9 0.2 HNRPC M16342 3.9 2.2 Ran GTPase activating protein 1 ZNF230 U95044 3.9 2.5 ZNF230 U95044 3.9 0.8 CTH S52028 3.9 0.1 CTH S52028 3.9 0.1 CTH S52028 3.9 4.4 Beneral transcription factor IIB GTF2B M76766 3.9 4.2 CRYStathion, beta 44 STRAIL INCOMPANIATION CONSTANCYS), member 1 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 U84487 3.9 0.1 LHCGR M63108 SCYD1 URGR	_	immunoglobulin mu binding protein 2	IGHMBP2	114754	000		1.1
Luteinizing hormone/choriogonadotropin receptor LHCGR MG10S MG		integrin, alpha 10	ITGA10	AE07401E	0.00	1.4	2.4
basic transcription factor 3, like 1 BTF3LIN M0354 3.9 3.2 heterogeneous nuclear ribonucleoprotein C (C1/C2) HNRPC M16342 3.9 2.2 Ran GTPase activating protein 1 RANGAP1 X82260 3.9 2.2 zinc finger protein 230 ZNF230 U95044 3.9 2.5 winor histocompatibility antigen HA·1 CTH S52028 3.9 2.5 DKFZP434D193 protein CTH S52028 3.9 4.4 Beneral transcription factor IIB GTF2B M76766 3.9 4.4 RAA1025 protein GTF2B M76766 3.9 4.2 coystallin, beta A4 CRYBA4 U59057 3.9 4.2 small inducible cytokine subfamily D (Cys.X3-Cys), member 1 SCYD1 U84487 3.9 1.1 1 fractalkine, neurotactin) Teurotactinin Till 1 1		luteinizing hormone/choriogonadotropin receptor	OTUNION I	M62109	200		8.5
HNRPC M3342 3.9 0.22 RANGAP1 X82260 3.9 2.5 ZNF230 U95044 3.9 2.5 CTH S52028 3.9 0.8 CTH S52028 3.9 0.1 U79263 3.9 4.4 U68494 3.9 7.2 2 GTF2B M76766 3.9 4.2 CRYBA4 U59057 3.9 0.1		basic transcription factor 3, like 1	BTE311	M90354			7.5
RANGAGO 3.9 2.2 ZNF230 U95044 3.9 2.5 ZNF230 U95044 3.9 2.5 CTH S52028 3.9 0.1 U79263 3.9 4.4 U68494 3.9 7.2 2 RB028948 3.9 4.2 2 CRYBA4 U59057 3.9 0 L SCYD1 U84487 3.9 1.1	_	heterogeneous nuclear ribonucleoprotein C (C1/C2)	HNDDO	M16347	000	0.2	
ZNF200 Column Column<		Ran GTPase activating protein 1	BANGAP1	X82260	. c	2.2	0.7
CTH S52028 3.9 0.8 CTH S52028 3.9 0.1 U79263 3.9 0.1 U68494 3.9 7.2 GTF2B M76766 3.9 4.2 AB028948 3.9 2.3 CRYBA4 U59057 3.9 0.1	_	zinc finger protein 230	7NF230	1195044		6.5	0.5
CTH S52028 3.9 0.8 CTH S52028 3.9 0.1 U68494 3.9 7.2 2 GTF2B M76766 3.9 4.2 CRYBA4 U59057 3.9 2.3 CRYBA4 U59057 3.9 1.1 1	_	minor histocompatibility antigen HA.1	000	220300	0.0	7	0.7
SCYD1 U79263 3.9 0.1	_	cystathionase (cystathionine gamma-lyase)	1110	0,600	0.0	0.8	0
GTF2B M76766 3.9 4.4 2 2 2.3 4.2 2.3 4.2 4.2 4.2 4.2 4.2 4.2 4.2 4.2 4.2 4.2	_	DKFZP434D193 protein	3	8202021	3.0	0.1	2.7
GTF2B M76766 3.9 7.2 2 GTF2B M76766 3.9 4.2 AB028948 3.9 2.3 CRYBA4 U59057 3.9 0	_			079203		4.4	1
G1F2B M76766 3.9 4.2 AB028948 3.9 2.3 CRYBA4 U59057 3.9 0	_	general transcription factor IIB		068494		7.2	23.3
CRYBA4 U59057 3.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	_	KIAA1025 orațein	G1F2B	M76766		4.2	2.5
CRYBA4 U59057 3.9 0 1.1 3.9 1.1 1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1	_	Andrews Protein		AB028948			3.2
1 SCYD1 U84487 3.9 1.1 1	_	ciyatanını, beta A4	CRYBA4	U59057		0	3.6
		Stridt ittuucible Cytokine subtamiiy D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)	SCYD1	U84487	3.9	1.1	13.9

Figure 11XXXX

37645_at	CD69 antigen (p60, early T-cell activation antigen)	CDE9 722	722576	3.0	lau	1
37912 at	TNF receptor-associated factor 4	1	200		0.0	4 C
37962_r_at	syntaxin binding protein 3	1_	202		0.7	0
39150_at	ring finger protein 11	┸	550	200	0.7	ر در
63313_at		┸.	003039 AAA10636	200	3.2	0.1
51174_at	spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	SCA7 AL043992	3992	3.9	4.4	3.2
56399_at	PABP interacting protein 2	16360714	1631		1:	
80913_at		A17010E2	1001		1:1	0.5
75996_at		719193	277		7 0	
59520_at	MARK	A103/4	2/4		2.8	2.8
53790_at	actin-related protein 3-beta	AAIZ	0250	3.9	1.5	1.1
77680 at	ı	AA//242	247	3.9	0.1	0.1
74525 at	enhancer of polycomb 1	AI809979	976	3.9	7.1	3.1
50563 r at		AI791534	534	3.9	2	3.4
61101 34		AI224126	1126	3.9	5.5	2.5
65/3/ 24		AI539443	9443	3.9	14.2	9.4
52005 at		N73778	778	3.9	1	5.2
18056 at		AI217733	733	3.9	2.9	4
53358 at	ijypotijeticai proteiti reuzdziji	N73934	934	3.9	2.6	9.9
72014 2 24		AI279946	946	3.9	0.7	=
90173 at	MADLS, Illelituer RAS oncogene family	RAB13 AW001549	1549	3.9	1.4	0
83915 at		AA203229	3229	3.9	0.1	0.8
81889 7 34		AI703123	1123	3.9	2.7	1.5
54633 at	hypothetical protein El 13070	AI819070	070	3.9	1	1.2
82223 at		AA19507	2022	3.9	1.9	0
82481 at		Af871160	160	3.9	2.3	3.4
		AI243249	1249	3.9	1.3	0
91935 at		AI148712	1712	3.9	1.3	3.3
62334 c at		AI694752	.752	3.9	2	60
47724 r at		T94015	115	3.9	4.8	0
54842 24		R92163	163	3.9	2.5	4
63069 24		AI758780	1780	3.9	0.7	0
67/01 at		AA521016	1016	3.9	0.1	0
62004 21		AA872025	2025	3.9	2.7	1.9
63094_at		R1031	311	3.9	6.0	07
	i					,

Figure 11 YYYYY

68186 at			AA465263	3.9	2.2	2.7
88152_at			AA706908	3.9	0.3	1.1
70238_at			AA521399	3.9	2.3	8.5
73171_at			AI953346	3.9	1.9	0.7
72375_at			AA316630	3.9	1.2	0
58913_at			AI916598	3.9	0.1	0
48136_at	hypothetical protein FLJ20371		AA032184	3.9	2.3	7.3
33180_at	protein phosphatase 1, regulatory (inhibitor) subunit 2	PPP1R2	U68111	3.9	2	1
58356_at			AA142978	3.9	2.3	3.8
66322_at			N95416	3.9	2.4	2.2
85177_at	H2B histone family, member R	HZBFR	AI336982	3.9	0.4	0.5
48589_s_at			N98652	3.9	0.3	1.6
65815_at	ZYG homolog		AI080334	3.9	2.1	0
84284_at			A1056418	3.9	1.6	0
64015 g at			AA130159	3.9	3.3	1.3
53485 at			AI521545	3.9	1.8	5.2
52540_at			AI467915	3.9	3.8	2.6
58577_at			A1392933	3.9	2.2	0
52090_at			AI198126	3.9	m	0
46732_at			AA075666	3.9	9.0	0
46090_at			AA806216	3.9	8.0	4.7
55289_at			W86056	3.9	0.3	0.2
			AA630405	3.9	2.5	2.8
47371_at			AA017037	3.9	7	13
47964_at	KiAA1014 protein		AI083506	3.9	1.5	0
37929_at	immunoglobulin superfamily, member 4	IGSF4	AB017563	3.9	0.2	0.5
44058_at			W60953	3.9	2	5.2
65579_at	SH3 and PX domain containing protein SH3PX1		AA455005	3.9	1.2	0
37747_at	annexin A5	ANXA5	U05770	3.9	1.5	1.8
37611_at	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	TNFRSF11B	AB008822	3.9	0	0
57717_at	CGG triplet repeat binding protein 1	CGGBP1	AA903358	3.9	1.6	6.0
49762_at			186307	3.9	2.6	3.4
64851_at			AA399994	3.9	1.3	4.3
47614_at			AI021988	3.9	2.9	1.5

Figure 11ZZZZ

1339_s_at			X14675	3.9	3.3	2
70261_at			AI808755	3.9	0.7	0
70832_at			AI739235	3.9	1	2
75686_f_at			AI734065	3.9	5.2	8.8
78611_at			AI378890	3.9	0.8	0.4
37454_at	small inducible cytokine subfamily A (Cys-Cys), member 13	SCYA13	AJ001634	3.9	0.2	3.6
40266_at	KIAA1036 protein		AB028959	3.9	3.7	4.3
33448_at	serine protease inhibitor, Kunitz type 1	SPINT1	AB000095	3.9	2	3.9
40139_at	FK506 binding protein 12-rapamycin associated protein 1	FRAP1	996880	3.9	2.2	3.3
36610_at	KIAA0029 protein		D21852	3.9	3.7	3.7
34314_at	ribonucleotide reductase M1 polypeptide	RRM1	X59543	3.9	2.9	2.8
41504_s_at	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene homolog	MAF	AF055376	3.9	3.2	4.1
35261_at	glia maturation factor, gamma	GMFG	W07033	3.9	2.6	4.3
36194_at	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)	LRPAPI	M63959	9.6	0.5	4.5
37298_at	GABA(A) receptor-associated protein	GABARAP	AF044671	3.9	1.6	7
37609_at	nucleotide binding protein 1 (E.coli MinD like)	NUBP1	U01833	3.9	0.8	8
52238_s_at	transforming, acidic	TACC3	A1990642	3.9	3.4	3.5
56821_at			A1963454	3.9	4.1	4.8
43422_at	CD27-binding (Siva) protein		AW025365	3.9	3.3	4.7
65813_at		2FP36	N32721	3.9	2.8	4.8
55718_at	hypothetical protein FLJ10890		AI494412	3.9	2.3	2.3
54662_at	ribosomal protein S9	RPS9	AA194261	3.9	3.4	3.9
54869_at			AA287799	3.9	3.7	4.4
63544_at			N33295	3.9	2.7	4.5
65761_at			AA525969	3.9	2.8	3.6
43495_at			192245	3.9	2.1	4.7
60863_s_at	hypothetical protein from EUROIMAGE 2021883		AA526910	3.9	2.8	4.3
50252 at			AA149410	3.9	2.9	3.9
88182_at	- 1		AI084454	3.9	5.6	5.8
51105_at	Rho guanine nucleotide exchange factor (GEF) 3	ARHGEF3	N57933	3.9	1	3.2
44343 s at			AI074877	3.9	3.1	3.8
47634_at			AW052044	3.9	3.6	2.8
56267_at	adaptor-related protein complex 1, sigma 2 subunit	AP1S2	AP1S2 AA151802	3.9	3.2	3.7
l						

Figure 11AAAAA

121.21 dt	neat snock protein hsp/U-related protein	!	AA742240	3.9	2.8	4
5309/at	clone FLB5214		AA532452		2.6	
5/210_at			AI862775		Si c	
43384_at			AWOOOGO		0.0	4 6
55564_at	spleen tyrosine kinase	SYK	1		0.7	4.0
57222_at			1	0.0	0.0	0
52313 at	hydroxyacyl-Coenzyme A dehydrogenase / 3 ketosoyl Coenzyme A		_1_	5.0	۲.۵	3.5
l 	thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	AHOHH	AI9/2144	რ რ	2.4	4.6
47640_at	Nedd-4-like ubiquitin-protein ligase		0020001			
41411 at	CGI-65 protein		A1000/00	3.9	4.1	5.1
38704 at	actin hinding protein; macrophin (migrafilament and acting		//899CIW	3.8	1.3	2.4
	cross-linker protein)		AB007934	ж Ж	3.6	4.7
39809_at	HMG-box containing protein 1		AF019214	αr	V &	,
724_at	adrenergic, beta, receptor kinase 2	ADRRKO	X69117	0.00	5 0	7.7
40094_r_at	40094_r_at Lutheran blood group (Auberger b antigen included)		X80026	ο α	0.0	O.O.
40462_at	DKFZP727M231 protein		A FOR FOR	0.0	7.0	2
41753_at	actinin, alpha 4	ACTNA	11/0724	0.0	3.3	٦
40932_at			H18080	0.0	0.1	ا
35408_i_at	zinc finger protein 44 (KOX 7)	ZNEZZ	71000		10.4	7.7
32905_s_at	tryptase, alpha	7001	102000	3.8	1.5	16.8
32809 at	Ithionurine S.methyltransferase	IFSI	M30038		2.3	3.6
34789 at	:12	TMH	AL118582	3.8	9.0	1.6
) - CO (+ C	some (or ejsteme) proteinase inflibitor, clade B (ovalbumin), member 6	SERPINB6	S69272	3.8	2.1	0
33541_s_at	leukocyte-associated Ig-like receptor 2	COIVI	24133346	C		
37694_at	KIAA0244 protein	7	1	0.0	5 1	0.1
38412_at	protein phosphatase 1, regulatory (inhibitor) subunit 11	1101000	00/007	0 0	3.5	0
58106 at		7717 1 1 1	000000	3.8	1.4	1.6
66357 at			AA496024	3.8	0.3	0.5
74270 r at			AA778876	3.8	1.8	1.5
78/00 24			AI733391	3.8	2.4	C
70430 at			AA206363	3.8	2.2	1-2
01324_dt	cargo selection protein (mannose 6 phosphate receptor binding protein)		AI636693	3.8		3.5
82566_at			AA285320	α m	7	
75243_s_at	75243_s_at basic transcription element binding protein 1	BTEB1	AA101758	0000) [-	20

Figure 11BBBBB

91452_at		4	41702022	0.0	2 .	-
82064_at		VV	AA552150		7.0	0.0
91683 at		{	V C C C C C C C C C C C C C C C C C C C		0.0	4.7
67375 at			9003/4			3.3
		A	AI829/0/		2.4	4.2
49/51 at		AA	AA169778	3.8	3.1	2.1
516/4_at			N28262	3.8	3.2	6.0
/8986_at	ubiquitin specific protease 25	USP25 AI	AI092963	3.8	1.7	2.8
63108_at		A	AI741779	3.8	3.3	2.2
49925_at	hypothetical protein FLJ10120	A	AI971227	3.8	1.5	0.5
43188_at	- 1	A	AI732568	3.8	1.9	1.4
50761_at	BANP homolog, S	A	AI738764	3.8	6.5	1-1-
63543_r_at	suppressor of S. cerevisiae gcr2	A	AI954776	3.8	3.4	00
63669 at		A	AI546970	3.8	2.2	0
58350_at	hypothetical protein FLJ20651	AW	AW014619	3.8	5.5	0.6
44347_at		Z	53347	3.8	1.3	4 8
59613_r_at		I	H78589	3.8	1.5	3.5
68675 at	ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen)	FCN3 AI	AI652910	3.8	4.7	8
43006 at		A	AI871342	3.8	2.1	2.1
/3095_at		A	AI335277	3.8	6.0	1.5
46196 at		A	AI580948	3.8	1.1	2.9
43049 at	hypothetical protein FLJ13433	1	H06431	3.8	2.9	0.8
48150 at		2	R02297	3.8	1.6	3.2
05255 r at		AA	AA393998	3.8	3.4	2.5
9020/ at	HDCMA18P protein	A	AI968653	3.8	2.7	0.2
49/69 at	hypothetical protein FLJ13611	2	61558	3.8	3.7	1.3
20318 at		A	A1497833	3.8	1.5	3.1
2/040 at		A	AI198956	3.8	2.3	2.9
20242 at	KIAAU493 protein		AA863228	3.8	4.8	2.5
48931_at		KIAA1085 AI	AI692989	3.8	1.5	0.6
65645 at	IGF-II mKNA-binding protein 2	A	AI675886	3.8	ō	C
68410_r_at			T96375		3.8	4
80380 at		A	AI278983		Ö	17
60349_at		AA	AA921855	3.8	1.1	0.6
53056 at		Z	N91168		2.2	
45932_at			D59841		2	

Figure 11CCCCC

45191_at	protein phosphatase 1, regulatory subunit 6	PPP1R6	A1680750	3.8	io c	C
51053_at			AI122787		0:7	7
54379_at			N56947	000	0.4	7.00
35281_at	laminin, gamma 2 (nicein (100kD), kalinin (105kD), BM600 (100kD), Harlitz innetional anidomolycie bulgasi	LAMC2	U31201			1.8
54215 at						
54049 at			AA/42993			2.5
57207 at			A1652991	3.8	5.9	0
36880 at	NADYON mondono ovidendi esta Constanti esta Constan		AL045641	3.8	1.2	0
50550 at	hypothetical protein El 112820	NMOR2	U07736	3.8	0.2	2
47052 at	וואסטוופווכם חוסופוע ברזוקאקט		AI745595	3.8	4.6	0.8
74664 at			AI139548	3.8	3.1	2.2
74004 S at	_	UBXDC1	AA430224	3.8	2.7	0.6
46283 at	nypotnetical protein FLJ10081		AL044171	3.8	2.4	0
40310 at			AA872062	3.8	1.9	3.4
46/10 at			AA480092	3.8	4.2	0
55559 at			AI266650	3.8		2.5
5882/ at			A1992368	38	4.2	11.1
48/6/ at	ALEX1 protein		A1693923	0 00	100	3.31
65982_at	hypothetical protein		AA740774	0.00	ο α	10.0
62888 r at			AI923987		1 7	0.0
/546/_at			AI917245	8 6	00	0 0
78852_at			AI076830	8,6	17	0.6
8892/ at			AA889052	3.8	22	68
70530 Lat			AA019714	3.8	1.5	1 2
41201 at	0000		AA456976	3.8	0.4	3.6
41301 dt			AB002306	3.8	1.6	3.4
3961/ S at	_		AF040105	3.8	2.3	27
120 at	as I	UQCRC1	L16842	3.8	1.7	4 1
1/2 at	Inositoi polyphosphate-5-phosphatase, 145kD	INPP5D	U57650	3.8	ď	
459_s_at	bridging integrator 1	BIN1	U68485	α κ	000	0 0
32824_at	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)	CLNZ	AF039704			4.3
33348_at	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	TCF12	M80627	3.8	1.5	3.6
40818_at	H-2K binding factor-2		D14041	3.8	2.4	000

Figure 11DDDDD

36188_at	tion fac	GTF3A	D32257	3.8	1 6	3.6
36635_at	ATPase, Class VI, type 11B	ATP11B	I٩		1.0	0.00
1768 s_at	c-src tyrosine kinase	CSK		α	000	1.0
36799_at	frizzled (Drosophila) homolog 2	FZD2		α		5.1
55755_at	growth suppressor 1		14	0 00		20.0
48066_at			AI768720	α		0.0
76484_at			AA789296		3.4	γ.ς
61126_at			N22262	8 8	0.0	0.00
67162 r_at			AI366683	8 %		a c
44712_at			AI139894	800	200	0 0
60046_at			AI796241	388	3.2	2.4
44097_at	DKFZP586C1324 protein		AI928466	38	27	
56323_at			AI890133	388	E	3.6
63997_s_at	vacuolar protein sorting 11 (yeast homolog)	VPS11	AW007365	3.8	1.6	5 1
49110_s_at			T48132	38	26	1.0 8 V
38487_at	KIAA0246 protein		D87433	3.8	3.6	300
44569_at			AA961420		3.6	3.5
54765 at	xeroderma pigmentosum, complementation group C	XPC			2.8	4.2
46132_at			AA210738		2.1	3.4
46569_at			AA552976		800	0.00
49197_at	solute carrier family 16 (monocarboxylic acid transporters), member 1	SLC16A1	Al129459		3.2	2.7
56980_at	hypothetical protein FLJ23309		AI762891	α		96
48952_at	hypothetical protein FLJ21634		A1985274		3.13	0.0
38697_at	DKFZP566C243 protein		AL050274		80	2:0
40/00 at	nuclear body protein Sp140		036500	3.7		101
37468_at	Janus kinase 2 (a protein tyrosine kinase)	JAK2	AF058925	3.7	4	3.1
3904 / at			AB020880	3.7	3.4	
39856_at		RPL36A	AI708983	3.7		
41853 at	yrophosphate synthet	PRPSAP2	AB007851	3.7	1 7	
31786_at	Sam68-like phosphotyrosine protein, T.STAR		AF051321	3.7	2.0	200
4/1_t_at	tubulin, beta, 4		U47634	3.7	2.2	200
40434_at		PODXL	U97519	3.7		149
40589_at	Syntrophin, beta 2 (dystrophin-associated protein A1, 59kD, basic component 2)	SNTB2	U40572	3.7	2.2	1.8

Figure 11EEEEE

32731_at	FE65-LIKE 2		AB018247	3.7	1.7	2.2
41226_at	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	DUSP3	L05147	3.7	1.9	2.2
35927_r_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	LILRB1	AF004230	3.7	1.5	2.2
39267 at	N-acetylglucosamine-phosphate mutase		AF102265	3.7	3.5	7.8
242 at	microtubule associated protein 4	MAP4	M64571	3.7	3.5	0.4
31671_at	RNA binding motif, single stranded interacting protein 1, pseudogene	RBMS1P	D82351	3.7	4.6	3.9
36968_s_at	Opa-interacting protein 2		AL050353	3.7	1.8	1
35214_at	T	NGDH	AF061016	3.7	2	5.6
1565_s_at	growth factor receptor bound protein 2	GRB2	M96995	3.7	3.6	1.1
39657_at	keratin 4	KRT4	X07695	3.7	0.3	3.4
34370_at	archain 1	ARCN1	X81198	3.7	2.7	3.1
36001_at	methyltransferase-like 1	METTL1	Y18643	3.7	2.5	0
35265_at	fragile X mental retardation, autosomal homolog 2	FXR2	U31501	3.7	m	0.4
41823_at	staufen (Drosophila, RNA-binding protein)	STAU	AJ132258	3.7	2.8	
32628_at	zinc finger protein 161	ZNF161	D28118	3.7	3.5	7.2
35847_at	ubiquitin specific protease 24	USP24	AB028980	3.7	m	4.7
40390_at	serine dehydratase	SDS	105037	3.7	5.2	16.9
37375 at	KIAA0638 protein		AB014538	3.7	1.3	2.1
38012_at	fibrillin 2 (congenital contractural arachnodactyly)	FBN2	U03272	3.7	2.4	2
37572_at	cholecystokinin	SCK	AW043690	3.7	0.7	7.1
38082_at	KIAA0650 protein		AB014550	3.7	m	12.1
840_at	zinc finger protein 220	ZNF220	U47742	3.7	2.5	2.6
37890_at	CD47 antigen (Rh-related antigen, integrin-associated signal	CD47	X69398	3.7	5.4	1
56042 at	phospholipase C. beta 3. neighbor pseudogene	PLCR3NP	A1023365	3.7	23	000
58005 at	Lie		A1480253	7.0	5.7	0.0
80067			0700740	200		0 0
00307 at			AA/03040	7.7	1,	0.0
00231 at			AA5/3860	3./	2.4	5.7
66316_at			N24645	3.7	0	3.3
52939_at			N36115	3.7	1.7	3.1
66473_at			AI677843	3.7	9.0	1.5
76576 at			AA813745	3.7	1.4	2.4

Figure 11FFFFF

4- 00001						
28893 at		Ai697856	7856	3.7	3	2.5
78005_at		AI459248	3248	3.7	0.8	2.7
74867_at		AI038997	3997	3.7	4.3	3
90852_at		AI147384	7384	3.7	6.0	2.8
90884_r_at		AA699634	9634	3.7	2.5	26
82382_at		AA921947	1947	3.7	2.5	17
75265_at		AI821772	772	3.7	0.2	0.3
51366_at		AI188748	3748	3.7	2.5	2.5
56575_at	CGI-108 protein	AW02552	5521	3.7	1.1	0
52074_at		AI218119	3119	3.7	1.8	2.5
80265_at		AI420422	1422	3.7	1.2	3.9
53351_at	epidermal growth factor receptor substrate EPS15R	AA083211	3211	3.7	1.6	0.7
83640 at		A1948	3598	3.7	1	9.0
51578 at		T91195	195	3.7	1.1	3.6
83566_at		AI366705	5705	3.7	2.3	1.4
54763_at	hypothetical protein FLJ20303	AL043081	3081	3.7	2.1	0.2
64149_at		N51587	587	3.7	1.6	0
59084_at		AA126814	5814	3.7	1.7	0
43173_at		AA661990	1990	3.7	0.5	1.1
68376_at		AA927862	7862	3.7	2.8	1.5
68146_at		AA66	1520	3.7	2.3	2
88280 <u>r_at</u>		AA703174	3174	3.7	6.0	5.4
88282_at		AA765234	5234	3.7	2	3.5
88805_at		AI761186	186	3.7	0.3	9.0
63554_at	•	N64735	735	3.7	1.1	1.9
70664_at		A182351	3511	3.7	6.0	0
72134_at		A1686860	9860	3.7	1.6	0
89772_r_at		AI567466	7466	3.7	9.0	1.8
49740_at	CGI-69 protein	AI279567	3567	3.7	3.1	8.6
65839_at	PC3.96 protein	AW022836	2836	3.7	4.4	6.3
43990 at	uncharacterized bone marrow protein BM040	AI676178	5178	3.7	3	0.8
66026_at		H44949	949	3.7	3.7	0.3
42804 at		W86160	160	3.7	5.1	5.4
51933_at		AW023193	3193	3.7	2	4.4
78757_at	selenoprotein X, 1	SEPX1 W92110	110	3.7	9	0.4

Figure 11GGGGG

1		7/00/7	ر. د	4.1	2.5
nypotnetical prot	FLJ23591	R91222	3.7	2.3	00
myeloid/lymphoid	MLL3	AI640514	3.7		
47324_at heat shock 90kD protein 1, alpha	HSPCA	AA199881	3.7	100	0.0
		AA205787	3.7	1 7	
43492_at hypothetical protein FLJ10439		AI818133	3.7	3.9	0.0
1		AI417988	3.7	2.4	000
<u>الہ</u>		AI694702	3.7	4.7	9 0
o]		N51557	3.7	2.2	0.0
		W31963	3.7	1.2	2.5
46114_at		AA121481	3.7	90	3.6
at		AA058944	3.7	000	5.6
PRO10/3 protein		AL037363	3.7		r l
lio	COX7A2	AI611424	3.7	2.6	
.1.		AI734899	3.7	5.1	1.6
71332 at		AW022635	3.7	1.1	0.5
		AA148929	3.7	5.7	4.9
19361 c at mudocan 1		N98235	3.7	4	5.4
- a - a -	SDC1	AI972735	3.7	5.1	0
66113 r at		AI123757	3.7	2.4	14.7
57345 g at		AI824210	3.7	9.0	2.4
33186 at		AI768674	3.7	1.4	2
62269 r at		AL046961	3.7	0.1	3.2
chromosomo 22 o		AI499298	3.7	0.7	4.1
Cyclin.denendent	C220RF5	AL096879	3.7	2	3
Τ	CDKN2C	AF041248	3.7	2.3	9.0
DKFZP4340156 p	BLCAP	AL049288	3.7	1.8	3.2
dinoid dibydront		AA447263	3.7	1.1	4
at seven transmemb	ODPR	M16447	3.7	1.9	2.2
		Y18007	3.7	1.5	3.9
54986 at Invoothetical profein MGC3103		AA582193	3.7	3.2	3.7
t high mobility group		AI992073	3.7	1.3	3.4
	HWG	AW005489	3.7	0.7	4
80889_at		80870308	7.0		

Figure 11HHHHH

Nir Hacohen, et al.

Inventors:

60009_at			AI673085	3.7	3.5	26
54698_at			W56253	3.7	2.9	3.5
68924_at			AA969377	3.7	3.1	3.6
44646_r_at	eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	EIF2S3	N38902	3.7	3.4	3.9
49591_at	hypothetical protein FLJ10504		AI888436	3.7	2.2	3.2
45607_at			AI810669	3.7	3.7	3.6
43801_f_at	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N- acetylglucosaminyltransferase, isoenzyme B	MGAT4B	1	3.7	2.7	5.7
57195_at			A1935271	3.7	2.2	3.6
47390_at			AA928060	3.7	3.7	3.7
65923_at			AI344311	3.7	3.2	4.2
55653_at			AA524700	3.7	2.1	3.5
34469_at	ABO blood group (transferase A, alpha 1-3-N-	ABO	X84746	3.6	0.3	9.1
	acetyigalactosaminyltransferase; transferase B, alpha 1-3. galactosyltransferase)					
39338_at	S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))	S100A10	AI201310	3.6	1.2	3.2
853_at	nuclear factor (erythroid-derived 2)-like 2	NFE2L2	\$74017	3.6	6.0	6
31410_at	transmembrane activator and CAML interactor		AF023614	3.6		3.7
40811 at	KIAA0576 protein		AB011148	3.6	1.7	0.4
38540_at	muscle RAS oncogene homolog	MRAS	AF043938	3.6	1.7	0.1
41155 at	catenin (cadherin-associated protein), alpha 1 (102kD)	CTNNA1	003100	3.6	1.7	0
41735 at	KIAA0870 protein		AI808958	3.6	1.2	0
40930_at	⊏1	SULT4A1	W25958	3.6	1.1	11.3
38900_at		PAX3	002309	3.6	1.1	3.1
33774_at	caspase 8, apoptosis related cysteine protease	CASP8	- 1	3.6	2.9	1.7
39243 s at	PC4 and SFRS1 interacting protein 2	PSIP2	U94319	3.6	2.8	4.5
3439/_at			AF069250	3.6	6.0	0
641_at		PSEN1	L76517	3.6	2.1	2.2
36042_at		NTRK2	X75958	3.6	0.4	3
34846_at	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	CAMK2B	AF112472	3.6	2	3.6
36/11_at	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F	MAFF	AL021977	3.6	2.6	0
895_at	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	MIF	119686	3.6	1.3	1.6
			-	_	-	

Figure 11IIIII

36906_at	cannabinoid receptor 1 (brain)	CNR1	U73304	3.6	0.4	4.6
1271 <u>g</u> at	v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65))	RELA	L19067	3.6	2.9	4.5
37368_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin dependent	NFATC4	NFATC4 AA292277	3.6		6.7
37399_at	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	AKR1C3	D17793	3.6	3.5	0.1
38732_at	chloride channel, nucleotide sensitive, 1A	CLNS1A	X91788	3.6	4	0
56186_at			AA745496	3.6	2.3	2.2
42300_at			AW006996	3.6	-	3.6
58119_at			AA481066	3.6	1.9	3.4
50666_at			AI911873	3.6	9.0	10.7
42449_at			AA609232	3.6	2.3	1.7
76140_at			K998891A	3.6	3.3	2.9
81453_at			A1243808	3.6	9.0	1.2
61896_at			AL038511	3.6	4.4	8.7
74374 at			AA923305	3.6	1.3	1.8
74681_at			AI018220	3.6	1.4	14.5
65239_at			941411A	3.6	4.2	0
51425 i at	- 1		AA971774	3.6	1.5	3.1
57028_at	RAB, member of RAS oncogene family-like 2B	RABL2B	AI760941	3.6	2.8	0
59252_at			AJ230805	3.6	2.4	2.3
91502_at			AA490519	3.6	2.1	1.9
85189_at			A1186064	3.6	2.1	1.6
48526_at	hypothetical protein FLJ10582		AI190311	3.6	4.6	1.1
63408_i_at			AA226131	3.6	2	1.3
43105_at			171861	3.6	3.7	9.5
85442_at			AI791175	3.6	1.7	1.3
87217_at			AA468768	3.6	0.7	3.8
59119_at			AL038787	3.6	0	0
68570_at			AA496390	3.6	0.3	0.2
70187 at			AL037446	3.6	2.9	1.3
71549_r_at			AA699538	3.6	2.2	5.4
44936_at			T93893	3.6	10.2	59

01270 g 2+			AI887362	3.6	6 2.8	
1013/0 r at			AA578920	3.6	C	
/2/32_s_at			AIGGORES	000		
50237_at	hypothetical protein FLJ11109		A1037500	0.0		
52273 s at	RAB10, member		_	3.6		1
74938 at	Secretory Carrier	KABIO		3.6		2.
52522 at	-	SCAMP2	_	3.6	5 1.3	
49477 24			H06408	3.6		4.4
			AA948400	3.6	5 1.1	
13738 24			AI807366	3.6	5 2.1	2
25505 + 2+			AA565834	3.6	5 2.9	
43852 at	Dirlaylar protein 3 (apostocic representation)			3.6	6.0	1.9
54708 at	medicale protein a (apopulasis repressor with CARD domain)	NOL3		3.6	1.7	0.7
64756 at	NAG22 protein		AI890286	3.6	5 2.1	
89366 at			AI826107	3.6		5.4
47048 at			AI085580	3.6	(C)	
49395 at			AI971235	3.6		
15557 r at	fibronoctio 1		_	3.6		C
55341 at		FN1	-1	3.6		
43383 s at	hypothetical protoin El 190707		AI351368	3.6	3	
80285 r at	Typogramma process response		AW000901	3.6	1.1	0.5
72742 at			R98495	3.6	2.4	
47874 at			AA250992	9.8		
53354 at			AA281757	3.6	2.5	
A9524 at	Alphant condrator advantage of the		_	3.6	0	
18-1-100	Apport syndronie, interital retardation, midface hypopiasia and elliptocytosis chromosomal region, gene 1	AMMECR1	1 AI032981	3.6	2.1	4.6
58996_at			H77502			
60568_at			2007/11		0.7	1.6
64422 at			N49962	3.6		2.3
61314 at	KIAAD203 gene product		AA634254	3.6	2.3	3.8
51817 at			AL043152	3.6		
62456 at			Al991014	3.6	0.2	0.3
53573 f at			AA207074	3.6	1.9	2.5
57628 at	Inplote (Drosophile) homolog		- 1	3.6	2.7	3.9
57.020 at	KIAA170E Stotein	PELO	O AA436974	3.6		
10100 at	Industrial profession		AA044207	3.6		

Figure 11KKKKK

57280 f at	57280 f at Imaior histocompatibility complex, class I, B	HLA.B	A!985880	3.6	m	7.1
91767 s at	peptidyl prolyl isomerase H (cyclophilin H)	HIdd	AA741049	3.6	6.0	3.2
63124 at			AA631399	3.6	1.7	7.8
52310 at			2969463	3.6	0.4	1.1
74606 r at			AA122219	3.6	2.4	1
			AI985333	3.6	1	6.3
38990 at	F.box only protein 9	FBX09	AL031178	3.6	1.6	4.5
41733 at			AC003007	3.6	2	3.9
38161 at	Not56 (D. melanogaster) like protein		Y09022	3.6	3.2	2.1
36372 at	hexokinase 3 (white cell)	HK3	U51333	3.6	0.7	3.6
40782 at	short-chain dehydrogenase/reductase 1		AF061741	3.6	2.3	3.2
32234 at		DYT1	AF007871	3.6	1.6	2.1
32832 at	macrophage erythroblast attacher	MAEA	AF084928	3.6	1.9	5.7
34332 at	glucosamine-6-phosphate isomerase	GNPI	D31766	3.6	6.0	3.3
34826 at	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	SDHA	L21936	3.6	0.8	4.4
36482 s at	36482 s at IATPase, Ca++ transporting, ubiquitous	ATP2A3	Y15724	3.6	2	3.5
33956 at	MD-2 protein		AB018549	3.6	0.2	3.6
36571 at	topoisomerase (DNA) II beta (180kD)	TOP2B	X68060	3.6	2.7	5.1
32578 at	MAX-like bHLHZiP protein		AW005997	3.6	0.3	3.5
38270 at	poly (ADP-ribose) glycohydrolase	PARG	AF005043	3.6	1.3	3.4
48052 at			A1936906	3.6	2.6	2.1
58206 at			W63702	3.6	3.7	2.5
47431 at			AI742206	3.6	1.5	m
57545 at			AA706499	3.6	1.7	4.9
90257 at	hypothetical protein DKFZp547D065		AI089323	3.6	2.6	3.7
58240 at	bridging integrator 2	BINZ		3.6	1.7	2.5
62850 at			AA703170	3.6	3.3	2.7
53966 at	second mitochondria-derived activator of caspase		AF039235	3.6	0	9
59595 at			AA045175	3.6	3.2	3.2
45249 at			AA775778	3.6	2.2	3.8
51056 at	hypothetical protein DKFZp434D0412		AW025176	3.6	3.3	5.6
53879 at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	B3GALT3	•	3.6	1.1	3.5
43992_at			R61748	3.6	3.3	3.1
51163 at	Invoothetical protein FLJ22405		AA115361		2.9	
65465 at			AI953614	3.6	2.8	3.5

Figure 11LLLLL

h. intors: Nir Hacohen, et al.

50845 at 64314 s at						
64314 s at	Dutative selenocysteine Ivase		0100710		3.2	1.7
			AA775419	3.6	1.5	2
60100			AI653557	3.6	3.4	3.8
02109 at	- 1		AI440192	3.6	2.0	3.4
63971_s_at	sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 2	SIRT2	AI984394		2.4	5.8
55678_at	hypothetical protein MGC10986		W77900E	000		
80251 r at	ATPase Ca++ transporting ubiquitous	0.00	C007/M	3.0	3.2	3.7
46217 at	ממה למה להמופלים ניונצי מחולמונסמפ	ALPZA3	AI380736	3.6	3.6	3.6
54062 24			AI439688	3.6	9.0	7
24002 41	LCA I-like Iysophospholipase		AA972732	3.6	2.3	3.1
81/54 g at	serologically defined colon cancer antigen 3	SDCCAG3	W02630	3.6	3.3	3.6
5//29_at	carbonyl reductase		AI382182	3.6		0.00
38659_at	suppressor of clear, C. elegans, homolog of		ABO20669	3.5	200	5.7
38670_at		ZNF313	$_{\rm L}$	3.5	2.5	4.0
39838_at	KIAA0622 protein; Drosophila 'multiple asters' (Mast) like homolog 1			3.5	2.2	3.0
30400					1)
39430 at	BULZ/adenovirus E1B 19kD interacting protein 3-like	BNIP3L	AF079221	3.5	1.6	C
38129 at	glycerol kinase	AR.	L13943	3.5	5.1	17
31845 at		ELF4	-	3.5	3.1	1
38158 at	extra spindle poles, S. cerevisiae, homolog of		l	3.5		1.1
32068 at	complement component 3a receptor 1	C3AR1	U62027	3.5	0	1
		PRKCBP2	U48250	3.5	1-	٥
닒	3B (H3.3B)	H3F3B	Z48950	3.5	- 13	7 7
41233_at	DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	<	3.5	5 0	
1925 at		CCNF	I	3.5	1 4	0
33814 at			AF005046	3.5	2.3	15.1
32904_at	egrinke module containing, mucin-like, hormone receptor-like sequence 1	EMR1	X81479	3.5	1.6	2.2
36239_at	POU domain, class 2, associating factor 1	POU2AF1	749194	٠ ٢	-	-
	S100 calcium-binding protein A11 (calgizzarin)	S100A11	D38583	2 2 2	7.7	0.1
	fatty acid binding protein 7, brain	FABP7	19	3.5	2.3	4.2
g at	G-protein coupled receptor		1	3.5	ά	100
34362 at		SLC2A5	M55531	3.5	2.6	4 1
T	Inypornetical protein FLJ10618		AL049246	3.5	2.5	
30834_at	JUKFZP564G202 protein		AL080058	3.5	0	4 4

Figure 11MMMMM

37023_at	(lymphocyte cytosolic protein 1 (L.plastin)	1001	102022	2 6	000	
37365 at	Dnaj (Hsp40) homolog subfamily R member 2		302323	0	0.7	1.1
37688 f at	For fragment of Ing. John afficient II a constant for (CD2)	DINAJBZ	A63368	3.5	2.3	0.5
27550	OF II CALL COURS OF THE STREET TO (CD3Z)	FCGR2A	M31932	3.5	0	0
3/558 at	IGF-II mKINA-binding protein 3		U97188	3.5	11.9	12.2
38020_at	KIAA0652 gene product		AB014552	3.5	3.2	ά.
37948_at	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD	ATP6C	_	3.5	2 4	0.10
56410_at	40S ribosomal protein S27 isoform		AA156232	2 2	90	0.1
48497_at	membrane-associated nucleic acid binding protein		A1380524	5.0	0.7	0.1
81276_at			NG 300	0.0	7	3.0
50825 at			1403094	3.5	5.5	7.2
76472 r at			W23499	3.5	2.8	12.4
10 07 20			AA910786	3.5	1.7	1.8
74200 at			AI732852	3.5	0.4	4.1
74390 at			A1740774	3.5	0.5	0.6
70401 r at			AW025517	3.5	6.0	X C
76/59 r_at			AI224653	3.5	1 1	
53869 at			H49544	3.5	0	7.0
54655_at	hypothetical protein FLJ12526		A1186169	2 0	1 0	ò
65272_at			AA492507	, c		200
83865_at			01703100	0 0	7.7	4:7
82643 at			6010010	0.5	/:1	2.9
47970 at			A1939451	3.5	1.8	9.0
43281 21			AA126059	3.5	1.3	2.6
86369 24			AA481181	3.5	5.5	7.1
50271 g of	100,000		A1500650	3.5	1.5	9.0
2007 1 K at	hypothetical protein		AW003291	3.5	1	C
25055 at	hypothetical protein FLJZZ609		AA700816	3.5	4.2	1.5
07.203 at			AA679812	3.5	1.1	5.9
09337 at			AI925894	3.5	9.0	C
20/22 at	hypothetical protein MGC41/4		AI291406	3.5	9.0	
25015 at			AW007238	3.5	0.1	C C
49000 at			AI936984	3.5	8	2
49485 at	PR domain containing 4	PRDM4	W22625	3.5		1
/2443_at			R95898			, ,
76006_at			A1953050	000		6.3
53659_r_at	DKFZP434D193 protein		AA453704	. w	2.4	4.1
73471_at			AWOON 1	2.0	100	7
			775	~		

49158_at	myosin IXA	MY09A	AI435029	3.5	3.6	5.2
52846_at	hypothetical protein from BCRA2 region		AI809961	3.5	1.7	2
78473_at			AW051926	3.5	0.7	9.0
90038_at	sin3-associated polypeptide, 18kD	SAP18	AW006624	3.5	5.8	5.5
42699_at			AA490077	3.5	2.1	2.1
54195_at			AA604910	3.5	2.1	2.9
87678_at			AI270326	3.5	6.0	0
84420_r_at			AI580853	3.5	9.0	1.2
75923_at			AI356228	3.5	1	0
68633_s_at	hypothetical protein		AI650829	3.5	6.0	0.3
49640_s_at			N21189	3.5	2.3	1.8
50284_at	LIM and cysteine-rich domains 1	LMCD1	AA156689	3.5	2.2	2.3
45711_at	hypothetical protein FLJ20396		N37049	3.5	2.6	2.8
45347_at			AA533633	3.5	1.8	3.6
63361_at	spondin 2, extracellular matrix protein	SPON2	AA570505	3.5	3.2	3.2
61871_r_at	WW Domain-Containing Gene		AI963349	3.5	4.3	1.5
64543_at			AI668557	3.5	2.4	7.9
87221_at			AA829405	3.5	5.4	3.1
72183 f at			AI587180	3.5	2.3	1.9
45206_at	zinc finger protein 277	ZNF277	AA102582	3.5	4	2.5
58622_at			AA463374	3.5	5.3	9
62167_at			AI866590	3.5	1.1	1.2
46608_r_at			AI885018	3.5	3.1	0
55933_r_at			AI732404	3.5	0.7	1.8
89908 f at	GDP dissociation inhibitor 1	GDII	AW004027	3.5	5.2	1
87890_at	folyipolyglutamate synthase	FPGS	AI745045	3.5	2.1	0
78749 g at	78749 g at heterogeneous nuclear ribonucleoprotein A2/B1	HNRPA2B1	AI963008	3.5	1.8	0
49709 at	hypothetical protein FLJ10116		AA127924	3.5	5.1	0.4
42093_at			AA398660	3.5	4.6	4.5
57452_at			AA451798	3.5	2.8	4.7
58958_f_at			H05039	3.5	2.3	4.5
70323 f at			AI743616	3.5	4.4	3.4
31432 g at		FCGRT	U12255	3.5	2.3	3.5
31820 at	hematopoietic cell-specific Lyn substrate 1	HCLS1	X16663	3.5	2.3	4.3

intors:

	glucosyltransferase		AJ224875	3.5	1.8	3.6
40504_at	paraoxonase 2	CNOG	AF001601	0	0	
40872 at	cytochrome c oxidase subunit VIb	COXER	T57872		3.5	2.5
41139_at	melanoma antigen, family D. 1	O COVE	2/0/61		7.0	5.8
41224 at	KIAA0788 protein	MAGEDI	W26633		1.8	1.9
33399 at	ribosomal protein C6	- 1	AB018331	3.5	1.1	4.2
33907 24	001		AA142942	3.5	1.8	2.9
35547 at	himsthatical action initiation factor 4 gamma, 3	EIF4G3	AF012072		2.4	3.5
3004/ 41	ilypotiletical protein rLJ10326		AA526812	3.5	17	3.5
34400 at	low molecular mass ubiquinone-binding protein (9.5kD)		AI540957	25.5	2.1	0.0
55545_at	Blutamic.oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	GOTI	M37400		3.4	2.9
32510_at	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	AKR7A2	AF026947	3.5	2.1	4.1
36136_at	p53-induced protein		75010315	1		
1427 g at		1	AF010313	3.5	1.7	2.4
37346 at	ADP-ribosylation factor 5	A C	1/0680	3.5	3.7	5.1
37900 at		0	M57567	3.5	1.6	3.8
38780 at	aldo-keto reductase family 1 member A1 (aldobuda 1111)	~	AF093670	3.5	2.2	2.9
39160 at	Dortivate dehydrogenase (lingmide) hets	AKR1A1	J04794	3.5	8.0	3.8
39172 at	The about the ab	PDHB	980060	3.5	2	3.3
65033 at			AL049319	3.5	2	3.3
59410 at	hypothetical protein FI 110688		AI052571	3.5	2.7	3.6
56238 at	PDZ-LIM protein mystigue		AA192438	3.5	3.8	1.4
56248 at			AI589776	3.5	3.4	3.5
63673 at			AI885374	3.5	2	6.0
45518 at	Chromosome 22 onen reading frame 4		AI635057	3.5	1.3	4
47982 at		- 1	AW026098	3.5	1.8	3.1
43798 s at	T	AQP3 /	AA630981	3.5	3.4	3.1
49165 at	hynothetical protein DD00013		AI347938	3.5	2.1	4.3
60062 s at	_	4	AW024795	3.5	0.7	3.4
18-5-3000			AI027140	3.5	2.9	3.7
57132_at	RNB6		41341482	3 5		
43857 s at			AA570070) w	500	x) (
72644_at			0 7 7 0 0 0 7 7	0 0	6.3	3.7
			14300440	3.5	2.3	9.0

Figure 11PPPPP

		MGP	AI140620	3.5	33	
57461_at			AI472111	3.5	3.0	0
82156_at			AW044081		2.5	0
52973_at	hypothetical protein FLJ10330		AA683501		0.0	7 6
50162_at			AA610838		2 2	
43795_s_at	43795_s_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV)	NDUFA8	1 -		2.6	4.1
45531_at			41970101	2 5	C	
62462_at	hypothetical protein dJ473B4		A1433432		3.5	77.
54547_at	hypothetical protein DKFZp434G0522		AA147848		000	3.3
52842_at			AI 110412			9.0
47057_at			D20714	, c	0.00	2.3
55446_at			A1199032		1.00	
55732_at			AWOONA	5 6	0.0	3.4
48354_at			A1000000	3.5	2.2	33
34470_at	transcription factor EC	TEEL	1	9.4	0.7	5.2
1313 at	proteasome (prosome macropain) subunit heta tupe 7	1000	1	4.0	3.2	
37824 at		LSMB/	D38048	3.4	4.6	0.5
1003	13		AB028997	3.4	1.2	1.4
1000 at		RAP1B		3.4	1	1.6
10110_at	aniyold beta (A4) precursor protein binding, family B, member 2 (Fe65-like)	APBB2	U62325	3.4	0.1	7.3
40598_at			W20138	70		
35488_at	small nuclear RNA activating complex, polypeptide 1, 43kD	SNAPCI	1144754	100	4.7	0.0
41185_f_at	SMT3 (suppressor of mif two 3, yeast) homolog 2	SMT3H2	A197172A	0.0	0.0	13.9
32259_at		F7H1	45/1/CIO	0.4	2.7	5.5
32786_at	jun B proto-oncogene	IND I	X51345	0.4	4.0	3.5
33779_at	vesicle-associated membrane protein 1 (synaptobrevin 1)	VAMPI	AF060520	1 5	1.6	7.7
32888_at	leukocyte tyrosine kinase	74-	200000	1.0	1.0	5.6
34104_i_at			A32413	9.0	1.2	2.5
39344 at	transformer-2 alpha (htra.2 alpha)		M14/23/	3.4	0.9	6.7
31690 at			053209	3.4	1.1	3.5
33835 at	KIAAA721 protein		008997	3.4	2.1	2.2
678 24	-13		AB018264	3.4	9.0	3.5
27070 at	۳. I	ALPP	J04948	3.4	1.1	6.9
37242 at	-1	MGC5149	U79260	3.4	1.9	
3351U S at	[pintamate recentor metabotropic]					

0	ב (איווות בע ו בעבטטוע ב)	RP2	AJ007590	3.4	2	4
T		CPD	062090	3.4	1 7	
hypothetical prote	5F1122 similar to axotrophin		AL050171		7	
N-ethylmaleimide	tor attachment protein, gamma	NAPG	1		1 2	2 3
T		GARS	1		20	5
t-complex-associa	pressed 1-like	TCTE1L	L		000	C
beta-2-microglobu		BZM	L		1.5	2.3
	leoprotein M	HNRPM	L			0
38033_at DKFZP564M1416 protein			□	1 0	2.1	
37956 at aldehyde dehydrogenase 8		ALOHA		0.4	70	
38817_at sperm associated antigen 7		SPACZ	15	100		2.
		10 AG		3.4	4.6	
eukarvotic transla	tion initiation factor 2.alpha kipasa 3	0.14011		3.4	2.8	14.8
		EIFZAKS	_1	3.4	2.6	5.
54885 at Ihynothetical protein			AA010757	3.4	0.6	o.
T			AI458882	3.4	1.4	
54751 at HSPC163 protein			AA470110	3.4	1	3.3
1			AA044747	3.4	1.6	
75653 24			AI004422	3.4	4.1	6.5
accitac potaioossa miseas			_	3.4	2.8	1.5
Т		SPAG4	_	3.4	1.9	0.4
76905 at			AI971242	3.4	3.1	1.1
90600 at			AI674760	3.4	0.7	7
66819 at			AA491286	3.4	0.4	1.2
59883 r at			AA984073	3.4	1.6	6.5
42599 at			Al150628	3.4	2.4	4.6
78618 at			T82459	3.4	2	1.2
78742 at			AI889955	3.4	0.3	0.5
58530 r at			AI939581	3.4	1.2	6.4
. J. n			T66185	3.4	2.5	5.3
83060 at			AI916523	3.4	3.4	
53934 at			AI335004	3.4	1.2	1.4
54720 at			AI291699	3.4	1.5	4.4
64506 at zinc finger protein 143 (close pHZ 1	17 17		- 1	3.4	10.4	
hypothetical areta	11.2:1)	ZNF143		3.4	1.7	0.7
inyporterinal profes			177176			

Figure 11RRRRR

83898_at	NADPH oxidase, EF hand calcium-binding domain 5	SXON	A1091544	3.4	8.0	0 1
82051_at	hypothetical protein FLJ20321		AA535115	3.4	2.2	0.5
91689_at			AA534953	3.4	7 7	-
82470_at			A1858051	3.4	1 C	C. T
47688_at			H78083	3.4		5 -
85291_at			A1467796	3.4		7.7
51942_at			AA142984	3.4	26	4.4
84709_at			AI700770	3.4		C
84761_at			AI476355	3.4	0.5	
46309 at		TUBB	AL039239	3.4	13	E E
43850_s_at	PP1201 protein		AA668732	3.4	5.4	2
59047_at			AI825998	3.4	9.0	3.5
87096_at			AA335058	3.4	1.5	2.2
87135_at	- 1		AI239715	3.4	86	1 2
74635_at		CDK2	AI989454	3.4	α.	
65764_at	RAB18, member RAS oncogene family	RAB18		3.4	6.3	0.3
71001_at			AI863286	3.4	27	2.6
71272_at			AI928726	3.4	80	- r
43439_at	hypothetical protein FLJ11252		AA741298	3.4	60	
43407_at	DKFZP586F1524 protein		AW014654	3.4	1 9	2.7
56662_at			AI627666	3.4	000	j
59278_at			Н98683		21	0 0
43376_at	LIS1-interacting protein NUDE1, rat homolog		AI863849	3.4	1.6	2 1
45092_at			AA029446	3.4	0.8	2.5
87894_at			H65062	3.4	1.9	1.6
6/593 at			AI033153	3.4	0.5	9.0
/1616_r_at			R27430	3.4	-	1.3
42/09_at	Wolf-Hirschhorn syndrome candidate 1-like 1	WHSC1L1	241537	3.4	0	7.2
			AA648525	3.4	1.6	2.4
-11	- 1		AA482950	3.4	2.6	3.4
	ribosomal protein L39	RPL39	1	3.4		1.2
60011_at	KIAA1255 protein		H62663	3.4		0.3
65660_at	nuclear transcription factor, X-box binding 1	NFX1	AA744238	3.4	1.6	
65086_at	hypothetical protein MGC3262		278349		1.2	1.2
65662_at			AA019910	3.4	1 9	0 0

Figure 11SSSSS

47079_at mannosyl (alpha-1,3)-glycoprotein beta-1,4-N. acetylglucosaminyltransferase, isoenzyme B mannosyl (alpha-1,3)-glycoprotein beta-1,4-N. acetylglucosaminyltransferase, isoenzyme B 87481_at mannosyl (alpha-1,3)-glycoprotein beta-1,4-N. acetylglucosaminyltransferase, isoenzyme B 87481_at hypothetical protein FLJ10698		32N	N78066	3.4	3.2	3.5
acetylglucosamin acetylglucosamin acetylglucosamin hypothetical protein proteasome (pros proteinsmembrane Extransmembrane CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer Extransmembrane Extrans		AI45	AI458735	3.4	2.4	
mannosyl (alpha- acetylglucosamin hypothetical protein proteasome (pros proteasome (pros proteasome (pros proteasome (pros proteasome (pros protein) transmembrane E alpha thalassemii cerevisiae) homol t CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer peroxiredoxin 2 homolog of mouse thydroxyacyl.Coen RecQ protein-like icitrate synthase citrate synthase citrate synthase concomposition	ne subunit 2	AA97	AA974493			1.3
hypothetical protein proteasome (prosent KIAA1096 protein proteasome (prosent KIAA1096 protein proteasome (prosent cytochrome b-5 transmembrane palpha thalassemic cerevisiae) homol to cerevisiae) homol to cerevisiae) homol to cerevisiae) homol to cerevisiae) homol to cerevisiae) homol to cerevisiae) homol to cerevisiae) homol to cerevisiae) homol to cerevisiae homologo finousse thypothetical protein ARF-binding protein hydroxyacyl-Coen RecQ protein-like citrate synthase contromiosome controlled control	ycoprotein beta-1,4.N.	MGAT4B AL04	AL049000	3.4	1.2	3.8
hypothetical protein proteasome (prosent proteasome (prosent proteasome (prosent proteasome (prosent protein)) It cytochrome b.5 transmembrane E alpha thalassemic cerevisiae) homolot to CCAAT/enhancer (CCAAT/enhancer CCAAT/enhancer peroxiredoxin 2 homolog of mouse thypothetical protein hydroxyacyl. Coent RecQ protein-like citrate synthase contromosome control	erase, isoenzyme B				-	
nypothetical protein proteasome (prospecial proteasome (prospecial proteasome (prospecial protein proteasome (prospecial protein) protein prot		D79	D79487	3.4	-	, c
t KIAA1096 protein proteasome (pros proteasome (pros transmembrane E transmembrane E alpha thalassemic cerevisiae) homol t CCAAT/enhancer CCAAT/enhancer cysteine and glyci peroxiredoxin 2 hypothetical protein ARF-binding protein ARF-binding protein ARF-binding protein and citrate synthase contransments.	86901	AIGE	41951927	400	10	5.4
proteasome (pros at cytochrome b-5 transmembrane E alpha thalassemic cerevisiae) homol t CCAAT/enhancer CCAAT/enhancer at CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer transmembrane go of mouse thypothetical prote KIAA1080 protein ARF-binding prote hydroxyacyl.Coen RecQ protein-like citrate synthase chromosome cont		2004	1367	4.0	0	0.5
transmembrane Etransmembrane Etransmembrane Edha thalassemic cerevisiae) homol cerevisiae) homol CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CAAT/enhancer CAAT/enhancer CAAT/enhancer CCAAT/enhancer CAAT/enhancer CAAT/enh	Jacronain) activator cliburate 1 /0400 -1-1-	- 1	AA9/0/41	3.4	1.5	2
transmembrane E transmembrane E alpha thalassemii cerevisiae) homol t CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CASteine and glyci peroxiredoxin 2 homolog of mouse thydroxyacyl. Coent KIAA 1080 protein ARF. binding protein hydroxyacyl. Coent RecQ protein-like citrate synthase controlings.	ich opain) activator subuille (PAZS alpha)	PSME1 AA66	AA662670	3.4	4.3	0.8
transmembrane paper alpha thalassemic cerevisiae) homol cerevisiae) homol to CCAAT/enhancer CCAAT/enhancer GCN5 (general co cysteine and glyci peroxiredoxin 2 homolog of mouse t hypothetical prote KIAA1080 protein ARE-binding protein hydroxyacyl. Coengree Commosome contraine contraine contrained		CVBE	20045	,		
alpha thalassemic cerevisiae) homol t CCAAT/enhancer t CCAAT/enhancer cysteine and glyci peroxiredoxin 2 homolog of mouse t hypothetical protein ARF-binding protein ARF-binding protein hydroxyacyl. Coent RecQ protein like citrate synthase conclumosome conclumosome conclumosome concluming alpha company and conclumosome conclumoso		1	343	3.4	6.8	5.6
alpha thalassemii cerevisiae) homol to CCAAT/enhancer CCAAT/enhancer to CCAAT/enhancer cysteine and glyci peroxiredoxin 2 peroxiredoxin 2 peroxiredoxin 2 peroxiredoxin 2 hypothetical protein ARF-binding protein hydroxyacyl.Coeng RecQ protein-like citrate synthase chromosome concurrent		MEM4 AI93	A1939329	3.4	4.4	2.5
cerevisiae) homol to CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CCAAT/enhancer CASTER CONTRATION PROPERTY IN A 1080 protein like CONTRATION CON		- 1	AA279956	3.4	2.2	
CCAAT/enhancer tt CCAAT/enhancer tt CCAAT/enhancer GCN5 (general co GCN5 (general co cysteine and glyci peroxiredoxin 2 homolog of mouse thydothetical prote KIAA1080 protein ARF-binding prote hydroxyacyl.Coen RecQ protein-like citrate synthase citrate synthase chromosome con	al retardation syndrome A-linked (RAD54 (S.	ATRX AA80	AA806986	3.4	1.8	1.4
CCAAT/enhancer GCN5 (general co cysteine and glyci peroxiredoxin 2 homolog of mouse t hypothetical prote KIAA1080 protein ARF-binding prote hydroxyacyl-Coen RecQ protein-like citrate synthase chromosome conc						
GCN5 (general co GCN5 (general co cysteine and glyci peroxiredoxin 2 homolog of mouse t hypothetical prote KIAA1080 protein ARF-binding prote hydroxyacyl-Coen RecQ protein-like citrate synthase Chromosome con	protein (O /EDD) Late		A1698684	3.4	4.7	5.3
GCN5 (general co GCN5 (general co cysteine and glyci peroxiredoxin 2 homolog of mouse thypothetical prote KIAA1080 protein ARF-binding prote hydroxyacyl.Coen RecQ protein-like citrate synthase	protein (C/EDr), beta	CEBPB AW02	AW025406	3.4	2.4	C
GCN5 (general co GCN5 (general co cysteine and glyci peroxiredoxin 2 hypothetical prote KIAA1080 protein ARF-binding prote hydroxyacyl-Coen RecQ protein-like citrate synthase		A183	AI830502	3.4	2.3	00
GCN5 (general co cysteine and glyci peroxiredoxin 2 homolog of mouse thypothetical protein MAR-binding protein hydroxyacyl-Coen RecQ protein-like citrate synthase concomposition of the concompositio		A120	AI209180	3.4	2	7.3
GCN5 (general co cysteine and glyci peroxiredoxin 2 homolog of mouse thypothetical protein AR-binding protein AR-binding protein hydroxyacyl-Coeng RecQ protein-like citrate synthase chromosome concompanion and		AA52	AA528592	3.4	α.	
GCN5 (general co cysteine and glyci peroxiredoxin 2 homolog of mouss at hypothetical protein KIAA1080 protein ARF-binding prote hydroxyacyl-Coenz RecQ protein-like citrate synthase		EOM	W03586	3.4	27	9 6
cysteine and glyci cysteine and glyci peroxiredoxin 2 homolog of mouss at hypothetical protein KIAA1080 protein ARF-binding prote hydroxyacyl-Coenz RecQ protein-like citrate synthase			AA883059	3.4	0.7	2 0
cysteine and glycir peroxiredoxin 2 homolog of mouse at hypothetical protein: KIAA1080 protein: ARF-binding protein hydroxyacyl-Coenz RecQ protein-like (citrate synthase chromosome cond	amino-acid synthesis, yeast, homolog)-like 2	GCN5L2 AF029777	2777	3.4	2.5	0.2
peroxiredoxin 2 homolog of mouse at hypothetical protei KIAA1080 protein; ARF-binding protei hydroxyacyl-Coenz RecQ protein-like (citrate synthase chromosome cond	protein 1	CCBD1 M23	M3314E			
homolog of mouse at hypothetical protein: KIAA1080 protein: ARF-binding protei hydroxyacyl-Coenz RecQ protein-like (citrate synthase chromosome cond			10185	4.0	3.1	4.4
ARF-binding protein, ARF-binding protei hydroxyacyl-Coenz RecQ protein-like (citrate synthase chromosome cond	R OKI (KH domain RNA binding protein)	┸	100	0.4	5.5	3.3
KIAA1080 protein, ARF-binding protei hydroxyacyl-Coenz RecQ protein-like (citrate synthase chromosome cond	1585	ALU31/81	1/81	3.4	1.4	4
ARF-binding protei hydroxyacyl-Coenz RecQ protein-like (citrate synthase chromosome cond	associated, gamma-adaptin ear containing	A1/4.	A1/43654	3.4	2.6	3.5
		AB0Z	AB029003	3.4	2.3	2.1
citrate synthase	dehydrogenase, type II	HADH2 AF035555	5555	3.4	1 6	2
chromosome cond	elicase (1. like)	RECQL A1685944	5944	3.4	2.4	2
ביין בייי ביייטקסש	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)		7042	3.4	2.1	4.2
	TING TIME	٩	0219	3.4	2.9	22
o contact in the might protein, I	111, 1	MKRN1 U41315	315	3.4	-	7 7

Figure 11TTTT

35289_at	rab6 GTPase activating protein (GAP and centrosome associated)	1	AJ011679	3.4	2.4	3.2
35159_at	tubulin specific chaperone e	TBCE	U61232	3.4	1.9	3.1
34381_at	cytochrome c oxidase subunit VIIc	COX7C	AI708889	3.4	1.6	5.4
1924_at	Syclin H	CCNH	U11791	3.4	2.3	3.2
36945_at	endoplasmic reticulum lumenal protein		X94910	3.4	6.0	(m)
37672_at	ubiquitin specific protease 7 (herpes virus associated)	USP7	272499	3.4	9.0	3.9
37264_at	zinc finger protein 131 (clone pHZ·10)	ZNF131	U09410	3.4	2.5	m
32610_at	LIM domain protein		X93510	3.4	2.4	3.4
33121 g at	regulator of G-protein signalling 10	RGS10 A	AF045229	3.4	1.5	4
138_at	mitogen activated protein kinase kinase kinase 1	MAP4K1	U66464	3.4	3.7	2.8
40745_at		AP1B1	L13939	3.4	2.7	3.2
41038_at	neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2)	NCF2	M32011	3.4	1.4	3.1
58498_at	KIAA1378 protein		AI082236	3.4	2.5	3.4
80436_at			AI935644	3.4	3.3	4
44713_at	HSPC009 protein		U18006	3.4	1.9	4
45577_s_at			AI471038	3.4	4.9	5
45276 g at	protein x 0001		W30943	3.4	m	4.9
43382_s_at	C-terminal binding protein 1	CTBP1	AI991853	3.4	2.5	3.8
65724_at	KIAA1423 protein		AI684729	3.4	3.5	3.6
57156_at	HSPC023 protein		W92964	3.4	3.2	4.9
51173_at	purinergic receptor P2X, ligand-gated ion channel, 4	P2RX4	AI872092	3.4	2.9	3.4
46261_at	hypothetical protein		AL045512	3.4	1.7	2.2
45543_r_at			AI359916	3.4	3.4	2.8
44842_at	COP9 complex subunit 7a		AI971871	3.4	2.9	8.4
46871_r_at			W32096	3.4	3.1	2.9
47101 g at			AI972460	3.4	2.6	3.4
64436_at	arginyl aminopeptidase (aminopeptidase B) like 1	RNPEPL1	AI926755	3.4	2	m
54483_at			AA760777	3.4	3.4	3.4
62559_at	hypothetical protein FLJ11230		W31010	3.4	1.6	3.3
44828 s_at	ATPase, Na+/K+ transporting, alpha 1 polypeptide	ATP1A1	AI610470	3.4	2.6	3.7
47082_at	NAG-5 protein	7)	AW003127	3.4	2.7	3.6
54507_at		/	AA912049	3.4	1.9	2.8
32464_at	defensin, beta 2	1 _1	AF071216	3.3	6.0	1.4
35074 at	jerky (mouse) homolog-like	JRKL	AF004715	88	c	36

		7]	A1 0/9923	33	4.6	O.4
41438_at	KIAA1451 protein		AR011165	3.3	1.9	9
41625 at	thyroid hormone receptor associated protein, 240 KDa Suburiit		AE007130	33	0	0
Γ	hynothetical protein		100/130	5 6	1 2	0
T	VIAAOSEO gene product		08/43/	3.3	2 0	
1	מנוננ	SAIL	AF051850	3.3	ס	7
1	supervillin	FIF4A2	D30655	3.3	2.4	8.
1420_s_at	eukaryotic translation initiation factor 4A, Isolofiii 2	CTNNA1	123805	3.3	1.4	0.2
		ALNXO.	103106	3.3	1.6	1.5
-1	cyclin-dependent kinase inhibitor 1A (pz.), Cip1)	┺	AA868382	3.3	1.2	1.3
32773_at	major histocompatibility complex, class II, UV alpha 1	+	AI 021366	3.3	2.8	3.3
40446_at	PHD finger protein 1	+	D83778	333	2.6	1.3
34221 at	KIAA0194 protein	2	000110	2 2	82	3.4
34678 at	fer-1 (C.elegans)-like 3 (myoferlin)	LERILS	-10		1 6	1.5
33829 at		· ·	0/0711	5 6	000	2.4
34755_at	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 2	ADPRTL2	AJ2368/6	J	7:7	
			U67322	3.3	2	2.8
ωı	HBV associated factor		W26762	3.3	6.9	٥
33285_i_at		RAB32	U59878	3.3	0.2	0
41523 at		MAP3K4	AF002715	3.3	1.9	0.2
35651_at	In Kinase Kinase Killase		AB007870	3.3	1.9	0
40018_at		GGPS1	AB019036	3.3	1.5	1.1
35296_at	geranylgeranyl diphosphate synthase 1	GARPRI	013317	3.3	2.5	1.1
35943 s at	GA-binding protein transcription lactor, beta submit 1 (Sons)	DTR	M60278	3.3	4.4	1.3
5-000	growth factor)		000000	3.3	0	5.4
38051 at	ere	MAL	VE2660	5.00		0.4
	CCAAT/enhancer binding protein (C/EBP), beta	כנסים	NGGGOR	000	2.3	4.2
55376_at	MIL1 protein		AA504346	3.3	2.2	4.9
61487_at		HIEX	1_	3.3	1.1	2.3
60070_f_at	H1 histone family, member X			3.3	1.3	4.5
50757 at			A1051390	3.3	O	0
80698_at			W87283	3.3	0	2.3
76039_at			A1276023	3.3	1.5	0
47427_at	hypothetical protein FLJZU339		AA829524	3.3	e	4.4
66523 at			A1732902	3.3	0	0
81813_at			1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2			

MARQBSS protein				00100	2.2	1 5	3.5
KIAA0853 protein	15 127 st		₹	19/2129	5.0	210	6
MARAGOSD protein MAGABSZA 3.3 0.8 4.1 AAGABSZA 3.3 0.5 0.5 0.5 AAGABSZA 3.3 3.5 0.5 0.5 AAGABSZA 3.3 3.5 0.5 0.5 AAGABSZA 3.3 3.5 3.5 3.5 AAGABSZA 3.3 3.5 3.5 AAGABSZA 3	1	1/18 A O O E D D D D D D D D D D D D D D D D D	ΑA	1528666	3.3		7.7
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	7	KIAAU833 protein	A	222203	3.3		4.1
AIGSTATE	1330_at		A	648374	3.3	0.2	5.8
H98190 3.3 3.3 2.3 2.8 2	53868_at		Ā	693524	3.3	0.5	0
AIRCREAN AIRCREAN	275 at			198190	3.3	3.3	7
Air Coll - Brotein Air Col	299_at		Ā	823793	3.3	0.2	2.8
AIRCOGEO	1859_at		\ 	1377276	3.3	1.9	2.3
AAEB932 33 1.5 1.4 AAEB932 3.3 1.5 1.4 AAEB932 3.3 2.2 AAEB9323 3.3 2.2 AAEB9323 3.3 2.2 AAEB9333 3.3 2.2 AAEB9333 3.3 2.2 AAEB9333 3.3 2.3 AAEB9333 3.3 3.3 AAEB9333 3.3 3.3 AAEB9333 3.3 3.3 AAEB9333 3.3 3.3 AAEB9333 3.3 AAEB93	1693 i at			1802667	3.3	0.8	1
AA922623	163 at		4	1658932	3.3	1.5	1.4
interferon gamma receptor 2 (interferon gamma transducer 1)	1089_at		A	A526232	3.3	2.2	9.0
Interferon gamma receptor 2 (interferon gamma transducer 1) IFNGR2 AB24688 3.3 0.64 2.2 Interferon gamma receptor 2 (interferon gamma transducer 1) IFNGR2 AB24681 3.3 1.9 7.9 CGI-58 protein CGI-13 pr	.762_at		A	4923551	3.3	2.8	4.4
interferon gamma receptor 2 (interferon gamma transducer 1) iFNGR2 AI826621 3.3 0.4 2.2 CGI-58 protein CGI-58 protein AA001263 3.3 1.9 7 Interferon gamma receptor 2 (interferon gamma transducer 1) AA001263 3.3 2.7 4.9 CGI-58 protein AA001263 3.3 2.7 0.4 AA001263 3.3 2.7 1.8 AA001263 3.3 2.7 0.4 AA001263 3.3 2.7 0.4 AA001263 3.3 0.1 1.8 AA001263 3.3 0.1 1.8 AA001263 3.3 0.1 4.1 AA001263 3.3 0.1 4.1 AA001263 3.3 0.1 4.2 AA001263 3.3 0.1 4.2 AA001263 3.3 0.1 4.2 AA001263 3.3 3.3 3.4 AA001263 3.3 3.3 3.2 AA001263 3.3	066_at		A	A234688	3.3	9.0	2
TEGRIA 3.3 1.9 7.8 MANGANGS 3.3 2.3 4.9 AANOTACE 3.3 2.9 4.9 AANOTACE 3.3 2.7 1.8 AANOTACE 3.3 3.1 1.1 1.1 AANOTACE 3.3 3.1 3.1 1 AANOTACE 3.3 3.1 3.1 3.1 3.1 AANOTACE 3.3 3.1 3.1 3.1 3.1	'936_at	(1) representation frameducer 1)	۰.	1826621	3.3	0.4	2.2
CGI-58 protein AA034063 3.3 2.3 4.9 CGI-58 protein CGI-13	102 at	reception 2 (miteriation garming transparent	L	T69814	3.3	1.9	7
CGI-58 protein AA174079 3.3 1.9 118 CGI-58 protein AA201265 3.3 2.7 0.4 CGI-58 protein AA201265 3.3 2.7 1.8 ACGI-58 protein AA2012065 3.3 2.7 1.8 ACGI-13 protein ACGI-13 p	090 at		A	A034063	3.3	2.3	4.9
CGI-58 protein AAO01263 3.3 2.7 0.4 CGI-58 protein AAO01265 3.3 2.7 0.4 AAO01263 3.3 2.7 1.8 AAO01263 3.3 2.7 1.8 AAO01263 3.3 0.1 1.8 AAO01263 3.3 0.1 1.8 AAO01263 3.3 0.1 4.1 AAO01263 3.3 0.1 4.1 AAO01263 3.3 3.3 3.4 2.6 AAO01263 3.3 3.3 3.4 2.6 AAO01269 3.3 3.3 3.4 3.4 AAO01269 3.3 3.3 3.4 3.2 AAO01269 3.3 3.3 3.4 3.2 AAO0136 AAO00126 3.3 3.4 1.3 AAO0000 AAO0000 AAO0000 3.3 3.4 1.3 AAO0000 AAO0000 AAO0000 AAO0000 AAO0000 AAO0000 AAO0000 <td>690 at</td> <td></td> <td></td> <td>A174079</td> <td>3.3</td> <td>1.9</td> <td>11.8</td>	690 at			A174079	3.3	1.9	11.8
CGI-138 protein AA412065 3.3 2.7 1.8 AI766604 3.3 5.3 0.1 1.8 AI766604 3.3 5.3 0.1 1.8 AI766604 3.3 3.3 0.1 1.8 AI766604 3.3 0.1 1.8 1.1 1.8 AI766604 3.3 3.3 0.1 4.1 AI766604 3.3 3.3 3.4 2.6 AI766604 3.3 3.3 3.4 2.6 AI766604 3.3 3.3 3.4 2.6 AI766604 3.3 3.3 3.4 3.4 AI766604 3.3 3.3 3.4 AI766604 3.3 3.3 3.4 AI766604 3.3 AI76660 3.3 AI7660 3.3	774_at		4	A001263	3.3	2	
Air Decision Air	232 at	Cal-58 protein	A	A412065	3.3	2.7	1.8
tropomodulin 3 (ubiquitous) at Golgi vesicular membrane trafficking protein p18 tropomodulin 3 (ubiquitous) at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking p18 at Golgi vesicular membrane trafficking protein p18 at Golgi vesicular membrane trafficking p18 at Golgi vesicular membrane trafficking p18 at Golgi vesicular membrane trafficking p18 at Golgi vesicular membrane trafficking p18 at Golgi vesicular membrane trafficking p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi vesicular membrane p18 at Golgi ve	1585 at		1	11766604	3.3	5.3	0
tropomodulin 3 (ubiquitous) tropomodulin 3 (ubiquitous) at hypothetical protein FLJ10143 tropomodulin 3 (ubiquitous) at hypothetical protein FLJ10143 tropomodulin 3 (ubiquitous) at hypothetical protein FLJ10143 tropomodulin 3 (ubiquitous) at hypothetical protein FLJ10143 tropomodulin 3 (ubiquitous) at hypothetical protein FLJ10143 at hypothetical protein tropomodulin 3 (ubiquitous) at hypothetical protein FLJ10143 at hypothetical protein tropomodulin 3 (ubiquitous) at hypothetical protein FLJ10143 at hypothetical protein FLJ101)319_at		-	41301513	3.3	0.1	1.8
tropomodulin 3 (ubiquitous) tropomodulin 4 (ubiquitous) tropomodulin 4 (ubiquitous) tropomodulin 4 (ubiquitous) tropomodulin 4 (ubiquitous) tropomodulin 4 (ubiquitous) tropomodulin 4 (ubiquitous) tropomodulin 4 (ubiquitous) tropomodulin 4 (ubiquitous) tropomodulin 4 (ubiquitous) tropomodulin 4 (ubiquitous) tropomodulin 4 ()825 at			1492230	3.3	1.1	1
tropomodulin 3 (ubiquitous) TMOD3 AI373630 3.3 3.4 26 at Golgi vesicular membrane trafficking protein PLJ0143 AI625962 3.3 3.4 2.6 at hypothetical protein FLJ0143 AI656132 3.3 4.6 0 Alsaysay AI859280 3.3 0.6 5. CGI-13 protein AA782992 3.3 1.9 1. ALGA-13 protein ALGA-13 protein<	2996 at			1123967	3.3	0.1	4.1
tropomodulin 3 (uniquitous) 4 (1525962) 3.3 3.4 2.6 at Golgi vesicular membrane trafficking protein FLJ10143 4 (1092890) 3.3 2.8 3.3 3.2 4.6 4.5 4.6 4.6 6.0 4.6 6.0 4.6 6.0 6.0 6.0 6.0 6.0 7.3 1.3 1.3 1.3 1.3 1.3 1.1 1.3 1.1 1.2 4.6 6.0 6.0 6.0 6.0 6.0 5.0 6.0 5.0 6.0	2563_at		Ь.	41373630	3.3	3	0
th Golgi Vesicular membrane branching protein FLJ10143 2.8 3.4 4.6 4.6 4.6 4.6 4.6 4.6 4.6 4.6 4.6 4	3032 at			41525962	3.3	3.4	2.6
at hypothetical protein FLJ0143 H65785 3.3 1.2 4.6 at hypothetical protein FLJ0143 Al656132 3.3 4.6 0.1 at hypothetical protein FLJ0143 Al656132 3.3 4.6 0.1 Al656132 3.3 1.3 1.3 1.3 Al656132 3.3 3.4 1.3 1.1 Al694438 3.3 0.6 5.1 CGI-13 protein Al6482992 3.3 3.8 3.8 Al644092 3.3 1.9 1.4	3435 r at	Golgi Vesicular illerilorare transcring protest pao		AI092890	3.3	2.8	3.4
at hypothetical protein FLJ0143 Al656132 3.3 4.6 0.0 at CGI-19 protein Al656132 3.3 4.6 0.0 Al656132 3.3 1.3 1.3 1.3 Al656132 3.3 3.4 1.2 1.2 Al656133 3.3 3.3 0.6 5.0 Al66613 Al66613 3.3 1.9 1.3 Al66613 Al66602 3.3 3.8 3.8 Al66613 Al66602 3.3 1 3.8 3.8	5525_at			H05785	3.3	1.2	4.7
hypothetical protein FL3 (2) 1.3 1.3 1.3 Al859280 3.3 3.4 1. Al394438 3.3 0 5 CGi-19 protein Al634944 3.3 1.9 1. AA782992 3.3 3.8 3. AL64092 3.3 1 1	5434 at			AI656132	3.3	4.6	0.2
CGI-13 protein AI859280 3.3 3.4 1. CGI-13 protein W07150 3.3 0.6 5. AA782992 3.3 1.9 1. AA782992 3.3 3.8 3. AL044092 3.3 1	0323 g at	nypothetical prote		H69779	3.3	1.3	1.2
at Al394438 3.3 0 at CGI-19 protein W07150 3.3 0.6 5. at CGI-113 protein Al634944 3.3 1.9 1. at CGI-113 protein AA782992 3.3 3.8 3.3 at AL044092 3.3 1	3263 r at			AI859280			1.3
at CGI-19 protein W07150 3.3 0.6 5. at CGI-13 protein AIG34944 3.3 1.9 1. at CGI-113 protein AA782992 3.3 3.8 3.3 at CGI-113 protein AA782992 3.3 1	0194_at			AI394438	3.3	0	
CGI-113 protein AIG34944 3.3 1.9 1. CGI-113 protein AA782992 3.3 3.8 3. AL044092 3.3 1	852/ at	in protein		W07150	3.3		5.6
Cd: 11.5 protein	5553 at	Cai-19 protein		A1634944	3.3	1.9	1.5
AL 044092	7004 at	Cal-113 protein		AA782992	3.3	3.8	3.6
	600/ at			AI 044092	3.3	-	

69376_at			AI655430	3.3	1.5	3.8
47902 at			W74622	3.3	1.6	1.1
62466_at	lymphoid blast crisis oncogene	LBC	AI797853	3.3	2.7	8.0
53334_at			H12612	3.3	1.1	6.9
49581 g at			AA779208	3.3	2.1	2.4
44421_s_at			D59337	3.3	0.8	1.4
51254_at			A1090139	3.3	3.6	4.9
60138_at			AI823497	3.3	1.1	5.1
52575_at			H66727	3.3	3	3.6
63980_at	hypothetical protein FLJ10618		H46637	3.3	2.9	
52083_at			AL040341	3.3	2.8	
46126_at			AI498592	3.3	0	0.8
63457_f_at			AA022988	3.3	2.2	4
64909_at	hypothetical protein DKFZp762B226		AI341683	3.3	3.6	1
58630_at			AA187854	3.3	1.7	
54900_at	f-box and leucine-rich repeat protein 3A	FBXL3A	AI983021	3.3	1.5	2.
64266_at	stromal antigen 2	STAG2	AA476504	3.3	1.2	1.0
72376 r_at	cathepsin K (pycnodysostosis)	CTSK	AI282317	3.3	6.0	0.8
46052_at			AA250767	3.3	4.2	6.5
47155_at			AI300571	3.3	2.2	0.5
48896_at	carboxypeptidase A3		AI082244	3.3	3.6	14.3
56710_at			AI762244	3.3	1.4	2.3
74710_s_at	epithelial membrane	EMP3	AW005790	3.3	2.4	3.9
34477_at	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	UTY	AF000994	3.3	1.9	2.8
40414_at	valyi tRNA synthetase 2	VARS2	X59303	3.3	2.8	m
40764_at	glutamic-oxaloacetic transamınase 2, mitochondrial (aspartate aminotransferase 2)	G0T2	M22632	3.3	2.4	
250_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	NFATC3	L41067	3.3	3.2	3.3
1287_at	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	ADPRT	J03473	3.3	2.1	
32455 s_at	proline and glutamic acid rich nuclear protein		U88153	3.3	2.6	m
33340_at	KIAA0438 gene product		AB007898	3.3	1.3	4.
36417_s_at	36417_s_at acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-	ACAA1	ACAA1 AF035295	3.3	8.0	3.9
	Cocile A Choleso,					

Ī			AR014514	3.3	3.1	3.3
Ţ	KIAAUb14 protein	SNRPN	U41303	3.3	2	3.1
34842_at	Small nuclear riboliucieoproteili polypeprote 17	FIF3SO	1178525	3.3	1.9	3.4
23_at	eukaryotic translation initiation lactor 3, subuint 3	ANXA11	1 19605	3.3	1.7	4.2
36637_at	annexin A11	BRF2	X78992	3.3	2.4	3.1
32588 s at 479_at	disabled (Drosophila	DAB2	U53446	3.3	e -	4.
	describe monophosphate deaminase 2 (isoform I)	AMPD2	M91029	3.3	3	2.9
	adeliosine mortain A1 (70kD)	RPA1	M63488	3.3	2.3	e l
38461 at		CENPB	X05299	3.3	3.3	m
3/931 at	bypothatical protein		T84485	3.3	2.7	3.5
48/13 B at	וואסחוובווכמו הוסנכווו		AI078187	3.3	2	2.6
75510 at	distriction protein	LRN	AI654857	3.3	2.5	4.3
90610 at	ءً اءُ		AA593768	3.3	m	3.1
/333/ s at	7055/ Sad hypometical protein reserves		A1992128	3.3	2	2.5
40/01 S at			A1090386	3.3	2.4	1.8
56263_dt 66112_at	translocase of inner mitochondrial membrane 17 (yeast) homolog A		AA234191	3.3	1.4	4.5
1000	heart of fire and		AI760042	3.3	3.1	m
49403 at	Don't lo lorest lotine		AA150502	3.3	1.5	3.1
56293 at	handthetical protein FI 120160		AA133311	3.3	3.3	3.5
44047 at			AA913312	3.3	2	3.2
45562 at	characterized hynothalamus protein HCDASE		R69311	3.3	1.9	2.5
32301 3 at	SLIMO.1 activating		H98166	3.3	2.6	4.7
52932_at		KAII	W51778	<u>ლ</u> ლ	6,	2.6
110			AA479016	3.3	3.1	3.1
5007/ at			H15571	3.3	1.3	3.1
43984 at			A1141764	3.3	3	1.6
85/01 at			AA740928	3.3	2.1	3.1
004 at	Icol 20 protein: cell death regulatory protein GRIM19		AA181145	3.3	3.7	4.4
45339 at	projecting regulatory element hinding	PREB	٠.	3.3	1.3	3.1
5/100 at	5) 100 at hypothetical profess FI 121794		AL046381	3.3	1.3	3.3
010+0 K at	יייייייייייייייייייייייייייייייייייייי		R55295	3.3	3.3	2.6

44550 24	hotassium voltage gated channel Tsk-related family, member 3	KCNE3	AI148745	3.3	2.9	2.9
			A1672040	3.3	2.1	3.2
F0071 at			AL042592	3.3	3.1	4.4
5307 1 at			AI953658	3.3	3.1	3.4
54502 c at	hypothetical protein FL J20859		AW006969	3.3	1.5	3.7
76220 at	peroxisomal short-chain alcohol dehydrogenase		A1131178	3.3	8	3.7
65042 at	Unionitin like 4	UBL4 /	AW043826	3.3	2.3	m
190001 5 24	-	CSNK1E	AI831641	3.3	2.8	2.9
51116 g at		L	AW021000	3.3	2.5	2.5
}						
46307 at	endomembrane protein emp70 precursor isolog		N24239	3.3	2.4	χ.
223 at	Ubiquitin-conjugating enzyme E2L 3	UBE2L3	S81003	3.2		1.1
39004 at	hypothetical protein FL J22512		AI432190	3.2	0.5	0
	linovitransferase		AB017566	3.2	0.1	8
1 ~	far unstream element (FUSE) binding protein 1	FUBP1	U05040	3.2	3.4	0
31826 at	KIAA0674 protein		AB014574	3.2	2.4	2.4
31389 at	oxidative stress induced like	TISO	U46752	3.2	2.2	1
40790 at	hasic helix-loop-helix domain containing, class B, 2	ВНГНВ2	AB004066	3.2		0.3
1367 f at		OBC	M26880	3.2	2.2	9
35868 21	advanced plycosylation end product-specific receptor	AGER	M91211	3.2	1	16.7
2082 s at	. E-cadherin (epithelial)	CDH1	L08599	3.2	2.9	5.3
32859 at	and activator	STAT1	M97935	3.2	18	8.2
39227 at		PTPRT	AB006621	3.2	1.8	2.9
31673 s at	cell matrix adhesid	CMAR	X65784	3.2	2.7	0
33935 at	calcyclin binding p		AL035305	3.2	1.7	2.3
32249 at	H factor (complement)-like 1	HFL1	M65292	3.2	6.0	0.9
34396 at	KIAA0978 protein		AB023195	3.2	2	m
36706 at	serine/threonine kinase 9	STK9	Y15057	3.2	1.3	3.6
35262 at	integrin beta 4 binding protein	ITGB4BP	AF022229	3.2	1.2	0.3
41789 r at	KIAA0669 gene pr		AB014569	3.2	3.6	2.8
32665_at	protein phosphata	PPM1B	AJ005801	3.2	0.4	1.3
	isoform		. 3000	100		
40034_r_at			D86864	3.2	Ø.	>
	endothelial celis		AE035387	0 %	0	2.1
35747 at	stromal cell derived factor receptor 1		AFU3320/	3.5	1,51	

					-
;	small inducible cytokine subfamily A (Cys.Cys), member 17	SCYA17 D43767	3.2	5.8	1./
Į.		FHIT U46922	3.2	9.0	1.2
	218	-	3.2	1.9	1.1
at	actor domain protein 1,	4	3.2	1.8	1.4
7	hinding of	L.	3.2	7.7	6.7
	ימחובי ש	L	3.2	0	6.2
	cathebsin K (pycriouysostosis)	≤	3.2	1	3.2
T	serine/threonine kinase 1/a (apopiosis:iiiduciiig/	_ـــــــــــــــــــــــــــــــــــــ	3.2	0.2	4.1
	nuclear receptor coactivator 4		3.2	0.4	3.4
58033_at		44524064	3.2	3.1	1.7
58435 at	lipopolysaccharide specific response od protein	A1376793	3.0	2	3.2
56199_at	hypothetical protein FLJ20445	A1150441	3.0	5.1	3.4
57737_at		A1130441	20.0	0.	1
63340 at	hypothetical protein FLJ20417	N99181	3.2	1.5	2
E7784 c at		A1525683	3.2	7	4.
37704 5 91		AA699653	3.2	1.8	5.6
54955 at		AI301060	3.2	1.1	1.4
56495_at		AI001809	3.2	0.5	2.3
75/21 at		H54203	3.2	2.9	5
66312_at	ومرامه والمسترسا والمسترسا والمسترسا والمسترسان	AI799087	3.2	2.4	0.5
88653 at	NBALL TOT Dasic Krupper line lactor	Al733141	3.2	4.4	1.6
/699/ at		AA862450	3.2	2.2	4.2
66685_at		AL079769	3.2	3.6	0
76513_at		AA806526	3.2	2.3	8.2
		AA886300	3.2	0.3	3.9
61//1 at		AA434579	3.2	0.7	1.6
77045 at		AA421929	3.2	1.2	2.6
52/95 r at		AI209116	3.2	0.8	5.8
62084 at		AI700571	3.2	3.9	2.3
54624 at		AI305286	3.2	3.4	5.8
54628 at	-	A1352449	3.2	0	1.6
	nypotnetical prof	AI917726	3.2	3.1	0.5
8119/ at		Al351861	3.2	2.5	1.9
63185_at		A1633758	3.2	1	0.9
83/69 at		AA602573	3.2	3.5	4.8
84320 at		R97050	3.2	1.5	2.4
62263_at					

		_	AA0244/7	,			_
35091_at			H92507	3.2	2.6		_
47667 at			A1394150	3.2	4.5	8.9	
85174_r_at			A1927605	3.2	2.2	٥	
at			A1952956	3.2	0.8	0.1	_
at	KIAA0729 protein		AA521504	3.2	0.1		
63106_at			A1652996	3.2	1.3	2.6	
79344_at			AA806200	3.2	2.9	2.3	م آ
68707_at		7NF265	AI 047537	3.2	2.4	1.6	ر در ا
63884_at	zinc finger protein 265		A1632101	3.2	1.6		ठा
59594_r_at			AI684748	3.2	1.7	0.7	_
69821_at	33000		AI417549	3.2	1.8	1.	ζij.
44153 at	hypothetical protein Locaby 33		AA910175	3.2	1.1		<u> </u>
71519_at 1957_s_at	transforming growth factor, beta receptor I (activin A receptor type II-	TGFBR1	AF054598	3.2	1.8	0.3	m 1
	like kinase, 53kD)		AI041279	3.2	2	7.5	ഗി
72313 at			AA010008	3.2	1.3	0	41
72703_at			AI288733	3.2	1.6	1.	ന
47011_at	G-substrate		AA806001	3.2	0.1		151
89838_at			AA151917	3.2	2.2	4	বা
49168_at	C VICE VICENCE OF THE PERSON O	ANKRAZ	A1829903	3.2	0		তা
61697 at	ankyrin repeat, family A (REXAIVE.IRE), 2 https://doi.org/10.112389 similar to acetoacetyl-CoA synthetase		AA640793	3.2	0.4	0.1	=
5/33/_5_41	2/33/_5_at ilypotitetical proton 2000 1		44105000	3.0	3.8		70
65562 at	twisted gastrulation		AA222718	3.2	2.4		N
60473_at			A1765698	3.2	4.6	E	3.4
50081_at	- 1.		AA324765	3.2	2.8	0	0.3
85965_at	two-pore channel 1, homolog		N54910	3.2	2.1	5	9.6
56228 r at			AA180358	3.2	2.7		ळा
42675 at			AA938414	3.2	1.1	0	80
79804_at			AI740499	3.2	0.3	1	ωj
86993 at			AI417686	3.2	2.1		ञा
64628_at	FI 110007 cimilar to kinesin light chain		A1144421	3.2	0.7		8
54439 at	hypothetical protein FLJ12307 Siltilial to Airiesii iigiit ciidii		H25689	3.2	2.3		3.1
44586 at			H29258	3.2	2.1	7	4.2
43004_at							

Figure 11BBBBBB

Ti. Response of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

84521_at			LEUCOON	0.0		1
72281_at			AA426104	2.0	2	0.7
58980_at	zinc finger protein 155 (pHZ-96)	7NF155	1	3.6	7.7	6.1
53402_at				3.6	7 0	6.1
44453_at			H51604	3.5	1.6	3.2
51995_at	cysteine knot superfamily 1, BMP antagonist 1	CKTSF1R1	4491244	3.5	4. 0	2.7
53156_at		10110	080679	3.5	5 ,	0.0
60607_r_at			N26011	3.6	10	4.8
53197 g at	Suppression of tumorigenicity 16 (melanoma differentiation)	0110	1	3.6	0	2.8
60647_at		2110	`	3.2	2.6	4.1
43545 at	zinc finger protein 281	7817001	W66422	3.2	1.2	1.6
55811 at	:1	7874N7	A1/96083	3.2	1.8	3.1
46221 at	MEK cartner 1		AA074601	3.2	2.2	0.7
46583 24	ואורא המינוופן ז		AA056667	3.2	1.9	1.5
40202 at	116B6142		AI640524	3.2	9.0	0.3
4022/ al	naro142 protein		AA186623	3.2	1.7	0.5
40002 at			AA524036	3.2		C
22019 at			AI859233	3.2	40	2
/5885_at	bromodomain-containing 2	BRD2	1	3.2		
76844_at	hypothetical protein FLJ20608		,	3.5	2.0	0
3/2/4 at	Diotinidase	BTD	1	3.5		000
44801_s_at	hypothetical protein FLJ21080			3.5	100	4 0
46305_at	CGI-44 protein; sulfide dehydrogenase like (yeast)		AI804917	3.5	0.0	0.0
73273_at	flightless I (Drosophila) homolog	FLII	A1696805	3.5	7 1	9.0
42055_at			AA282531	3.0		
			AI817130	3.5	7 7	3.5
52909_at			3096417	3.2	2.1	5 6
53000 at			3144365	3.2	1 6	200
70000			AI016237	3.2	5.4	26
20057 at	المستومية		H53956	3.2	9.0	C
3037F 24	nypouletical protein r_JZ0134		AF070644	3.2	1.4	3.2
39417 at	Epidiolyfilal secretory protein (19.5kD)		AI525834	3.2	1.5	4.7
39441 24	land (hacterial lantihistic control		AB028951	3.2	1.3	2.9
2077A at	oxidate (ortechrams a) asserted in	LANCL1	Y11395	3.2	2.9	2.8
21021 21	=1	OXA1L	X80695	3.2	3.1	5.4
31921_at	olfactory receptor, family 2, subfamily F, member 1	OR2F1	U56421	3.2	2.8	0.3

	the first properties	GOLIT	1,0001	0.0	1 2	3.7
	tubuiii, beta polybeptide	900	300314	3.6	7.1	110
40478_at	hypothetical protein		AL021396	3.2	2.8	2.6
40568_at	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2	ATP6B2	L35249	3.2	1.8	4.3
294 s at	cell division cycle 2-like 1 (PITSLRE proteins)	CDC2L1	U04815	3.2	2	1.4
100	MD-1, RP105-associated		AB020499	3.2	2.3	2.9
34291_at	phenylalanine-tRNA synthetase-like	FARSL	U07424	3.2	1.6	3
	lactate dehydrogenase B	LDHB	X13794	3.2	2.4	4
41309 g at	C-terminal bindin	CTBP1	U37408	3.2	2	3.6
39637_at	solute carrier fam	SLC26A2	U14528	3.2	3.2	3.2
39672_at	protein tyrosine phosphatase, non-receptor type 7	PTPN7	M64322	3.2	4.4	4.6
40296_at	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	XPNPEP2	AL023653	3.2	2.7	3.2
36846_s_at	36846_s_at U6 snRNA-associated Sm-like protein LSm7		AA121509	3.2	2.8	3.3
36957_at	protein kinase C binding protein 1	PRKCBP1	W22296	3.2	2.5	3
36974 at	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	PSMF1	D88378	3.2	1.4	2.7
37385 at	CIk-associating RS-cyclophilin		U40763	3.2	1.2	2.2
37700 at	bleomycin hydrolase	BLMH	X92106	3.2	1.4	2.7
38811_at	5-aminoimidazole-4-carboxamide ribonucleotide	ATIC	D82348	3.2	1.9	3.1
	formyltransferase/IMP cyclohydrolase					
56483_at			AA309047	3.2	2.1	4
75801_at			AI620827	3.2	2.4	3.2
at	p47		96020M	3.2	2.3	3
63374_at	mucolipin 1	MCOLN1	AI816064	3.2	1.5	3.8
47463_at	eukaryotic translation initiation factor 2C, 1	EIF2C1	AA453723	3.2	3.1	2.9
54865_at	coronin, actin-binding protein, 1C	COROIC	N27805	3.2	2.9	3.2
60471_at	hypothetical protein FLJ22439		AA625133	3.2	2.9	3.1
65736_at	hypothetical protein FLJ20671		AA165689	3.2	0.5	4
72108_at	FSHD region gene 1	FRG1	AA856746	3.2	1.5	3.2
72643_i_at			AI758570	3.2	2.8	3.2
50235_at			AA207254	3.2	2.6	2.2
49242_at			N51263	3.2	2.6	3.2
43408 g at	DKFZP586F1524 protein		AW014654	3.2	1.6	3.3
43926_at			N36085	3.2	2.7	3.2
43967_at	ATP-dependant interferon response protein 1		AI826411	3.2	0	2.5
45331_at	hypothetical protein FLJ10355		AA102468	3.2	3	2.7

52691 at			AW014700	3.2	3.2	3.2
56441_at			W05842	3.5	1.7	33
65900_at	KiAA1436 protein		AI694579		3	3.7
56638_g_at			AI436183	3.2	1.8	3.2
53956_at			AA449296	3.2	2.6	2.8
46232_at	COP9 complex subunit 4		AI745197	3.2	1.6	3.5
54093_at	hypothetical protein		AI307252	3.2	2.7	2.4
74764 g at	testis enhanced gene transcript (BAX inhibitor 1)	TEGT	AW013869	3.2	2	5.4
55664_at	annexin A11	ANXA11	AI923271	3.2	1.9	3.9
61119_at	CCAAT/enhancer binding protein (C/EBP), alpha	CEBPA	AI971171	3.2	2.7	3.1
52340_f_at		MAZ	AA025883	3.2	2.4	2.6
	factor)					
54978_at	solute carrier family 25 (mitochondrial carrier; ornithine transporter)	SLC25A15	AI885329	3.2	m	1.4
	member 15					
64517_at	KIAA0747 protein		AI972594	3.2	2.4	m
68682 f at			AI636095	3.2	2.8	2.8
55565_at	hypothetical protein FLJ20424		AI745491	3.2	2.5	3.2
47156_at			AI032786		2.5	2.9
46714_at	kiaa iso protein		AA524098	3.2	2.2	4.1
38688_at	KIAA0461 protein		AB007930	3.1	3.3	7.4
37472_at	mannosidase, beta A, lysosomal	MANBA	U60337	3.1	5.6	3.5
31851_at	ret finger protein 2	RFP2	AJ224819	3.1	0,4	1.9
31853_at	embryonic ectoderm development	EED	AF080227	3.1	4.3	C
34997_r_at	frizzled (Drosophila) homolog 5	FZD5	•	3.1	1.7	4.1
31884_at	hypothetical protein		L40399	3.1	0.8	0
40049_at	death-associated protein kinase 1	DAPK1	X76104	3.1	0.7	0
40282_s_at	_	DF	M84526	3.1	2.4	0
452_at	SWI/SNF related, matrix associated, actin dependent regulator of	SMARCC1	U66615	3.1	6.0	0
32804_at	RNA binding motif protein 5	RBM5	AF091263	3.1	1.3	1.2
33887_at	hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	D84064	3.1	1.6	0
39099 at	Sec23 (S. cerevisiae) homolog A	SEC23A	X97064	3.1	2.2	0
39620_at	POU domain, class 6, transcription factor 1	POU6F1	221966	3.1	1.8	2.2
35335_at	Rho associated, coiled coil containing protein kinase 2	ROCK2	AB014519	3.1	2.7	9.9
35703_at	platelet-derived growth factor alpha polypeptide	PDGFA	X06374	3.1	1.2	0.8

Figure 11EEEEEE

40013_at	chloride intracellular channel 2	CLICS	Y12696	3.1	1.4	2.4
1660_at	ubiquitin conjugating enzyme E2N (homologous to yeast UBC13)	UBEZN	D83004	33.1	61	7.0
37172 at	carboxypeptidase B2 (plasma)	CPB2	M75106	3.1		12
31481_s_at	thymosin, beta 10	TMSB10	M92383	3.1	2	2.9
362_at	protein kinase C, zeta	PRKCZ	215108	3.1	0	0.2
37278_at	tafazzin (cardiomyopathy, dilated 3A (X.linked); endocardial	TAZ	X92762	3.1	0.1	3.1
	fibroelastosis 2; Barth syndrome)					
37564_at	DKFZP434F162 protein		AL080201	3.1	0	2.7
38046_at	IK cytokine, down-regulator of HLA II	포	AJ005579	3.1	2.6	0
38065_at	high-mobility group (nonhistone chromosomal) protein 2	HMG2	X62534	3.1	2.1	1.4
36423_at	p8 protein (candidate of metastasis 1)		W47047	3.1		15.6
36442_g_at	_	KCNMA1	U02632	3.1	1.5	2.3
	-					
559_s_at	homeo box 11 (T-cell lymphoma 3-associated breakpoint)	HOX11	S38742	3.1	0.4	1.9
38842_at	Leman coiled coil protein		AB023206	3.1	3.1	4.9
52653_at			AI360291	3.1	2	2.3
63919_f_at	_	ENC1	M85329	3.1	2	0.8
43421 g at	kinesin protein 9 gene		AA625821	3.1	1.8	1.4
57786_at			W02232	3.1	3.1	2
50975 s at	sex comb on midleg (Drosophila)-like 1	SCMLI	AW022735	3.1	1.4	1.5
43835_at		KIAA1449	N91136	3.1	2.9	2
83661_r_at	hypothetical protein FLJ22215		AI972942	3.1	1.2	0.5
50801_at			AI276956	3.1	1.7	2.4
66258 at			AA648468	3.1	1.8	3.3
60263_at			AA126730	3.1	0.4	3.2
57524 at			AI821146	3.1	2.2	2.5
81672_at			W38444	3.1	6.0	0
46523_at			AA703310	3.1	1.2	1.8
76786_at			AI733079	3.1	0	3.3
74425_at			AI742694	3.1	1.2	0.7
74487_at			AI733562	3.1	3.4	2.3
78234_at			AI733569	3.1	0.3	2.5
75049 g at	hypothetical protein FLJ13984		AA041295	3.1	2.4	0.7
82436_at			AI242023	3.1	0	0.5
42613_at			N64684	3.1	1.2	2.3

Figure 11FFFFFF

80048_at	AA406555	3.1	9.0	
53509_at	AI247411	3.1	2.3	1.7
Sat	AI640222	3.1	8	2.4
03310_at hypothetical protein PROU9/1	AI807379	3.1	1.1	1.2
830/1 at	R52673	3.1	0.4	1.9
84194 at	T52159	3.1	1.3	5
4/946 at	H04453	3.1	3.5	2
21010 at	AI740822	3.1	1.7	4.9
02340 at	R44193	3.1	6.0	1.8
05140 at	AA749167	3.1	6.0	0.8
GODOU at	A1569653	3.1	2.3	
10000/_at	AI457453	3.1	1.6	0
49302,at Cur. 149 protein	AA167070	3.1	3.2	0.7
V0134_at	AA291194	3.1	4.8	10
40222 at	AA243661	3.1	2.2	2.4
1000/2 at	AA993965	3.1	0.2	0.1
7930g at	AA287513	3.1	1.2	0.3
75725 at	AI793256	3.1	1.5	0.0
3832U at	T85261	3.1	4.2	2.6
00500 at	AI679563	3.1	0.3	2.2
00/30 Tal	A1680842	3.1	2.3	1.3
20,200 at	AI183829	3.1	1.3	m
+	AI703451	3.1	9.0	1.5
64345 S at MAA1102 protein	AW003533	3.1	3.5	2.3
70554 at	A1743273	3.1	8.0	0.3
70142 24	AI798146	3.1	1.8	6.0
20C17 21	AI800042	3.1	1.3	2.8
70876 at	AI422384	3.1	0.4	0.7
Τ		3.1	0.3	0.7
60851 r at	REST AI872294	3.1	1.1	1.6
80073 34	AW024260	3.1	4.1	2.4
75330 at	W15168	3.1	1.1	1.4
73322 at 61400 i at	AL045360	3.1	2	1.9
01400 41	AI952593	3.1	1.8	0
82057_at	AA181363	3.1	25	

Figure 11GGGGGG

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dors:

52685 at					
		A1991451	3.1	1.5	3
hypothetical protein clone Tolothocyltel: 0413 Ct. 1200000		AI378363	3.1	2.7	2.7
Thomself protein, clone reletion(rialy_b41)_stratt022/0_FL142		AI628609	3.1	0	0
ribosomal protoin 010		AA928698	3.1	2.6	5.8
indestrial protein 510	RPS18	AI990458	3.1	2.6	
		AI253134	3.1	m	4.1
		AI472026	3.1	0.7	0.2
		AA777488	3.1	1.6	1.4
		AI792647	3.1	2.3	0.7
		AI521246	3.1	1.7	6.0
		AA626793	3.1	3.6	1.7
61705 f at hypothetical protein El 190036		AI554439	3.1	0.2	2.2
	`	AW006276	3.1	0.4	2.5
		N22751	3.1	7.2	9.1
		AI972964	3.1	1.7	2.5
		AA165313	3.1	2.3	1.8
		A1446414	3.1	3.8	127
		AI761595	3.1	1.5	2
		N72845	3.1	1.8	0.7
caspase 4, apop	CASP4	AI246018	3.1	60	000
74600 g at uroporphyrinogen III synthase (congenital erythropoietic porphyria)	UROS A	AW016762	3.1		2.5
TERE! (TRE1) interacting purplace feeting		N98637	3.1	1	0.3
KIAA1460 SSASS	TINF2	W25667	3.1	3.9	
-1	\dashv	N32192	3.1		0.7
at transmentaling and the anarogen induced KNA	TMEPA! /	AA535819	3.1	1.9	0
		AA968576	3.1	1.9	0.5
KIAA1101 protein		AI765321	3.1	4.3	5.6
		N23782	3.1	2.4	0.7
		AI768697	3.1	1.6	8.6
hypothetical protein MCC10264		AA151719	3.1	6.7	3.4
Porterior protein mac 10/04	,	AA602884	3.1	1.8	8
		AI150454	3.1	2.2	5
		N30122	3.1	1.8	1.6
		2825184	3.1	2.9	1.2
	1	AA632741	3.1	0.3	3.2

Figure 11HHHHHH

dors.

Ti

86451_at			AI683426	3.1	2.8	
38613_at	putative cyclin G1 interacting protein		U61837	3.1	2.1	2.4
1933 g at	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	ABCC5	U83661	3.1	2.5	3
38976_at	coronin, actin-binding protein, 1A	CORO1A	D44497	3.1	3.1	3
943_at	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1	. RUNX1	D43968	3.1	1.8	E .
37835 at	CDIC antigen, c polypeptide	CDIC	M28827	3.1	2.7	5.0
	hematopoietic protein 1	HEMI	M58285	3.1	1.6	3.3
39783_at	KIAA0100 gene product		D43947	3.1	2.4	3.1
40077_at	aconitase 1, soluble	AC01	211559	3.1	1.9	2.8
40127_at	paired mesoderm homeo box 1	PMXI	M95929	3.1	1.5	3.3
40537_at	KIAA0741 gene product		AB018284	3.1	1.7	2.9
38242_at	B cell linker protein		AF068180	3.1	2.7	3.1
40801_at	DKFZP434C212 protein		AA643063	3.1	1.3	2.8
40879_at	KIAA0699 protein		AB014599	3.1	2.2	3.3
34660 at	ribonuclease, RNase A family, k6	RNASE6	AI142565	3.1	2.7	2.9
35165_at			AF070582	3.1	0.2	m
174_s_at	intersectin 2	ITSN2	U61167	3.1	1.7	2.7
514_at	Cas-Br-M (murine) ectropic retroviral transforming sequence b	CBLB	U26710	3.1	1.3	3.2
41600_at	proliferation-associated 2G4, 38kD	PA2G4	U59435	3.1	2.9	m
880_at	FK506-binding protein 1A (12kD)	FKBP1A	M34539	3.1	1.2	4.1
36592_at	prohibitin	РНВ	S85655	3.1	2.9	2.1
37031_at	C9orf10 protein		D80005	3.1	1.2	3.4
37268_at	vascular endothelial growth factor B	VEGFB	U43368	3.1	6.0	2.2
32589_at	chromatin assembly factor 1, subunit A (p150)	CHAF1A	U20979	3.1	2.1	1.9
38078_at	filamin B, beta (actin-binding protein-278)	FLNB	AF042166	3.1	1.7	2.1
38000_at	pyruvate carboxylase	PC	S72370	3.1	5.6	m
38338_at	related RAS viral (r·ras) oncogene homolog	RRAS	AI201108	3.1	2.4	2.2
48123_s_at			AI022930	3.1	2.1	3.3
61287 f at	similar to rat nuclear ubiquitous casein kinase 2		AI380204	3.1	2.2	3.8
62311 g at			W96015	3.1	1.9	2.7
57030_at			W26295	3.1	3.1	3.1
53860_at			AA453352	3.1	1.7	1.8
47909_at	zinc finger protein 106		N26630	3.1	2.6	2.6
62889_at	KIAA0675 gene product		D29070	3.1	3.1	3.1

Figure 11IIIII

52811_at	aryl hydrocarbon receptor nuclear translocator	ARNI	A1768497	3.1	0 1	,
54/58_at			AA256195	3 -	1 7	1 0
44083 at			A1/179056	100	, , ,	7.7
65745_s_at			0,500,4	7.0		3.1
65750 fat	hypothetical protein		AI685/14	3.1	0.7	3.6
٠,, -	ה שלים היים היים היים היים היים היים היים ה		N75645	3.1	0.1	2.9
00100			AW021173	3.1	2.9	3.2
4034E 21			AA677588	3.1	2.5	2.6
49345 at			AI770110	3.1	9.0	2.2
03//4 4	TOT2 (100)		AI556963	3.1		100
64272 at	I Cr.3 (EZA) Iusion partner (in childhood Leukemia)	TFPT	AI309849	3.1	2.4) (m
10/28 24			AW024964	3.1	3.4	3.6
57171 at	() Control () Co		`	3.1	2.8	2.4
55500 24	carbotypriate (ivacetylglucosamine b.U) suitotransferase 6	CHST6		3.1	2.4	E
51203 at	יואסטיויפנוכמי איטיפוון רריסטעו		AI936523	3.1	1.7	2.9
90501 at			AA775177	3.1	2.5	000
64504 of	unit-interacting protein		A1660343	3.1	3.5	3.0
04304 at			H87175	3.1	C.	200
32000 at			AI860012	3.1	2 1	200
22109 at			AI302185	3.1	2.2	3
45000	L		AA613328	3.1	1.5	300
45609 at			AA725071	3.1	2.4	6.7
5/39/ at	Platelet/endotnelial cell adhesion molecule (CD31 antigen)	PECAM1	L34657	3.1	2.1	2.0
45170 21			M63805	3.1	3.1	3 2
45176 at	KAPIA, member of KAS oncogene family	RAP1A	AI476340	3.1	2.5	2.2
50238 at			AA627644	3.1	2.9	2.9
37883 i at	hypothetical protein		AI801902	3.1	2.2	2.4
39727 at	dual enecidicity absorbation 11 (DAIA (DAIA		AI375033	e	1.6	99
39744 at	DEAD/H /Aso Ch. Als Ass /Usb Late (RIVA/ RIVP complex I-interacting)	DUSP11		က	2	0.3
40000	host chock transfer of the second of the sec	DDX3	AF000982	ĸ	1.5	8
40200 at	lical silock transcription factor 1	HSF1	M64673	3	3.6	900
40638 at	on licing factor proling (*) in the second proling of the second p			m	1.5	27
	spirchig lactor promite/glucamine rich (polypyrimidine tract-binding protein-associated)	SFPQ	X70944	m	2	0.1
40928_at	DKFZP564A122 protein		2013CW	1	,	
1388 g at			1	n	1.8	2.4
		NOX.	103258	۲,	- 7	

Figure 11JJJJJJ

territin, heavy polype programmed cell der sialyltransferase 4A (pleckstrin homology, tr melanoma antigen, f unc.51 (C. elegans)-1 fatty acid binding pri growth inhibitor) meningioma express nuclear receptor coa nuclear receptor sub phosphogluconate d platelet-activating fa (45kD) ORF KIAA0321 protein lymphocyte antigen at adenylosuccinate sy thyrold hormone rec protein phosphatase ewing sarcoma breal at	32833 at	CDC-like kinase1	CLK1	M59287	č	2.2	30
se at ferritin, heavy polype at programmed cell de fat sialyltransferase 4A (at a sialyltransferase 4A (at melanoma antigen, fat melanoma antigen, fat melanoma antigen, fat unc-51 (C. elegans). at fatty acid binding pract meningioma express at muclear receptor coa at nuclear receptor sub at phosphogluconate dat phosphogluconate dat (ASAD) at (ASAD) at thyroid hormone recept in at thyroid hormone recept in at thyroid hormone recept at thyroid hormone recept at thyroid hormone recept at thyroid hormone recept at thyroid sarcoma breat at the protein phosphatase at the phosphatase	33470_at			AF052177	m	i 0	000
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f_at sialyltransferase 4A (35218_at		PDCD10	AF022385	m	60	C
at pleckstrin homology, at melanoma antigen, fat unc.51 (C. elegans)-lat fatty acid binding pragrowth inhibitor) at meningioma express at meningioma express at nuclear receptor coa at nuclear receptor sub at phosphogluconate dat phosphogluconate dat (45kD) at (ASkD) at (ASkD) at (ASkD) at protein phosphatase sy at thyroid hormone receptor sub at thyroid hormone receptor at thyroid hormone receptor at thyroid sarcoma breal at those at the protein phosphatase at the protei	40290_f_at		SIAT4A	L13972	m		2.2
f at melanoma antigen, f at unc-51 (C. elegans)-lat fatty acid binding programmer and fatty acid binding programmer and inclear receptor coast inclear receptor subset in nuclear receptor subset phosphogluconate diat phosphogluconate diat (45kD) at phosphogluconate diat (A5kD) at phosphogluconate diat (A5kD) at phosphogluconate sylvation for an inclear receptor subset in nuclear receptor subset in nuclear receptor and the phosphogluconate sylvation for an inclear sylvation phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the protein phosphatase at the phosphat	38741_at	pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin-2)	PSCD2	U70728	3	2.7	0
at unc-51 (C. elegans)-lat fatty acid binding progression and progression and proceeding at meningioma expression and phosphogluconate do at phosphogluconate do at phosphogluconate do at phosphogluconate at thyroid hormone recent and adenylosuccinate sylate at protein phosphatase at protein phosphatase at protein phosphatase at Ewing sarcoma breal at expensesion and at expensesion and at expensesion and at expensesion and at expensesion and at expensesion and at expensesion and at expensesion and at expensesion and at expensesion and at expensesion and at expensesion and at expensesion and at expensesion and and and and and and and and and an	34575 f at	amily A,	MAGEAS	010689	m	0.4	4.3
at fatty acid binding programment fatty acid binding programment for the program and phosphogluconate dat phosphogluconate dat phosphogluconate dat (45kD) at (A5kD) at (A5kD) at (A5kD) at (A5kD) at (A5kD) at (AM0321 protein at hymphocyte antigen at hymphocyte antigen at thyroid hormone recent and adenylosuccinate sylate at thyroid hormone recent at thyroid sarcoma breal at a fail and a fail at thyroid and at thyroid and at a fail and a fail	34827_at	unc-51 (C. elegans)-like kinase 1	ULK1	AF045458	e	0.3	0.5
at meningiome appress at meningiome appress at nuclear receptor cab at nuclear receptor sub at phosphogluconate di at platelet-activating fa (45kD) at (A5kD) at (AA0321 protein at KIAA0321 protein at kimphocyte antigen at tymphocyte antigen at tymphocyte antigen at thyroid hormone recept at thyroid hormone recept at Ewing sarcoma breal at Ewing sarcoma breal at Ewing sarcoma breal at adenylosuccinate syruate at adenylosuccinate syruate at thyroid hormone recept at thyroid hormone r	34867_at	fatty acid binding protein 3, muscle and heart (mammary-derived	FABP3	AI041520	m	2	2.1
at nuclear receptor coa at nuclear receptor coa at nuclear receptor sub at phosphogluconate di at platelet-activating fau (45kD) at (A5kD) at (AA0321 protein at Wiphocyte antigen at thyroid hormone recept at thyroid hormone recept at thyroid hormone recept at thyroid hormone recept at the protein phosphatase at protein phosphatase at Ewing sarcoma breal at a fait at the protein at at the protein phosphatase at at the protein phosphatase at the phosphatase at the protein phosphatase at the phosphatase at the protein phosphatase at the phosphatase at the phosphatase at the phosphatase at the phosphatase at the phosphatase at the phosphatase at the phosphatase a		Browth Hillionical					
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at nuclear receptor sub at phosphogluconate dat platelet-activating far (45kD) at (A5kD) at ORF at (MAA0321 protein at Iymphocyte antigen at Iymphocyte antigen at thyroid hormone recept at thyroid hormone recept at protein phosphatase at protein phosphatase at Ewing sarcoma breal at a thyroid at at a thyroid at at a thyroid at at a thyroid at at a thyroid at at a thyroid at at a thyroid at at a thyroid at at a thyroid at at a thyroid at at a thyroid at at a thyroid at at a thyroid at at a thyroid at a thyro	36118_at	nuclear receptor coactivator 1	NCOA1	AJ000882	ĸ	4.5	4.4
at phosphogluconate dat platelet-activating far (45kD) at (A5kD) at (A6kD) at (AA0321 protein at kiAA0321 protein at imphocyte antigen at imphocyte antigen at thyroid hormone recent protein phosphatase at protein phosphatase at Ewing sarcoma breal at Ewing sarcoma breal at Ewing sarcoma breal at at Ewing sarcoma breal at at Ewing sarcoma breal at at at at at at at at at at at at at	1102_s_at	Inuclear receptor subfamily 3, group C, member 1	NR3C1	M10901	8	1.1	6.4
at platelet-activating far (45kD) at (A5kD) at ORF at KIAA0321 protein at kipphocyte antigen at thyroid hormone receat thyroid hormone receat thyroid hormone receat the protein phosphatase at Ewing sarcoma breal at Ewing sarcoma breal at at Ewing sarcoma breal at at Ewing sarcoma breal at at at at at at at at at at at at at	36963_at	phosphogluconate dehydrogenase	PGD	U30255	С	1.3	0.1
445kD) at ORF at KIAA0321 protein at Imphocyte antigen 117 at adenylosuccinate synthase at thyroid hormone receptor associated protein, at protein phosphatase 4 regulatory subunit 2 at protein phosphatase 4 regulatory subunit 2 at Ewing sarcoma breakpoint region 1 at Ewing sarcoma breakpoint region 1 at at at at at at a at at a at at a at at	37317_at	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit	PAFAH1B1	L25107	e	1.4	3.5
at KIAA0321 protein at KIAA0321 protein at Iymphocyte antigen 117 at adenylosuccinate synthase at protein phosphatase 4 regulatory subunit 2 at protein phosphatase 4 regulatory subunit 2 at Ewing sarcoma breakpoint region 1 at Ewing sarcoma at at at at at at a sarcoma breakpoint region 1 at at at at a sarcoma breakpoint region 1 at at at at at at a sarcoma breakpoint region 1 at at at at at at at at at at at at at a		(45kD)					
at KIAA0321 protein at Iymphocyte antigen 117 I at adenylosuccinate synthase at thyroid hormone receptor associated protein, at protein phosphatase 4 regulatory subunit 2 at Ewing sarcoma breakpoint region 1 at Ewing sarcoma breakpoint region 1 at at at at at a at at at at at at at at	37376_at	ORF		M68864	8	1.6	0
at KIAA0321 protein at lymphocyte antigen 117 rat adenylosuccinate synthase at thyroid hormone receptor-associated protein, at protein phosphatase 4 regulatory subunit 2 at Ewing sarcoma breakpoint region 1 at Ewing sarcoma breakpoint region 1 at at at at at at at at at at at at at a	38372_at			U66042	3	7.5	C
at lymphocyte antigen 117 Tat adenylosuccinate synthase at thyroid hormone receptor associated protein, at protein phosphatase 4 regulatory subunit 2 at Ewing sarcoma breakpoint region 1 at Ewing sarcoma breakpoint region 1 at at at at at at at at at at at at at a	37943_at	KIAA0321 protein		AB002319	m	1.5	0
r at adenylosuccinate synthase at thyroid hormone receptor-associated protein, at protein phosphatase 4 regulatory subunit 2 at at at Ewing sarcoma breakpoint region 1 at a	37968_at	lymphocyte antigen	LY117	AF031137	m	0.7	2.5
thyroid hormone receptor associated protein, at protein phosphatase 4 regulatory subunit 2 at the factor of the fa	33167_r_at	adenylosuccinate syr	ADSS	X66503	e	0.1	0.2
at protein phosphatase 4 regulatory subunit at at Ewing sarcoma breakpoint region 1 at at at at at at at at at at at at at a	54686_at	eptor-associated		AA122265	3	2.5	4.5
at at Ewing sarcoma breal at at at at at at at at at at at at at	52207_at	4 regulatory subunit		W87465	m	0.8	-
at at Ewing sarcoma breal at sarch at at at at at at at at at at at at at	/6949_at			AI187760	3	0.1	2.4
Ewing sarcoma breal	888/9_at			AI378857	e	0	0.8
at at	59096_at	L		AI082856	3	0.5	1.5
66880_at 76704_s_at 78992_at 79240_at 80275_at 62048_at	9003/_at	Ewing sarcoma breakpoint region 1	EWSR1	AW001288	က	2.8	0.5
76704 s_at 78992_at 79240_at 80275_at 62048_at	66880_at			AI733050	m	m	5.7
78992 at 79240 at 80275_at 62048 at	/6/04_s_at			AI817195	m	1.7	0.5
/9240_at 80275_at 620048_at	/8992_at			AI791323	m	0.5	1.3
80275_at 62048_at	/9240_at			AI435163	m	0	3.9
102048 at	802/5_at			R25709	3	1.2	1.9
20000	62048 at			AI192486	8	6.0	3.2
00315_d1	80313_at			AI215686	3	1.9	3.8

Figure 11KKKKKK

47221_at		HERROR	7	3.01	C 1
55135 at		0000014		0.0	4.6
67251 at		A1300034	200	C.1	0.0
47040		Al3/9/41	3	0.2	0.5
4/240_at		R02354	m	1.1	0.2
85242_at		AI472855	m	2.1	0
85667_at		A1932342	m	1.7	1.5
48363_at		AA651889	m	6	5
67091_at		AI081782	3	6.0	1.5
91495_r_at	major histocompatibility complex, class I, A	HLA:A R99989	m	1	0.8
88013 at		AI332638	m	1.2	2.9
88052 at		AI018179	e	0.7	2.9
79512_at		AI248270	m	2.5	8.5
88/60_at	- 1	\Box	m	1.9	2.4
5//92 at	zinc finger protein, subfamily 2A (FYVE domain containing), 1	ZNFN2A1 AA399630	e	2.7	3.6
70500 at		AI884831	က	1	3.2
70582_at		M79158	m	2	9.0
/0/98 at		A1400344	e	0	0.4
64293_at		AI971000	m	0.8	25.6
71543_at		A1935074	m	2	1.7
89/18_at		AI051304	m	0.8	2.6
85190_at		AA737437	ĸ	0.7	0
/3424 r at		A1962748	e		0
66099_at		A1983166	m	2.4	0.2
74354 at		AI982590	m	2.4	1.5
44/83 s at	hairy/enhancer-of-split related with YRPW motif 1	HEY1 R61374	m	1.5	2.6
78114 r at		AW016419	3	1.8	0.5
06047 st		AI018560	8	1.4	0.5
200047 at]	3	0.3	6.0
70002 at	core promoter element binding protein	COPEB A1355637	3	0.3	10.1
40229 at		H23103	m	0.8	0
6/6/6 at		AI040114	m	2.3	1.5
88909 at		AA528441	e	2.5	0
32010 at		AI672414	8	2.6	3.1
3010/ dt		AI684439	3	2.3	10.3
491/2 at	Inudix (nucleoside diphosphate linked moiety X) type motif 5	NUDT5 AI694646	3	2.5	1.1

Figure 11LLLLLL

ntors:

56366_at			AA700906	3	4	1 5
			AI686949	m	~	
[g	hypothetical protein FLJ10474		AA142988	m	2 9	#.1 D.C
28297 s at			N53553	m	12	7.0
46005 at			N81145	C.	0	200
64443_at	EH-domain containing 4	EHD4	Ľ	2 6	0.0	3.5
62489_at	hypothetical protein FLJ13078		AA897088	0 0		
54487_at			AA044626) (m	2 1	4.0
48573_at	zinc finger protein 161	ZNF16	AA452188	0 0	1.0	3.1
45556_at	KIAA1235 protein		AWOO1066	2 0	0.1	9.0
54902_at			N63582) (r	7.7	7 -
59066_at			AL 0.36615	0 6	000	1:1
56065 at			AA524267	n m	2 0	1 7
52892 at			AI761092	i c		1.1
54825 at			AAR10923	2 (200	7
61108_at			AA831618	2 6	1.0	٥
63110_at			W01020		2 1	3.1
86346_at			001001	2	3.5	1.9
39830 at	ribosomal profein 27		_	5	0.3	0.8
39041 at	1.	KPL2/	٩	3	2.7	5.8
מיסיוד ביים	dniyd oilpoariilde Stacetylitansierase (EZ component of pyruvate dehydrogenase complex)	DLA	Y00978	m	1.6	1.6
37769_at	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4	EDG4	AF011466	m	6.0	1.8
39751_at	DHHC1 protein		AE0E2102	0		
40110_at	isocitrate dehydrogenase 3 (NAD+) beta	10.10	1	n	9.0	3.1
33396_at	glutathione S-transferase pi	CCTD1	\perp	n (1.8	m
1468_at	heat shock protein 75		0124/2	2) (.3	3.9
41778_at	Solute carrier family 1 (neutral amino acid transporter), member 5	10.00		2)	1.6	2.7
41000_at	checkpoint suppressor 1	SLCIAS	\perp	m	1.3	2.9
33397_at	CDP-diacy/glycerolinositol 3-phosphatidy/transferase	CHEST	008723	20	1.4	2.8
		ב ב	ALU2U3&3	Y)	<u></u>	3.2
35167_at	KIAA0433 protein		AROUZSG3	6		
39593_at	fibrinogen-like 2	FGIO	1	2 0	7.7	2.9
33485_at	ribosomal protein L4	RPIA	1	200	X) 0	2.6
35329_at	cytochrome b5 reductase 1 (B5R.1)	1 1	- 1	010	2.0	4.6
	/		AF091084	m	<u>~</u>	ας

Figure 11MMMMMM

35221_at			X91648	3	1.9	1.6
34369_at	KIAA0214 gene product		D86987	m	1.4	2.3
36011_at	syntaxin 10	STX10	AF035531	e	1.6	1
34837_at	KIAA0376 protein		AB002374	m	1.9	2.9
40024_at	src homology three (SH3) and cysteine rich domain	STAC	ı	m	3.1	3.3
35773_i_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18)	NDUFB7	AA527880	m	2.7	2.6
35796_at	protein tyrosine kinase 9-like (A6-related protein)	PTK9L	Y17169	m	1.4	2.9
37306_at	KIAA0068 protein		D38549	e	1.8	4.2
37345 at	calumenin	CALU	AF013759	3	1.1	3.4
36792_at	tropomyosin 1 (alpha)	TPM1	224727	m	8	2.9
37680_at	A kinase (PRKA) anchor protein (gravin) 12	AKAP12	U81607	е	1.1	2.9
37647 at	acyloxyacyl hydrolase (neutrophil)	AOAH	M62840	m	2.2	2.7
38336_at	KIAA1013 protein		AB023230	e	2.5	2.9
43459_at	KIAA0680 gene product		AI472209	m	6.0	3.2
38680_at	small nuclear ribonucleoprotein polypeptide E	SNRPE	M21259	e	2.1	2.9
56426_at	hypothetical protein FLJ22351		AA177127	m	2.6	2.6
65125_at	dolichyl-phosphate mannosyltransferase polypeptide 3	DPM3	AI817330	m	2.7	3
48498_at			AA868896	e	2.7	3.4
53730_at			W60775	m	2.9	m
83320_at			AI494453	e	2.4	2.3
56544 g at	eIF4E-transporter		R50754	m	1	1.4
90724_at			AA885833	m	3.3	3.3
80095_at			AI271326	m	1.5	2.5
54648_at			AA810864	က	Э	1.8
58321_at			AL048542	e	2.3	2.4
82998 at			AI380429	m	2.6	2.8
54810 i at	KIAA1143 protein		AI745170	æ	2.8	2.2
48595_at	hypothetical protein FLJ10210		AA707400	m	2.8	2.8
54867_at			R41296	င	1.8	3.3
63323_at	hypothetical protein MGC3234		C05777	m	2.4	3.1
59616_at	- 1		AI621286	3	1.1	1.9
32800_at	retinoid X receptor, alpha	RXRA	908990	3	2.9	5.6
50219_at	mRNA for FLJ00023 protein		W27853	3	1.3	2.8
43827_s_at			103298	e	2.4	3.7

64061 at	hypothetical protein McC3180		AW006145	3	6	,
64934 at	J22195		AL121007	m	0	000
46315 at	edial your trailslation initiation factor 2B, subunit 3 (gamma, 58kD)	EIF2B3	AI660531	m	α α	5.9
1385A 24			AA233808	o cr		9.0
F1267 at			AW004730) (*	0.0	8.4
3120/ at			A1858023	7 (8.7	2.9
864 at	homeo box HB9	HI YBO	1107664	2)	2.2	2.6
51997_at		ILABO	400/00	n	2.6	1.9
45205_at			AA/04/89	3	2.7	2.7
46403_at			N21193	ĸ	2	24
52094 at	Similar to glucosamine. 6. sulfatases		AI984021	c	2.6	000
52120_at	hypothetical protein FI 120534		AI688582	æ	2.8	m
52124_at			AA628439	3	1.9	25
64368_s_at	hypothetical protein FI 110470		AI805463	3	2	i c
53031_s_at			AW001184	3	2	3.4
46097_at			AA521316	3	2.9	3
53626 at			AI831258	æ	2.7	24
46677_at			AI417834	m	2.6	26
47046_at			AI762760	3	1.6	2.7
49549_at	CD36 antigen (collagen type I recentor thrombonnal		06086Н	3	1.3	3.1
43499_at	tropomyosin 1 (alpha)	CD36	R20784	က	m	20
55611_at	ote	TPM1	N76371	e	2.6	26
48910_at	110000		AA242757	'n		3.4
39427_at	ubiquinol-cytochrome c reductase binding protoin		AI742347	Э	3.1	3.2
1158_s_at	calmodulin 3 (phosphorylase kinase delta)	UQCRB	T79616	2.9	2.2	3.6
40220_at	HMBA-inducible	CALM3	J04046	2.9	1.5	1.7
40546_s_at			AB021179	2.9	2.5	22
	Secretarions of appreasance of the second press, Z (BKD, BB)	NDUFA2	AF047185	2.9	1.8	3.3
40435_at	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	SLC25A6	103592	2.9	1.8	3.7
32774_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI)	NDUFB8	AI541050	2.9	1.3	4.2
41243 at			AB007916	00	C	
04140 at	Titulitati tibilibiog di Drosopnila Scribbie		D63481	000	200	2.3
				4.7	3.5	5.8

Figure 11000000

33828_at	SWI/SNF related, matrix associated, actin dependent regulator of	SMARCE1	SMARCE1 AF035262	2.9	1.5	4.2
	chromatin, subfamily e, member 1					
39588_at	turnor necrosis factor (ligand) superfamily, member 12	TNFSF12	AF055872	2.9	2.5	2.9
39516_at	hypothetical protein		AI827793	2.9	2.2	2.7
32696_at	pre-B-cell leukemia transcription factor 3	PBX3	X59841	2.9	6.0	2
33432 at			AI547308	2.9		1.6
33641 g at	allograft inflammatory factor 1	AIF1	Y14768	2.9	2.3	2.8
36030_at			AL080214	2.9	1.5	2.7
36076 g at	putative GTP binding protein similar to RAY/RAB1C		AL037167	2.9	2.3	2.9
35342_at			AF052159	2.9	2.5	2.6
41824_at	CGI-48 protein		A1140114	2.9	1.6	2.7
35779_at	vacuolar protein sorting 45B (yeast homolog)	VPS45B	AJ133421	2.9	2	2.1
36135_at	nucleolar protein p40, homolog of yeast EBNA1 binding protein		U86602	2.9	2.7	2.9
36624 at	ouc	IMPDH2	L33842	2.9	2.2	4.2
36644 at	CD151 antigen	CD151	D29963	2.9	1.8	2.8
32971_at	Friedreich ataxia region gene X123		L27479	2.9	2.6	2.6
33660_at	ribosomal protein L5	RPL5	U14966	2.9	2.4	4.1
37736_at	protein-Lisoaspartate (Diaspartate) Oimethyltransferase	PCMT1	D13892	2.9	0.7	3
38107_at	unc119 (C.elegans) homolog	UNC119	U40998	2.9	3.2	2.2
40695_at	IMP (inosine monophosphate) dehydrogenase 1	IMPDH1	J05272	2.9	2.7	3.7
37966_at	beta-parvin		AA187563	2.9	9.0	4.3
38770_at	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	ADAM12	AF023476	2.9	2.9	2.7
37978_at		QPRT	D78177	2.9	2.8	2.7
	pyrophosphorylase (carboxylating))			-		
38841_at	putative glialblastoma cell differentiation-related		AF068195	2.9	2	2.6
38282_at	a disintegrin and metalloproteinase domain 15 (metargidin)	ADAM15	U41767	2.9	2.9	1.7
38290_at	regulator of G-protein signalling 14	RGS14	AF037195	5.9	2.6	2.7
38292_at	Homer, neuronal immediate early gene, 2		AF093264	2.9	0.5	3.4
48010_at			W02538	2.9	3.3	4.4
48079_at			AI824079	2.9	2.4	2.5
56881_at			AI807211	2.9	1.6	3.1
76983_at			AI822003	2.9	2.4	2.5
48271_at	- 1		AI683752	2.9	2.8	2.9
78442_at	hypothetical protein MGC4692		AI819340	2.9	2.9	2.9
57818_at	hypothetical protein dJ462023 2		A1363216	2.9	2.9	3.2

Figure 11PPPPPP

10012	040105		AI077662	2.9	2.5	
Т	K10A0788 25555		AI761602	2.9		200
T			AI183987	2.9	1.3	
T	John Mainstation initiation factor 20, 2	EIF2C2		2.9	2.4	28
1			AI819630	2.9		3.5
Т	manage de la company de la com	WAS	ı	2.9		3.1
44041 at			AW023188	2.9	3.4	2.5
44069 at			AA570398	2.9	2.9	1.6
T	KIAAOR76 protein		H03287	2.9	1.5	0.1
T			AA524529	2.9	2.7	5.5
Τ	anglinoprotein C.I		W75954	2.9	2.1	2.8
Γ	hypothetical protein El 1904E4	APOC1	AW005911	2.9	1.1	2.7
T			AW003067	2.9	æ	3.3
Īŧ	FH domain-hinding mitotic phosphosystic		AI768100	2.9	1.5	2.5
1			F30336	2.9	2.1	3.3
-		TM9SF2	AI540695	2.9	2.1	4.8
50979 s at			AA999701	2.9	2.4	2.7
-	hypothetical protein FI 110656		AI968170	2.9	2.1	2.9
-			AI684281	2.9	2	2.3
1	WD repeat domain 3		AW009920	2.9	1.9	2.8
Ī		WDR3	AI880771	2.9	2.1	(*)
Г	beta-site APP-cleaving enzyme		- 1	2.9	3.6	1.4
±		BACE	- 1	2.9	2.9	2.9
\top	hynothetical protein El 110669		AA604243	2.9	2.4	(m)
Γ	biphenyl hydrolase-like (serine hydrolase: hreast enithalial mindin	200	- 1	2.9	2.6	3
T		D T T	AA526961	2.9	1.8	2.7
at			W02300	00	c	
4626/ at hypoth	hypothetical protein FLJ14153		AI949941	29	1 0	3.0
T	- 1`		AA127629	2.9		8 6
T	endocytic receptor (macrophage mannose receptor family)		AW007248	2.9	000	2.5
te 0	isaged 1 (Alacilla condema)		AI125581	2.9	2.1	26
÷	FH1/FH2 domain containing protein	JAG1	AI739154	2.9	6.0	2.9
7 7	יב עטוומווויבטוונמוווון אוטוניים		N90883	2.9	2.7	2.8
מון			0000			

Figure 11QQQQQQ

Inventors: Response of Dendritic Cells to a...

Inventors: Nir Hacohen, et al.

17007			W61056	29	1 6	000
20702 at			H93046	286	, c	2.5
20/05_dt	instante ford protein CHRAC17; UNA polymerase epsilon p17 subunit		AF070640	2.8	2.2	3.1
41462_at	sorting nexin 2	CAINO	VEOCE 400	0		
10720_at	adenosine A2b receptor pseudogene	SAVIO ACCOUNT		7.8	9.0	2.5
39700 at	Rho GTPase activating protein 1	ADORAZBP	AL022398	2.8	0.5	3.6
40196 at	HYA22 protein	ARHGAP1	AI961929	2.8	1.8	4.3
39772 at	hypothetical protein MGC2683		D88153	2.8	2.1	2.2
674 a at	mothylonototrohydrofolot- 4-		AF007157	2.8	-	2 2
B 9	inetriylerietetialiyurololate denydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase formyltatrahydrofolate	MTHFD1	J04031	2.8	1.9	2.6
	synthetase					
41209_at	lipoprotein lipase					
254_at	H3 histone, family 3A	TAL	M15856	2.8	2.6	2.3
1676 s at		H3F3A	M11353	2.8	1.3	4.6
33466 at	Barrier actor - Ballina	EEF1G	M55409	2.8	2.6	4.6
37034 at	Putative human HI A class II associated		AF038182	2.8	2.1	2.4
34330 at			U73477	2.8	2	2.3
33632 p at		COX7A2L	AB007618	2.8	1.7	4
35338 at			AF023612	2.8	1.4	3.5
	receptor protein)	PACE	X17094	2.8	3.1	3.5
1375_s_at	tissue inhibitor of metalloproteinase 2	F				
35761_at	aminoadipate-semialdehyde dehydrogenase phosphococtatheim	ZAIMIL	M32304	2.8	0.1	3.7
	transferase	AASDHPPT	AL050073	2.8	1.3	2.5
36856_at			07.000747			
37333_at	DNA (cytosine-5-)-methyltransferase 1		W28/43	2.8	1.7	3.3
1138_at	solute carrier family 20 (phosphate transporter) member 1	LIMMIT	X63692	2.8	1.7	2.2
32585_at	erythrocyte memb	SLCZUAI	L20859	2.8	1.8	3
36798 g at	sialophorin (gpL11	EPB4112	AF027299	2.8	0.8	8
31638_at	Ruanidinoacetate N	NHS	J04168	2.8	1.2	2.2
1815 g at	th factor	GAMT	AC005329	2.8	1.2	23
39113 at	Drotein distilline isomerase related protein (2015)	TGFBR2	D50683	2.8	1.4	2.5
•	intestinal-related)		AI262789	2.8	1.6	2.6
39165_at	nitrogen fixation cluster-like		1017101	0		
89930_s_at			047101	8.7	1.1	2.8
			VCC34 1/VV		,	

Figure 11RRRRRR

56431 at	hematological and neurological expressed 1	HN1 N90863	α' c'	1.6	9 C
48119 at	nuclear hody profein Sn140	L		2	0.1
100		7/06/14		4.1	3.6
58872_at		AI983986	36 2.8	1.5	1.6
53749_at	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	NDUFC2 AL050278	2.8	2.3	5.6
	(14.3KU, B14.3D)				
89919_s_at	Tax interaction protein 1	AW00734	43 2.8	2	m
31804 fat	sulfotransferase family, cytosolic, 1A, phenol preferring, member 1	SULT1A1 X78283	3 2.8	2	1.7
84903_f_at		AI264299	99 2.8	2.6	2.6
at .	ras responsive element binding protein 1	RREB1 A1097330	30 2.8	1.6	2.6
65507_at	eukaryotic translation initiation factor 4 gamma, 2	EIF4G2 AI749642	12 2.8	1.6	2.4
48599_at		AA824370	70 2.8	1.4	2.5
57086_at	protein kinase C and casein kinase substrate in neurons 2	PACSIN2 AA814516	16 2.8	2.7	3.9
59113_at		AA513002	22 2.8	0.8	2.1
75059_at	bridging integrator 1	BIN1 AW009683	83 2.8	2.1	2.8
69646_i_at		AA75858	31 2.8	2.5	2.8
82472_at	hypothetical protein FLJ10392	A187328	31 2.8	6.0	2.7
71094_at		AA02779	91 2.8		2.8
57026_s_at	secretory carrier membrane protein 2	SCAMP2 AA825494	94 2.8	2.1	3.1
45515 s at	45515_s_at methionine sulfoxide reductase A	MSRA R55759	9 2.8	3.1	3.3
44071_at	anaphase promoting complex subunit 4	AA604393	93 2.8		3.4
45739_at	hypothetical protein FLJ11210	8E5950VV	38 2.8	1.5	2.3
59452_at		791617IA	57 2.8	2.8	2.9
76856_at		Z09520MV	02 2.8	1.8	2.6
65830_at	FXYD domain containing ion transport regulator 5	FXYD5 AA04421	11 2.8		2.9
60871_at	AD023 protein	A1924180		2.5	2.8
61712_at	hypothetical protein PR00823	Z13066IY	12 2.8	2.1	3.7
45114_at		W1815763	53 2.8	2.5	2.7
60289_at	KIAA1323 protein	A1160081	31 2.8		3.8
51960_at	COPZ2 for nonclathrin coat protein zeta COP	A1984000	2.8	m	2.6
75258 f at	ets variant gene 5 (ets-related molecule)	ETV5 AA224344	44 2.8		2.8
57918 at	DKFZP586G1517 protein	AA77961	17 2.8	2.6	2.8
46887_at		A1887726	26 2.8		3.4
46225 at	MO25 protein	AA524350		3.3	3.4
51139_at	vacuolar protein sorting 29 (yeast homolog)	VPS29 AI650545	15 2.8	2.1	3.6
64005_at	integral inner nuclear membrane protein	AA218866	66 2.8	2.4	2.4

Figure 11SSSSSS

7/205 24	on don forming the first of the		AI/39473	2.8	2.6	0
47056 at	endoplasinic reticulum glycoprotein		A1986375	2.8		ilıc
48511 24	TDIANS systems		AA496318	2.8	1.2	2
65798 24			H08320	2.8	1.4	i
55658 24			AI684486	2.8	14	23
57200 c 24	- 1		R76178	2.8	2.5	ic
1800E 24	related RAS VItal (r-ras) oncogene homolog	RRAS	T54317	2.8	200	4 6
20010 at			AI862553	28	ας	
39012 dt	mitocnondriai ribosomai protein L12	MRPL12	X79865	27	0.00	7
38985 at	leptin receptor overlapping transcript-like 1		AF063605	27	25	7.7
39043 at		ARPC1B		27	5.1	1
b//_s_at	acid phosphatase 5, tartrate resistant	ACPE	١	1,1,0	210	4.3
34946 at		1000	<u> </u>	7.7	0	2.2
34960 g_at	Fc fragment of IgE	01001	_	7.7	1.7	2.7
31852_at	hypothetical protein DKFZp5640	ruerk	_L	2.7	1.8	2.8
31583 at			≤	2.7	1.2	2.6
32120 at	mitotic spindle coiled coil related materia	RPS8		2.7	2.2	3.8
39184 at	transcription along the forth Protein		AF063308	2.7	2.4	2 1
	B)	TCEB2	AI857469	2.7	1.9	2.9
32212_at	programmed cell death 8 (apoptosis inducing factor)	ACCOURT ACCOURT	AI 0/9703	100		
33815_at	uridine monophosphate synthetase (orotate phosphoriposyl		1	7.7	7	2.7
	transferase and orotidine-5' decarboxylase)	N N	J03626	2.7	2.2	2.9
412/1_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	SLC7A8	Y18483	2.7	2	2.6
41642_at	SMA5		V7E040	ľ		
810_at	Rho guanine nucleotide exchange factor (GFF) 1	10100	04667	7.7	2.4	2.5
33925_at	neurogranin (protein kinase C substrate RC3)	ANTIGERI	064105	2.7	1.5	2.9
33244_at	chimerin (chimaerin) 2	NAGN	9/066X	2.7	2.7	2.7
34866_at		CHNZ	U0/223	2.7	2.5	2.5
35306 at	DEAD/H (Asp.Glu-Ala-Asp/His) hox polymentide 15		AF055029	2.7	1.2	2.7
36758 at	CT application you (suit day and a land)	DDX15	AB001636	2.7	2.1	3.3
37310 at	plasminogen activator urokipase		AF070578	2.7	2.2	2.7
37652 at	Calcineurin binding protein 1	PLAU	X02419	2.7	1.8	26
37272 at			AB002328	2.7	2.1	2.8
37690 at	live (hacterial acetalactate continuos D	ITPKB	X57206	2.7	0	2.5
10000	ייים (מתכנכו ומן מכרנסומרומום אווווומאם) וואפ					

Figure 11TTTTT

	(subunit 9), isoform 1	ATP5G1	20669X	2.7	2.4	2.4
38098_at	lipin 1	10101	0.000			
38115_at	lung cancer candidate		080010	2.7	1.4	1.8
37895 at	1		AF055479	2.7	1.4	2.4
1795 g at	Cyclin D3	SLC35A1	D87969	2.7	2	-
38727 at		CCND3	M92287	2.7	2.6	3.5
	KIAAN962 protein		M23161	2.7	1.2	000
39126 at	polyamine-modulated factor 1		AB023179	2.7	2.7	1.9
56336 at	מלו מלו מלו מלו מלו מלו מלו מלו מלו מלו	PMF1	AL080101	2.7	1.4	388
56492 at	epithelial protein lost in peoplesm bots		H45858	2.7	3	3.5
56458 at	- 1		A1147040	2.7	2	5.9
50809 at	hebaran sulfate (plucosamina) 3.0 sulfatzanfazza a		Z99408	2.7	1.4	2.5
56531 at	Chromosome 11 onen reading frame 15	HS3ST2	AI831517	2.7	2.3	2.2
17921 at		C110RF15	A/188389	2.7	1.9	3.9
76804 r at			AA744496	2.7	2.4	2.5
80157 at			AI582206	2.7	2.5	2.5
57823 at			AI130690	2.7	2.1	2.6
79089 at			H18472	2.7	3.1	18
51614 at			AI797610	2.7	1.4	27
64335 at	Orontein-kinase interferon inducible death.		N98756	2.7	2.7	00
	inhibitor, repressor of (P58 repressor)	PRKRIR	A1990010	2.7	1.9	2.7
60493_at			000777	,		
63791_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3 (9kD, B9)	NDUFA3	T95412	7.7	2.5	2.6
69537 at			31100	77	<u>0</u> . 1	3.4
			A1086592	2.7	2.4	26
84451 f at	NADH dehydrogenase (libialinaid) 5 5 3 (cacalinaid)		AI695399	2.7	1.2	600
	coenzyme () reductase)	NDUFS7	F23536	2.7	1.6	2.7
89816_r_at			, , , , , , ,			
44776_at	MUM2 protein		AA/43454	2.7	2.5	2.2
56344_at	vacuolar protein sorting 35 (yeast homolog)	VDCOE	AW020///	2.7	2.2	3.2
48218_at		VF 333	A190122/	7.7	2.9	5.1
57187_at	general transcription factor IIIC polynentide 5 (63km)	10011	186283	2.7	0.8	2.3
51192 at	hypothetical protein FL J20515	G1F3C5	A1688411	2.7	2	2.2
			- 40000			

Figure 11UUUUUUU

44583 at			W89075	2.7	2	2.6
56690 at			AA603344	2.7	2	29
44562 24			AW001815	2.7	α-	212
15541 c at			AA478664	2.7	2.4	2.5
64297 s at	hynothetical proto		AW015697	2.7	2.7	10
53131 at			AW026502	2.7	0.4	4
52112 at			N25670	2.7	6.0	3.9
74729 f at	anchor attachment protein 1 (Gaal p. 1920t) homeles			2.7	2.8	9
45659 at	Comment of Carter, yearly nomotog	GPAA1	1	2.7	1.7	3.2
45690 at	CGI-133 protein		AA582196	2.7	1.8	28
46890 at			AA887118	2.7	1.9	3.6
53015 at	hypothetical protein El 120720		AA203361	2.7	2.7	23
80415 at	=		1	2.7	2.2	27
49914 at	hypothetical protein d 1511516 of	MAT2A	_	2.7	2.1	33
37497 at	hematopoletically expressed homeobox		٩	2.7	2.3	4.3
32059 at		HHEX		2.6	2.5	1
31952 at	ribosomal protein 6			2.6	2.2	2.5
32197 at		RPL6	X69391	2.6	23	5 7
) - (C + -)	source carrier failing 23 (filltochondrial carrier; oxoglutarate carrier), member 11	SLC25A11	AF070548	2.6	1.5	3.2
1307_at	xeroderma pigmentosum, complementation group A	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \				
40961 at	SWI/SNF related, matrix associated actin dependent acting	AFA	1	2.6	2.4	2.5
	chromatin, subfamily a, member 2	SMARCAZ	X72889	2.6	2.1	2.7
32/88 at	RAN binding protein 2	CARNAG	0.0000			
32826_at	ectonucleoside triphosphate diphosphohydrolase 1	FNTPD1	A 11 221 22	0.70	1.8	2
35229_at	carnitine palmitoyltransferase I, liver	CPT1A	1 30211	0.0	7	2.5
36013 at	chromosome 4 open reading frame 1	CAORET	AE006621	6.0	1.4	2
35223_at	alpha integrin binding protein 63	1 1010	12000010	4.0	1.4	3.7
31901_at	potassium voltage gated channel, shaker related subfamily, beta	0041407	- 1	2.6	1.6	2.7
		VOIVABA	Ar 044253	2.6	1.6	2.5
35252_at	KIAA0528 gene product		00111004			
34882_at	Inucleolar protein (KKE/D repeat)		AB011100	5.6	2.3	2.1
36519_at	excision repair cross-complementing rodent repair definition		Y12065	2.6	2.2	2.5
	complementation group 1 (includes overlapping antisense sequence)	ERCC]	M13194	2.6	1.8	2.2

Figure 11VVVVVV

(points 0 = 0.5)	TUC	024132	2.0]	1.7	2.3
tein 1 (chaperonin)	HSPD1	M22382	2.6	1.6	3.4
Ras association (RalGDS/AF-6) domain family 2	RASSF2	D79990	2.6	1.3	2.5
		L10379	2.6	2.3	2.3
NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH: coenzyme O reductase)	NDUFS8	AF038406	2.6	1.7	2.7
stor	YY1	M77698	2.6	80	29
ribosomal protein L22	RPL22	AI526079	2.6		2.7
rotein		AI468699	2.6	2.3	2.5
		AI924940	2.6	2.4	2
bility complex, class II, DN alpha	HLA-DNA	AI692538	2.6	2	2.6
isocitrate dehydrogenase 1 (NADP+), soluble	1DH1	AI971036	2.6	1.1	2.7
		AI937449	2.6	2.2	3.5
		AI765712	2.6		2
		AW016356	2.6	2.2	2.5
- 1		AA932206	2.6	2.6	2.5
hypothetical protein FLJ20668		T66305	2.6	2.4	2.7
		W72919	2.6	2.6	2.7
		A1632438	2.6	1.6	2.5
		AI674163	2.6	2.6	2.5
hypothetical protein FLJ11151		AA570555	2.6	2.1	2.4
		U83510	2.6	2.6	3.1
tumor protein p53-binding protein, 1	TP538P1	AW008856	2.6	1.6	3.2
		AI701895	2.6	2.1	3.8
		AA601045	2.6	2.6	2.6
		AW004635	2.6	1.7	m
		N36764	2.6	2.6	2.4
		AA209239	2.6	0.4	2.1
BCM-like membrane protein precursor		AI697841	2.6	1.9	2.2
		AI652721	2.6	2.2	2.4
density-regulated protein	DENR	AA149864	2.6	1.4	3.5
		AI760531	2.6	1.9	2.6
		N37023	2.6	1.8	2.2
		N90917	2.6	2.4	2.2
		COVCVC14			

Figure 11WWWWWW

in cors:

44740_at	hypothetical protein FLJ20343		000000	0		
50429_at	hypothetical protein FLJ20640		W/328U	2.6	1.8	2.8
43977_at	hypothetical protein FL 120422		MA29221/	2.6	1.8	2.5
55526 at			AI660497	2.6	2.5	2.7
45714 at	hypothetical profein FI 120568		AA923355	2.6	1.7	4.2
58595 f at	CD24 antigen (small feel lung carcinoma clineter 4		- 1	2.6	1.8	1.5
64104 at	hypothetical protein of 155100 5	CD24	~1	2.6	8	43
51099 s at	coactivator indep		AI627538	2.6	2.2	2.5
53802 at			AA526554	2.6	2.6	E
60521 at			AA151838	2.6	1.8	2.6
64087 i at	hypothetical protein El 112171		AL043931	2.6	2.4	σ e.
53361 at			AI022065	2.6	1.9	2.6
	kelch-like protein C3IP1		H40238	2.6	2.4	24
54186 at			09569N	2.6	1.1	26
44143 at	McKusick-Kaufman syndrome		1	2.6	1.6	23
64263 s at		MKKS	_ 1	2.6	3.1	3.5
46226 at	HSPC142 protein		AA725421	2.6	1.7	1 7
54026 at			AA610145	2.6	2.3	7
75187 f at	alpha-2-macroplobulin		┙	2.6	2	
47405 f at	prohibitio	A2M	- 1	2.6	0.5	00
50341 s at	riboniclease 6 preciirsor	PHB	AA512948	2.6	1.5	2.5
55091 at	phosphoinositol 3		AI986481	2.6	24	000
75352 s at	Cytosolic acyl coenzyme A thioester hydrolog		AI341312	2.6	2.5	286
74541 at	low density linoprotein related protein 1 / 2 - 2 -		AW025033	2.6		2.5
•	receptor)	LRP1	AI969879	2.6	1.7	2.5
47611_at	phosphodiesterase 4A, cAMP-specific (dunce (Drosophila) homolog	PDF4A	AA523395	2 6		
41406 24	phosphodiesterase E2)			0.	7.7	2.9
41400 at	hypothetical protein FLJ21919		01 080 1A			
39000_at	N-myristoyltransferase 1	LEWN	AE043334	7.5	2.1	2.5
/63_at	glia maturation factor, beta			2.5	1.4	1.7
652 g at	replication protein A3 (14kD)	GWILD	٦.	2.5	1.1	3.6
40843 at	integrin cytoplasmic domain-associated protein 1	KFA3	- 1	2.5	2.1	2.3
37200 at	Fc fragment of IgG, low affinity IIIb, recentor for (CD16)	1000	AF012023	2.5	2.3	2.1
41205 at	Ubiquitin protein lipase F38 (human papilloma vivis 56	FUGRAB	- [2.5	0.5	2.3
		UBE3A	U84404	2.5	0	2.2
					_	_

Figure 11XXXXXX

	Dosollia Proteil 94, 1-1110cd	APS4Y	M58459	2.5	2	2.7
41732 at			AA310786	2.5	1.1	2.4
41746_at	non-histone chromosome protein 2 (S. cerevisiae) like 1	NHP2L1	Z83840	2.5	2.4	2.4
954_s_at	protein phosphatase 1, catalytic subunit, alpha isoform	PPP1CA	X70848	2.5	2.6	3.3
33333_at	KIAA0403 protein		AB007863	2.5	1.9	2.3
34191_at			AB002445	2.5	1.2	2.9
33915_at	melanoma adhesion molecule	MCAM	W22655	2.5	1.4	2.5
34256_at	sialyltransferase 9 (CMP-NeuAc;lactosylceramide alpha 2,3	SIAT9	AB018356	2.5	0	2.5
	stalyticalisterase, GM3 synthase)					
39248_at	aquaporin 3	AQP3	N74607	2.5	2.5	2.4
41236 at	hypothetical protein		U79252	2.5	2.1	2.5
34748_at	KIAA0846 protein		AB020653	2.5	0.8	2.3
35172_at	tyrosylprotein sulfotransferase 2	TPST2	AF049891	2.5	2.2	2.6
39076_s_at	DR1-associated protein 1 (negative cofactor 2 alpha)	DRAP1	AI991040	2.5	0.1	2.9
34402_at	unr-interacting protein		AB024327	2.5	1.6	4.4
35309_at	Suppression of tumorigenicity 14 (colon carcinoma, matriptase, epithin)	ST14	U20428	2.5	2	1.3
36561_at	propionyl Coenzyme A carboxylase, beta polypeptide	PCCB	X73424	2.5	1.9	2.5
36169_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE)	NDUFA1	N47307	2.5	1.3	4.2
36938_at	N-acylsphingosine amidohydrolase (acid ceramidase)	ASAH	U70063	2.5	0	2.8
32553_at	MYC-associated zinc finger protein (purine-binding transcription factor)	MAZ	M94046	2.5	1.9	2.5
32569_at	platelet activating factor acetylhydrolase, isoform lb, alpha subunit (45kD)	PAFAH1B1	L13385	2.5	1.5	2.7
37408_at	endocytic receptor (macrophage mannose receptor family)		AB014609	2.5	2.2	2.3
37740_r_at	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	SLC25A5	102683	2.5	1.8	2.5
38090 at	phosphatidy/serine decarboxylase	PISD	AL050371	2.5	2.5	2.5
38443 at	son of sevenless (Drosophila) homolog 1	SOS1	U79291	2.5	1.4	2.1
40756_at	nucleophosmin/nucleoplasmin 3	NPM3	AF081280	2.5	2.2	2.2
40758_at	immature colon carcinoma transcript 1	ICT1	X81788	2.5	1.3	2.5
2028_s_at	E2F transcription factor 1	E2F1	M96577	2.5	2.5	2.8
39155_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	PSMD3	D67025	2.5	1.6	3.7
41084_at			AI659108	2.5	1 7	•

57346_at	Mad4 homolog		AA831438	2.5	m	3.6
56197 at			AI783924	2.5	2.3	2.6
48852_at			AI346327	2.5	1.8	2.8
51684_at	hypothetical protein DKFZp434F0272		W76160	2.5	1.8	2.3
66269_at			AA669114	2.5	2	2.1
88767_at			AW008519	2.5	2.5	2.5
55586_at	period (Drosophila) homolog 3	PER3		2.5	1.6	3.9
50890_at	L2DTL protein		AI800576	2.5	2.5	2
57809_at	presentlins associated rhomboid-like protein		W63675	2.5	2.8	3
61541_at			AI160808	2.5	2	2.7
62273_at			AI766808	2.5	2.5	2.3
91825_at			AI375222	2.5	2.5	2.5
54787_at			AA046849	2.5	1.6	1.4
59809_f_at	poly(A) binding protein, cytoplasmic 1	PABPC1	AW020548	2.5	2.2	4.1
43403_at	methylenetetrahydrofolate dehydrogenase (NADP+ dependent),	MTHFD1	AA618429	2.5		2.3
	methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase					_
59681_at	laminin receptor 1 (67kD, ribosomal protein SA)	LAMRI	AA468402	2.5	2.1	3.1
48597_at			AI871648	2.5	1.3	0.2
45268_at			AA205531	2.5	1.5	2
59091_at			AI799698	2.5	2.4	2.8
45475_f_at	hypothetical protein		AW006786	2.5	1.3	2.8
48417_r_at	hypothetical protein PR02849		AA636101	2.5	2.1	2.4
56287_at			AI801756	2.5	1.8	2.2
60821_at	KIAA1226 protein		AW006938	2.5	2.3	2.1
50198_at			AI208272	2.5	2.5	2.5
44036_at			N28741	2.5	1	1.8
50251_at			AA524283	2.5	2	2.6
45354 at	1		AA658561	2.5	2.1	2.5
43947_at	hypothetical protein FLJ11323		AA669327	2.5	2.5	2.7
89584_at	\neg	PRSS15	AI817597	2.5	6.0	2.9
	putative secreted pro		AI830110	2.5	2.1	2.3
48051_at	cell death-inducing DFFA-like effector b	CIDEB	AA148543	2.5	1.8	2.7
51186_at			AI743603	2.5	2.3	1.5
44519_at			A1140754	2.5	2.2	3.1

Figure 11ZZZZZZ

40,40	C/ C/ - 14					
	supplessor of variegation 3-9 (Prosophila) nomolog 1	SUV39H1	AA604816	22	2.2	25
64651_at			AIR18631	2 5	1 0	51-
74703_f_at	74703_f_at ATP synthase, H+ transporting, mitochondrial F0 complex subunit c	ATPECS	ATPECS NO1/12	2.5	0.0	0 0
	(subunit 9) isoform 3		0/4100	C.7	4.1	3.1
45217_at	platelet derived growth factor C	PUGEC	PUGEC AA631149	2 5	, ,	C
45599_at	triggering receptor expressed on myeloid cells 2		CHICOLO	2.7	6.1	7.7
53215 at			000001	6.3	6.2	2.5
			A163625U	2.5	1.7	1.7
51/93_s_at	51/93_s_at INADH denydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9kD, MLRQ)	NDUFA4	NDUFA4 AA890044	2.5	1.3	3.5
57828_at	ubiquitin A-52 residue ribosomal protein fusion product 1	IJRA52	A1857945	2 5	2 6	
46130 at		70, 100	2100001	63	2.3	4.2
64467 24			AL04281/	2.5	1.9	1.7
1			N21390	2.5	1.5	25
48/4/_at	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	PIPSK2B	PIP5K2B AI982873	25	2.2	ic
63259_s_at	63259_s_at docking protein 2, 56kD	CXCC	DOKO AABEAAOO	5 1 0	5.7	6.0
47139 at		2/100	00110000	2.5	7.5	7.4
47 133 at			AA481256	2.5	2.1	α α
46688_at	phenylalanyl-tRNA synthetase beta-subunit		AA639795	2 5	2.0	010
47627 at	47527 at cytochrome P540 subfamily IIS polynostide 1		20,7500.01	7.3	2.1	7.7
130 /			AI445492	ر د د	ر ب	0.00

Figure 11AAAAAAA

l _ l	Gene Name	Gene Symbol	GBA	Score Ecoli	Score Candida	Score Influence
1520_s_at	endothelin 1	LNCH LNCH	105008	7777	200	L C. I
563_at	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	IL12B	M65290	2449.1	761.6	1.2
1369_s_at	interleukin 8	11.8	M28130	2300.5	32.6	122 1
35822_at	B factor, properdin	BF	L15702	1635.7	787 1	17.3
38299_at	Interleukin 6 (Interferon, beta 2)	971	X04430	1566.4	101.3	7 700
40385 at	smail inducible cytokine subfamily A (Cys-Cys), member 20	SCYA20	U64197	943.4		
1400 at			AI652725	886.7	27.7	
1404 - 41		SCYA5	M21121	834.8	134.8	250 1
27107 ct	pentaxin related gene, rapidly induced by IL-1 beta	PTX3	M31166	827.3		
1272 04	troc oncogene	GR02	M36820	785		26.1
2002 g at	Idnition Hecrosis Tactor, alpha-induced protein 6	TNFAIP6	M31165	573.9	37.7	75.1
1050 st	BULZ-related protein A1	BCL2A1	U27467	547.8	65.2	
1009_a1	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	PTGS2	U04636	495.3		
77706_at			AA641972	793	50	7.0
408_at	GRO1 oncogene (melanoma growth stimulating activity, alpha)	GR01	X54489	486.7		
32818_at	hexabrachion (tenascin C, cytotactin)	HXB	X78565	474 9	27.3	1
39402_at	interleukin 1, beta	118	M15330	468 F		1.5
36067_at	α	SCYA19	AB000887	394.2		12.2
926 at	metallothionein 1G	MT1G	J03910	370.2		2.7
_' 1	aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)	АГДНЭ	AI127172	326.5	i m	2.1
	S100 calcium binding protein A9 (calgranulin B)	S100A9	W72424	313.3	0.5	C
21	hypothetical protein		AA618602	296.2	15	186
		DNJI	300219	289.9		36.2
41531_at	transmembrane 4 superfamily member 1	TM4SF1	AI445461	278		30.5
61818 at			A1970348	265	(*,	2 5
35577_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin). member 7	SERPINB7	AF027866	262.3		5.6
34929_at	tumor necrosis factor receptor superfamily, member 8	TNFRSF8	M83554	255.9	0	0
33335_at	Interleukini 12A (riatural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)	IL12A	M65291	250.2	18.4	14.6

Figure 12A

41096_at	S100 calcium-binding protein A8 (calgranulin A)	S100A8	AI126134	249.4	0	6.9
39827_at	hypothetical protein		AA522530	245.1	38.4	14.6
41468_at	T cell receptor gamma locus	TRG@	M30894	245.1	2	1
35000_at	tumor necrosis factor (ligand) superfamily, member 9	TNFSF9	U03398	232.3	2.9	3.1
33965_at	small inducible cytokine A1 (1-309, homoiogous to mouse Tca-3)	SCYAI	M57506	216.3	0	7.8
36116_at	thyroid hormone receptor interactor 10	TRIP10	AJ000414	215.9	56.7	7
1400_at	colony stimulating factor 2 (granulocyte-macrophage)	CSF2	M13207	210.9	0.1	1
47855_at	Interleukin 19	1119	AA151656	205.5	0	0.5
33789_at	small inducible cytokine A5 (RANTES)	SCYA5	AF088219	191.5	64.1	1.2
33513_at	signaling lymphocytic activation molecule	SLAM	U33017	178.3	14.3	1
58918_at			AA210892	176.1	24	34.8
41104_at	small inducible cytokine B subfamily (Cys.X.Cys motif), member 13 (B.cell chemoattractant)	SCYB13	AF044197	171.2	0	2.3
1334_s_at	colony stimulating factor 3 (granulocyte)	CSF3	X03656	167	1.2	7.2
31623 f at	metallothionein 1A (functional)	MT1A	K01383	160.3	22.3	49.7
33364_at	similar to rat myomegalin		U51694	156	58.9	2.9
36296_at	lymphotoxin alpha (TNF superfamily, member 1)	LTA	D12614	154	62.8	28.5
72840_at	19A24 protein		AI638519	149.1	43.6	23.3
49076_at	SGRF protein, Interleukin 23 p19 subunit		AI 796983	147.7	0.3	2.3
41870_at	lung type-I cell membrane associated glycoprotein		AF030428	143.7	0	1.2
34666_at	superoxide dismutase 2, mitochondrial	SODS	X07834	141.3	63.1	42.3
32114 s at	adenosine A2a receptor	ADORA2A	846950	137.9	31	27.9
48919_at	potassium inwardly rectifying channel, subfamily J, member 2	KCNJZ	AA393850	130	11.2	13.1
63335_at	sorting nexin 10		AI285531	127.4	55.8	74.2
48753_at	PPAR(gamma) angiopoietin related protein		N57259	126	7.9	14.7
37319_at	insulin-like growth factor binding protein 3	IGFBP3	M35878	125.2	7	1.3
46468_at			AI735586	122.3	4.7	0.2
1548 s at	interleukin 10	110	U16720	121.9	4.3	3.2
57440_r_at			AW014801	120.2	4	10.2
84995_at			AA769482	117.4	12.2	9.9
50978_at	putative secreted ligand homologous to fix1	hfjx	AI338625	117.2	3.8	3.3
609 f at	(metallothionein 1B (functional)	MT1B	M13485	116.3	11.1	20.1
63066_at			AA001735	113	12.6	9.6

58957_at	hypothetical protein FLJ20637		AI620475	108.9	42.7	28.3
36070_at	KIAA1199 protein		AL049389	108.4	0	2.9
33282_at	ladinin 1	LAD1	U42408	107.2	2.4	4 4
36454_at	carbonic anhydrase XII	CA12	AF037335	103	0	1.1
70594_at			AI819198	102.7	8.4	2.5
82795_at			AI793037	102.4	0	1 4
31622_f_at	metallothionein 1F (functional)	MT1F	M10943	101.8	13.1	32.6
33055_at	cytochrome P450, subfamily VIIB (oxysterol 7 alpha-hydroxylase), polypeptide 1	CYP7B1	AF029403	99.5	17.6	1.2
70097_at	indoleamine pyrrole 2,3 dioxygenase	OUNI	AI302268	99.5	29.8	30.0
73341_at			AA678425	99.2	1 2	
59805_f_at			AI636743	98.2	26	99
38909_at	cytochrome P450, subfamily XXVIIB (25-hydroxyvitamin D.1-alpha hydroxylase), polypeptide 1	CYP27B1	AB005038	98.2	17.2	2.9
87651_at			AI800110	95.3	10.5	F
75146_at			AL047300	94.9	18.8	0.5
76710_at	cardiotrophin-like cytokine; neurotrophin-1/B-cell stimulating factor-3		AI040033	92.7	4.7	4
32984_s_at	chloride channel Kb	CLCNKB	Z30644	92.3	5	ľ
1004_at	Burkitt lymphoma receptor 1, GTP binding protein	BLP1	X68149	92	0.2	11.5
56246_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	PFKFB3	AI765775	91	6.2	11.3
1911_s_at	growth arrest and DNA damage inducible, alpha	GADD45A	M60974	88.7		2.7
38428_at		MMP1	M13509	87.8	0	0.3
37407_s_at		MYH11	AF013570	87	17.5	1
45237_at	superoxide dismutase 2, mitochondrial	SOD2	AA142976	84.4	32.6	17.71
1549_s_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4	SERPINB4	U19557	81.2	0.7	1.1
1693_s_at	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	TIMP1	D11139	79.8	1	6.0
60032_at			AI984197	79	00	60
36130_f_at	metallothionein 1E (functional)	MT1E	R92331	78.7		8.6
57711_at			AA576959	78.3	8.6	0.7
35844 at	syndecan 4 (amphiglycan, ryudocan)	SDC4	079206	77.4	5.8	20.7
85561_at			AL079435	76.5	7.7	9.0
40687_at	gap junction protein, alpha 4, 37kD (connexin 37)	GJA4	68296W	74	13.5	4.2

Figure 12C

		AI635522	72.4	7.8	8.6
hypothetical protein FLJ22318		AI250747	72.4	0	C
tumor necrosis factor receptor superfamily, member 9	TNFRSF9	U03397	72.2	7.8	19.5
interleukin-1 homolog 1		AI814314	71.5	4.1	2.3
RNA helicase-related protein		H68340	71.4	10.1	219
similar to rat myomegalin		AI659612	71.11	8 6	11.8
		AI219461	70.7	4.8) Ir
nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NFKB2	876638	70.6	13.3	7.8
matrix metalloproteinase 7 (matrilysin, uterine)	MMP7	L22524	70.6	1.3	
		H72723	70.4	8.2	8.5
		AI680833	69.2	1.3	1.2
		AI535730	68.4	21	15.8
matrix metalloproteinase 10 (stromelysin 2)	MMP10	X07820	67.5	2.4	3.6
		AA926689	66.3	1.8	1.1
ninjurin 1	NIN	U91512	65.2	35.7	16.7
interleukin 15	1115	U14407	64.7	16.6	22.1
bHLH factor Hes4		AI380603	64.7	15.4	23.6
NK homeobox (Drosophila), family 3, A	NKX3A	AI557413	63.8	2.8	12.5
hypothetical protein FLJ20764		A1684508	62.7	4.1	2
v-ets avian erythroblastosis virus E26 oncogene homolog 2	ETS2	J04102	61.9	3.6	4.4
		AI244908	61.5	3.8	4.4
disintegrin protease		Y13323	61		1.5
snail 1 (drosophila homolog), zinc finger protein	SNA11	AA613301	8.09	0.3	1.8
p53-induced protein PIGPC1		AI525592	59.9	9.0	0.5
NY-REN-18 antigen		AA587445	59.8	23.1	1.9
		AA127641	58.7	2.4	7.4
		AI347073	57.3	2.1	11.6
DKFZP586C1619 protein		AL050374	56.3	9.1	10.6
		AI082042	55.4	14.7	1.9
testis zinc finger protein		AI798147	55.2	2.9	20
annexin A8	ANXA8	X16662	55.1	0	0.8
solute carrier family 1 (glial high affinity glutamate transporter), member 2	SLC1A2	U01824	55	0	1.2
signal transducer and activator of transcription 4	STAT4	L78440	54.6	103	5.9

Time: Response of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

1891_at	mitogen-activated protein kinase kinase 8	OVEDAM	014407			
76762 at		ONC TAIN	┙	53.8	4.5	11.2
48757 at	FH domain containing 1		AI246590	53.8	6.8	102
	Eri contant contantilly 1	EHD1	AI986040	53.8	000	100
04003 at			N47335	537	710	4.6
4/28/ at			VIA7EA72	133.7	2.7	8.2
48676_at			A14/34/3	53.5	2.5	6.9
37185 at	Serine (or externo) proteins a catalytic and a catalytic		9	53.3	0	C
5	member 2	SERPINB2	Y00630	52.6	0	0
40670_at	kynureninase (L-kynurenine hydrolase)	III	4			
37137 at	granzyme B (granzyme 2 cytotoxic T. lymphocyto agginted	ONIA	`	52.5	13.6	7.9
	serine esterase 1)	GZMB 6ZMB	M17016	52.3	9.1	15.3
80773_at			01011			
48025 at	INCK adaptor protein 2		- 1	51.8	8.6	13.9
222 at	exostoses (multiple) 1	NCKZ	7	51.7	5.9	6.9
37451 at		EXTI	879639	50.9	S	9.6
	KIAA1031 protein		AL109695	50.6	4.8	2,5
37716 at	1-		_	50.6	24.1	4 6
82532 at	and a supplied by monocional antibody MRC 0X.2	MOX2		50.5	7	
36100 24			AI821392	50	4	2
48506 at	hypothetical protein El 13611	VEGF		49.9	11.8	άσ
51075 24	passocia 1		AI358871	49.8	0	0 0
32527 at	adinon consists 2	PANX1	AA115920	49.5	3.0	ţ -
55022 at	ממלחמים שלפיתור ל		AI381790	49.3	14	
25701 04			N58182	49.2	1.0	1.0
30/01_41	serine (or cysteine) proteinase inhibitor, clade A (alpha-1	SERPINA1	X01683	48.8	2.5	21.8
38870 24	S100 coloinase, antitrypsin), member 1				;	4.4
1583 24	times acciding protein A12 (calgranulin C)	S100A12	D83664	48.3	5	9 9
72721 at	tanio, necrosis ideior receptor superfamily, member 18	TNFRSF1B	M32315	48	3.4	, e
41779 at	regulator of Generating signalling 16		AI830607	47.1	3.3	1 4
56302 24	Society of protein alguarming to	RGS16	U70426	46.6	α	12
57025 at	prostagianum E synthase	PTGES	103380	46.5	0,0	21
37027 41	retiriorc acid induced 3	RAI3	A1990405	76.51	7 0	0
44/90_s_at			A1120210	10.0	0.4	0.2
54565_at			7070710	40.7	0.8	0.8
58667_at			A4149730	45.6	8.7	10.3
529 at	dual specificity phosphatase 5	100	AA442239	45.4	0.4	5.5
		DUSP5	U15932	45	12.1	0

		_	W3/880	8.04	2.5	3
53970_at	dual adaptor of phosphotyrosine and 3-phosphoinositides		AF150266	43.8	9.5	m
84364_at			AA665185	43.3	3.1	1.7
75246_s_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3	SLC1A3	W26838	43.1	7.2	4.8
45647_s_at			AW005111	42.5	1.5	1.7
38131 <u>a</u> t	prostaglandin E synthase	PTGES	AF010316	42.1	0	1.2
43524_at	KIAA1170 protein		C14031	42.1	18.4	7.2
42363 r at	STAT induced STAT inhibitor 3		AI680350	41.7	5.3	5.8
48822 s_at	adenylate kinase 3	AK3	AW015546	41.5	6.1	0.5
35694_at	mitogen activated protein kinase kinase kinase 4	MAP4K4	AB014587	41.4	2.7	0.6
37225 at	KIAA0172 protein		D79994	41.4	3.6	10.9
33849_at	pre-B-cell colony-enhancing factor		002020	41	8.3	16.3
34439 at	absent in melanoma 2	AIM2	AF024714	40.9	18.1	16
58737_at			N27438	40.2	2.4	4.3
44640_at			W30985	40.2	11.6	8.4
64333 s at	pyrophosphatase (inorganic)	ЬР	AW009649	39.9	10.9	5
41654 at	adenosine deaminase	ADA	X02994	39.7	4.1	3.2
40456_at	up-regulated by BCG-CWS		AL049963	39.4	1.8	0
1022_at	GRO3 oncogene	GRO3	M36821	39.3	1.9	1.4
53609_at			C14904	39.3	13	22.8
48014_at			N54957	38.8	5.2	2
54147 at	pyruvate dehydrogenase kinase, isoenzyme 4	PDK4	AI763378	38.3	4.5	9.0
68652_at			AI431778	38	3.8	0.6
67259_at			R56235	37.9	0	6.3
1343_s_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3	SERPINB3	968995	36.4	0	0.3
43456_at	serine/threonine protein kinase MASK		AI299952	35.5	2.6	0
52729_at	CD44 antigen (homing function and Indian blood group system)	CD44	AA037772	35.3	3.3	0.6
64170_at			AI609751	35	3.2	0.5
32686_at	prostaglandin E receptor 3 (subtype EP3)	PTGER3	960980	34.9	2.2	2.2
53261_at			AI337231	34.9	10.4	1.6
53100_at	hypothetical protein FLJ10307		AA747448	34.8	5.3	1.3
33730 at	retinoic acid induced 3	RAI3	AF095448	34.7	1.2	4.6

Figure 12F

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36609_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3	SLC1A3	D26443	34.2	2.8	3.4
52255_s_at	collagen, type V, alpha 3	COL5A3 A	AI984221	33.9	2.1	3.9
55353_at		¥	AA760977	33.6	6.9	9
46760_r_at			H38110	33.5	9.1	5.8
36780_at	clusterin (complement lysis inhibitor, SP-40,40, sulfated	OTO	M25915	32.9	5	8.7
	glycoprotein 2, testosterone repressed prostate message 2, apolipoprotein J)					
51026_at	hypothetical protein PRO0813		N30257	32.6	3.3	O
36543_at	coagulation factor III (thromboplastin, tissue factor)	F3	102931	32.3	6.6	4.2
66529_at		A	AA843926	32.2	3.6	9.6
55063_at	glutamate decarboxylase 1 (brain, 67kD)	GAD1 A	AL042399	31.4	5	0
19664_s_at		A	AW001427	31.3	0.1	1.4
32518_at	zinc finger protein 259	ZNF259 A	AF019767	30.5	2.7	0
42524_at		L.,	R37337	30.1	6.4	3.6
47076_at			W87690	29.9	2.6	3.4
64911_s_at	hypothetical protein FLJ11305	4	AA854113	29.8	3.8	0
75742_at		4	AI870617	29.7	1.4	0
38994_at	STAT induced STAT inhibitor-2	d	AF037989	29.2	6.3	1.8
67764_r_at		ď	AA004879	29	4.4	11.8
32863_at	similar to calcium/calmodulin dependent protein kinases	A	AL023754	28.7	7.3	1.9
36139_at	DKFZP586G0522 protein	A	AL050289	28.5	1.5	20.1
53799_at	hypothetical protein similar to mouse Dnaji1	Ø	AA628434	28.3	5	0
40098_at	EH domain containing 1	EHD1	AF001434	28.1	9.0	3.9
42769_at			N46441	27.9	0.7	0.4
51278_at		1	AI 139543	27.7	2.8	2.6
49670_at			W96225	27.7	2.1	0
	FOS-like antigen 2	FOSL2	X16706	27.6	1.7	2.1
47971_at	ferritin, heavy polypeptide 1	FTH1	192243	27.6	6.3	0.8
54491_at		A	AA043562	27.5	Э	3.1
48105_at	latexin protein	-	AI672094	27.4	6.5	0.9
63380_at	hypothetical protein DKFZp434P0531		AI732727	27.4	5.9	4.9
56500_at	junctional adhesion molecule	,	AI241578	27.4	3.9	0
65628_at		A	AW023171	27.4	1.6	3.4
38617 at	LIM domain kinase 2	LIMK2	D45906	27.3	4.4	4

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34/// at	adrenomedulin	ADM	D14874	27.2	X	7 7
49249 s at			AA533079	27.1		7.
	hypothetical protein from EUROIMAGE 588495		AAA8650A	27.1	2.0	2.5
56641_at	liver expressed antimicrobial peptide		70005F01	27.1	3.1	3.8
52958_at			NC2450	17	10.1	2.5
38970 s at	Nef-associated factor 1		N03438	26.5	0.8	0
44344 at	1		AJ011896	26.4	7.6	4.2
40496 24	complement component 1 contract	HZBFL	AA557205	26.4	3.9	0.5
52665 34	complement component 1, s subcomponent	C1S	104080	26.3	5.6	7.9
75700 at	This of the fact o		H16258	26.3	9.0	2.6
56871 at	Hypothetical protein from EURUIMAGE 195596/		AI807170	26.2	0.8	C
59105 21	mitochondrial polito carrior		AI953847	25.7	8.6	12.8
39942 at	basic lauring almost transcription (1977)		- 1	25.7	4.2	2.1
56769 at	B2.H1 protein	BATF		25.6	6.3	0
37388 at	totididai verm		~1	25.6	8	6.1
35362 at	mosin X	TFPI2		25.5	0	1.2
33706 24	ADD ribonitation tooks Ill. 4	MYO10	~1	25.1	0	1.2
337.30 at	Contathiogram (2001) Ideas	ARL4	U73960	24.9	1.1	40
907709	Cystatinoriase (cystatinorine garnma-lyase)	CTH	A1955061	24.8	2.8	
76/07 at			AI653230	24.7	4	1.0
50702 2+			AI826091	24.6		
30702 at			155716	24.5	2	
1200 g at		PTPN2	M25393	24.4	6.4	10.1
33331_at	dual-specificity tyrosine-(*)-phosphorylation regulated kinase 3	DYRK3	Y12735	24.3	0.2	1.9
36564_at			W27/19	2.50		
36175_s_at	human immunodeficiency virus type I enhancer binding protein 2	HIVEP2	AL023584	24.2	7.7	5.7
48964_at						
59133 at			A1629027	24.2	17.2	9.1
89881 at	Chloride intracellular chappel 4		AA131626	24.1	1.2	0.7
35094 f at		CLIC4	AA675919	24	4.4	0.7
	domain), member 3	LILRA3	AF025527	23.9	5.9	1.5
55334 at			A1249019	73.7	C	
32186_at	solute carrier family 7 (cationic amino acid transporter, y+	SLC7A5	M80244	23.6	3.5	0 %
	Isystem), member 5				;	1

88550_at	[hypothetical protein FLJ12929		AI468004	23.6	6.7	0
54744_at			AA582287	23.5	8	8
37032_at	nicotinamide N-methyltransferase	L ₩ZZ	U08021	23.4	0	1.2
34481_at	vav 1 oncogene	VAV1	AF030227	23.3	0	0
39839_at	cold shock domain protein A	CSDA	M24069	23	1.1	
1779_s_at	pim-1 oncogene	PIM1	M16750	23	3.5	9.9
34770_at	mitogen-activated protein kinase kinase kinase 8	MAP3K8	Z14138	22.9	9.0	3.3
88906_at	KIAA1442 protein		AL110312	22.8	0	1.8
54782_at			AI281068	22.7	9	1.1
38582_at	serine protease inhibitor, Kazal type 1	SPINKI	AI961220	22.6	9.0	10.6
44906_at			AI916646	22.6	0.7	2.1
84601_at			AI469960	22.6	2.9	4
889_at	integrin, beta 8	ITGB8	M73780	22.5	2.1	1.2
56979_at			AA133395	22.5	3.4	3.4
35036_at	complement component C1q receptor		U94333	22.4	1.2	6.0
68355_at			AI655376	22.2	0	0.7
49364_at			AL041551	22.2	1.7	2.7
47544 at			AA741324	22.1	4.8	5.3
80151_at			AA031832	22	0.7	0.3
36453_at	KIAA0711 gene product		AB018254	21.9	1.1	0.3
38272_at	MKP.1 like protein tyrosine phosphatase		AF038844	21.7	2	0
40606 at	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR		U88629	21.6	4.4	2.6
69197_r_at			AA508552	21.6	6.1	0
1508_at	integrin, alpha 9	ITGA9	D25303	21.2	0	0.4
			AI554946	21.1	4	1.9
53757_at			AA131524	21.1	1.8	3.6
36933 at	N-myc downstream regulated	NDRG1	D87953	21	2.3	0.5
1776 at	Ras-related associated with diabetes	RRAD	L24564	20.8	0	1.2
39071_at	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen (CD51)	ITGAV	M14648	20.8	1.6	1.3
1237_at	immediate early response 3	IER3	\$81914	20.8	4.7	0
TO I	UDP-N-acteyiglucosamine pyrophosphorylase 1	UAP1	AB011004	20.7	1.9	1.2
47500 i at	c-myc promoter binding protein		AA805337	20.6	7.1	2.8
44370 at			AI589469	20.6	0.3	2.5
64247_at			H40631	20.6	4	3.1

			0.01	ò	5.4
		AI435160	20.5	8.7	2
Norrie disease (pseudoglioma)	NDP	ı	20.5	0.8	0.3
KIAA0481 gene product		AB007950	20.4	1.2	0
ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR		C75510	20.4	4	2.1
		W72194	20.3	0.3	1.5
		AI732347	20.3	-	0.1
RAS guanyl releasing protein 1 (calcium and DAG regulated)	RASGRP1	AF081195	20.2	2.4	2.7
insulinoma-associated 1	INSM1	M93119	20.2	4.5	6
nuclear factor of activated T-cells, cytoplasmic, calcineurin-	NFATC1	U08015	20.2	1.8	0
cyclin K	CCNK	X84721	202		0
clusterin (complement lysis inhibitor, SP-40,40, sulfated	CLU	AI982754	20.2		32
glycoprotein 2, testosterone-repressed prostate message 2,					
		AI674404	20		σ-
glutamine-fructose-6-phosphate transaminase 2	GFPT2	AB016789	19.9		4 4
hypothetical protein		AI346913	19.8	1 1	4
		AA975511	19.7	1	2
		AI810399	19.7	5.7	3.4
discs, large (Drosophila) homolog-associated protein 1	DLGAP1	AB000277	19.6	2.1	0.1
		AI373122	19.6	0.1	1.1
heat shock 70kD protein 1B	HSPA1B	W28645	19.5	0	2.2
BCL2/adenovirus E1B 19kD interacting protein 3	BNIP3	AF002697	19.5	5.8	0.2
lymphocyte antigen 94 (mouse) homolog (activating NK-receptor ; NK-p46)	LY94	AJ001383	19.3	0	8.0
intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ICAM1	M24283	19.2	5.5	1.4
		AI800735	19.2	0.2	0
KIAA0635 gene product		AA910186	19.2	1.5	3.4
		AA195108	19.2	1.3	2
chondroitin sulfate	CSPG2	X15998	19.1	1.3	4.6
		AA284560	19	2.9	1.5
		AI291314	18.9	3.7	1.5
		KIAA0481 gene product ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR RAS guanyl releasing protein 1 (calcium and DAG-regulated) Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated 1 Insulinoma-associated protein 1 Insulinoma-fructose-6-phosphate transaminase 2 Insulinoma-fructose-6-phosphate transaminase 2 Insulinoma-fructose-6-phosphate transaminase 2 Insulinoma-fructose-6-phosphate transaminase 2 Insulinoma-associated protein 1 Insulinoma-associated protein 1 Insulinoma-associated protein 1 Insulinoma-associated protein 1 Insulinoma-associated protein 1 Insulinoma-associated protein 2 Insulinoma-associated protein 2 Insulinoma-associated protein 3 Insulinoma-associated protein 3 Insulinoma-associated protein 3 Insulinoma-associated protein 3 Insulinoma-associated protein 3 Insulinoma-associated protein 3 Insulinoma-associated protein 3 Insulinoma-associated protein 3 Insulinoma-associated and Insulinoma-associated protein 3 Insulinoma-associated protein 3 Insulinoma-associated Insulinoma-associated protein 3 Insulinoma-associated Insulinoma-associated protein 3 Insulinoma-associated Insulinoma-ass	KIAA0481 gene product ELL.RELATED RNA POLYMERASE II, ELONGATION FACTOR RAS guanyl releasing protein 1 (calcium and DAG-regulated) Institutional associated 1 Inclear factor of activated T-cells, cytoplasmic, calcineurin RAS guanyl releasing protein 1 (calcium and DAG-regulated) Institutional associated 1 Inclear factor of activated T-cells, cytoplasmic, calcineurin RATC1 Gependent 1 CCNK Cyclin K Cyclin K Cyclin K Cyclin K CCNK Gyclin K CCNK Gyclin K CCNK Apolipoprotein 2, testosterone-repressed prostate message 2, apolipoprotein 3, Control apolipoprotein 1B BCL2/adenovirus E1B 19kD-interacting protein 3 BCL2/adenovirus E1B 19kD-interacting protein 3 BCL2/adenovirus E1B 19kD-interacting protein 3 BCL2/adenovirus E1B 19kD-interacting grotivating Nk-receptor; Intercellular adhesion molecule 1 (CD54), human rhinovirus RIAA0635 gene product Chondroitin sulfate proteoglycan 2 (versican) CSPG2	RELATED RNA POLYMERASE II, ELONGATION FACTOR C75510	AB007950 20.4 1.

solute carrier family 12 (potassium/chloride transporters),	SLC12A7	AI816843	18.9	1.9	0
member 7					
novel retinal pigment epithelial gene		AI973108	18.7	5.4	4.1
hypothetical protein DKFZp434F2322		AI632223	18.6	2.7	0.3
Alg5, S. cerevisiae, homolog of		AA425251	18.6	4.7	3.8
		AL050227	18.5	0	4.8
CD44 antigen (homing function and Indian blood group system)	CD44	L05424	18.5	9.0	
integrin, beta 8	ITGB8	A1129512	18.5	2	9.0
		AW014148	18.5	6.0	0.4
interleukin 2 receptor, alpha	IL2RA	X01057	18.4	0.2	1.8
hypothetical protein FLJ23231		AA011633	18.3	2.1	2.2
guanylate cyclase 1, soluble, alpha 3	GUCY1A3	Y15723	18.2	3.1	3.6
		AI768334	18.2	0	6.0
		AI050855	18.1	1.9	1.6
		AA999894	18.1	2.5	9.9
sterile alpha motif and leucine zipper containing kinase AZK		N95341	17.4	0.5	0
		AI982723	17.4	1	0.2
hypothetical protein FLJ20373		AW021103	17.4	9.0	5.2
KIAA0942 protein		AI073412	17.4	0.2	5.1
		AI991958	17.2	0.4	1.2
	HSD11B1	M76665	17.2	3.2	2.5
inositol 1,4,5 triphosphate receptor, type 3	ITPR3	001062	17.1	0.2	6.3
hypothetical protein FLJ13868		AI814485	17.1	3.4	1.7
		AI951161	17	1.9	3.4
hypothetical protein FLJ21162		AL046389	17	0.4	0.3
hypothetical protein FLJ20559		AA478923	17	3.7	1.4
		AA195829	16.9	0.2	0.7
		AI298599	16.8	5.1	2.9
single-stranded-DNA-binding protein		AL080076	16.7	4.5	3.8
KIAA0062 protein		D31887	16.6	0	2.3
solute carrier family 21 (organic anion transporter), member 11	SLC21A11	AA053855	16.6	2.5	0
		AI720898	16.6	6.1	1.3
HIV TAT specific factor 1	HTATSF1	AA581365	16.4	6.4	4.2
	solute carrier family 12 (potassium/chloride transporters), member 7 member 7 Megs, 5. cerevisiae, homolog of Alg5, 5. cerevisiae, homolog of copy for the family pigment epithelial gene hypothetical protein Dresport, alpha integrin, beta 8 integrin, beta 8 integrin, beta 8 integrin, beta 8 interleukin 2 receptor, alpha 3 guanylate cyclase 1, soluble, alpha 3 kypothetical protein FLJ23231 kypothetical protein FLJ20373 KIAA0942 protein hydroxysteroid (11-beta) dehydrogenase 1 inositol 1,4,5-triphosphate receptor, type 3 hypothetical protein FLJ21162 hypothetical protein FLJ21162 hypothetical protein FLJ20559 single-stranded-DNA-binding protein kilAA0062 protein solute carrier family 21 (organic anion transporter), member 11 HIV TAT specific factor 1	nuly 12 (potassium/chloride transporters), SLC ment epithelial gene tein DKFZp434F2322 se, homolog of tein DKFZp434F2322 se, homolog of tein FLJ23231 e 1, soluble, alpha tein FLJ23231 n n tif and leucine zipper containing kinase AZK tein FLJ20373 n tein FLJ20373 n tein FLJ20373 tein FLJ20373 tein FLJ20373 mily 21 (organic anion transporter), member 11 SLC mily 21 (organic anion transporter), member 11 tein FLJ20579	mily 12 (potassium/chloride transporters), SLC12A7 Then tepithelial gene Tein DKFZp434F332 Se, homolog of Tein FLJ2333 E1, soluble, alpha Tit and leucine zipper containing kinase AZK Tein FLJ20373 Thin the fluttor and leucine zipper containing kinase AZK Tein FLJ20373 Tein FLJ20373 Thin the fluttor and leucine zipper containing kinase AZK Tein FLJ20373 Thin fluttor alpha Tit and leucine zipper containing kinase AZK Tein FLJ20373 Thin fluttor and leucine zipper containing kinase AZK Tein FLJ20373 Thin fluttor and leucine zipper containing kinase AZK Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipper CD44 Tit and leucine Zipp	mily 12 (potassium/chloride transporters). SLC12A7 A 1816843 mily 12 (potassium/chloride transporters). SLC12A7 AI816843 nent epithelial gene tein DKFZp434F2322 A445521 se, homolog of tein DKFZp434F2322 A445521 oming function and indian blood group system) CD44 L05424 eptor, alpha ILCRB AI129512 eptor, alpha AW01448 tein FLJ23231 AW01143 tein FLJ23231 AV01657 tein FLJ20373 AV05341 tein FLJ20373 AV053923 tein FLJ20559 AA178923 tein FLJ20559 AA178923 tein FLJ20559 AA178928 ANB AND AND AND AND AND AND AND AND AND AND	Name

Figure 12K

55692_at	hypothetical protein FLJ11656		DCPCCW.	16.1	13	6
75007_at			AI079327	16.4	0.00	4.7
80084_at			A1889019	10.01	0.0	1.0
35275_at	adaptor-related protein complex 1, gamma 1 subunit	APIGI	AI 050025		0.0	0.8
49353_at	hypothetical protein FLJ20216		70070014	10.5	0.0	0.3
745 at	transcription elongation factor A (SII) 2	101	7577	10.1	0.3	0
55081 at	hypothetical profein hA3951 14 2	ICEAZ	D50495	15.8	4.9	1.2
η.			_	15.8	3.3	0
	inhibitor)	9	M59499	15.5	3.2	1.2
70631_at			VC000004			
73800 at			A402024	15.4		0
80408 at	ribosomal protein 1 37a		AI890347	15.2	2.3	0.0
64879 at	honoran cultate G.O. cultaternateure	RPL3/A	AA961504	15.2	0.3	0
51923 34	sobjection kinds 1	HS6ST	AA206625	15.2	0.2	0
77567 24	Springosnie Kinase 1	SPHK1	AI769914	14.8	m	16
17504 at			AI694316	14.7	0.5	0.0
/0034 at			AW007125	14.6	1 3	1.2
44008 at			AI921877	14.6	7-6	5.1
34 / 26 at	calcium channel, voltage-dependent, beta 3 subunit	CACNB3	U07139	14.5		0.7
44/28_at			AI819734	14.5		0.0
36980_at	proline-rich protein with nuclear targeting signal		003105	14.4	000	2.7
4253/_at			AA281239	27.3	2.7	4.0
/9494_at			177813	17.0	200	0.0
54077_at	hypothetical protein FLJ10430		W18181	2.4.5	5.0	1./
1440 s_at			X83490	14.2	D. C.	6.5
/2541_at			AIGEORGE	7	7.0	2.8
57833_s_at	NY.REN.45 antigen		AWOO1803	17	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	1.6
5/5/9 at			AI680721		1.1	
8/95/_r_at			AA513538	139	0 4	0.4
4/5/8 at			AA160156	130	0)-	0.0
58935_s_at	hypothetical protein MGC5363		AWOORAS	13.7	1,	٥
71889_at			AIGEBORE	13.7	1.1	2.5
37393_at	hairy (Drosophila)-homolog	200	10011	13.7	0.0	9.0
88283_at		ואנו	119314	13.6	0	9.0
45606 at			AI961/40	13.6	1.8	0.5
38463 c at	adenosine monophosphato dosmissos (instanto)		AA846692	13.6	0	0.5
Ta c COLLOC	(aucilosine illoilophosphate deaminase (isotorm E)	AMPD3	U29926	13.6	2.6	0.1

Figure 12L

77134 at			AA939344	13 5	V 2	
566/1_at	lipase, endothelial	LIPG		13.5		1 2
46043_t_at			AW009767	13.5	-	1.0
54968_at		HMGCS1	AI 048840	12.5	1.1	3.0
44795_at	STAT induced STAT inhibitor.2		A1129818	13.4	1 1	
6/329_at	hypothetical protein FLJ22833		AA610377	133	1 1 2	7.0
51030_at			AA843962	13.3	1 9	0.0
46238_at			AI193110	13.3	1.0	2.2
66903 r at			A1002222	132	00	000
42803 at	E2F transcription factor 5, p130-binding	E2F5	AI377305	13.2	3.5	7.0
6236/ at			AI220446	13.1	0.3	2.5
25102 s at	CGI-22 protein		AA627551	13.1	26	010
35992_at	musculin (activated B-cell factor-1)	MSC	AF087036	129	ο α	
3/951_at	deleted in liver cancer 1	DLC1	AF035119	129	0,0	7 0
39120 at	metallothionein 1L	MT1	AA224832	120		2.0
65281 f at			H22954	12.0	0.1 0.2	0.3
1573_at	platelet-derived growth factor beta polypeptide (simian sarcoma	POCED	M12702	12.0	, ,	1.2
	viral (v-sis) oncogene homolog)	5	IN1127.03	12.8	0	0.5
72558_at			AIRER718	120		
52850_at	KIAA1151 protein		AA128296	120	1.0	0.7
39857_at	syntaxin 11	CTV11	0000000	16.0	6.0	4.7
57094_at	transmembrane protein 2	TANCAN	A1100201	12.7	5.6	12.9
41385 at		INIEMZ	A1189381	12.7	1.9	2.1
75796 at			AB023204	12.6	1.1	1.9
76037 at			AI028528	12.5	1.3	0.6
76688 at			W86659	12.5	2.5	0
38840 s at	profilin 2		AI312606	12.5	0	1.3
64959 at		PFNZ	L10678	12.4	0	1.2
45266 at	hypothetical protein El 190977		AI733528	12.4	9.0	1.1
83364 at	hypothetical protein DKE7-K47-D00c		AI818338	12.4	0.5	0.5
36742 at	ring finger protein O		AW022249	12.4	1.7	C
39581 at	Costatin A (stefin A)	RNF9	U34249	12.3	0	4
55400 at	major histocompatibility complex place in	CSTA	AA570193	12.3	0.3	1.2
56234 r at	The second parently complex, class I, r	HLA·F	AI732773	12.3	4.2	5.8
60127 24			AA053401	12.3	2	C
1217			AA157886	12.3	6.0	α.

Figure 12M

53053_r at complement C1r.like 550320_g at 58412_at retinal degeneration 87114_at 56252_at 76493_at 60544_at 33767_at neurofilament, heavy 81351_at 76515_at hypothetical protein 36197_at chitinase 3.like 1 (ca	를 F		N91560	0 0 0		
ज व व व व व व व व व व व व व व व व व व व				12.3	17.0	
g at at at at at at at at at at at at at			AA160945	121	1 -	
at at at at at at at at at at at at at a			AI497833	12.1	1.1	X. I.
at at at at at at at at	Teration B Deta		AA807607	11.0	0.0	2.7
at at at at at at at at at at at at at a			AW001674	11.0	7.0	
at at at			4/0010/4	11:3	8. 0	0.5
at at at			4100100	211.3	2	1.3
at at at			A1393100	11.7	2.4	0
at at	t heavy polypeptide (2004)		N30562	11.7	0.7	3.7
at at		NEFT	X15306	11.6	0	0.3
Π	protein DVEZ-EGGO1404		AA527332	11.6	1.8	0
T	₹I⊷		AA777011	11.6	5.5	0
17 XX 71	ne 1 (cartinage grycoproteill-39)	CHI3L1	Y08374	11.5	1.2	0.7
1084 at wahl Aboleon m			AA913703	11.5	1.1	2.2
	i niutilie leukemia viral oncogene nomolog 2 (arg, ted gene)	ABL2	M35296	11.3	1	7.9
	ne product		1071701	-		
	phila) homolog 2	NOTCHO	VVV024050		0.0	0
		7	N024300	11.3	1:1	0
84950_at			47/261	11.2	2.8	0
64937 at popeve protein 2	in 2		A1581868	11.2	0	1.6
at	drogenase		AA044/32	11.2	0.5	0.0
s at		SORD	L29254	11.2	0	0.4
1919 at vay 1 oncogene	ne	***************************************	AA91//34	11.1	4.8	1.9
at		VAVI	X16316	11	0.4	0
54961 r at			R67370	11	3.1	2.7
53442 at			AA203620	10.9	4.9	1.1
39776 at KIAA0623 gene	product		R99605	10.9	3.1	8.1
	4		AB014523	10.8	1.4	1
1211 s at CASP2 and BIBK1	IPK1 domain containing		AA035736	10.8	1.3	6.4
	in vit domain containing adaptor with death domain	CRADD	U84388	10.7	0	0
_at	core binding factor, runt domain, alpha subunit 2; translocated to.	CBFA2T3	AB010419	10.6	1.5	1.3
36451_at			AI743299	10.6	3	C

Figure 12N

entors:

			CO407044 VIVIOR	0.0	0.2	0.1
63093_at			R06655	10.6	0.2	0.7
34713_at kinesin fa	kinesin family member 3B	KIF3B	AB002357	10.4	1.2	0.8
62711_at			AW021631	10.4	0.5	2.9
59488_at ADP-ribo	ADP-ribosylation factor-like 4	ARL4	Ai142552	10.4	1.4	3.2
	guanine nucleotide binding protein (G protein), gamma 2	GNG2	AA738022	10.4	0.2	0.7
2036_s_at CD44 an	CD44 antigen (homing function and Indian blood group system)	CD44	M59040	10.3	0.4	0
at			AW044646	10.3	9.0	0.5
1	KIAA0833 protein		AI796797	10.3	0	1.2
	bone morphogenetic protein 6	BMP6	M60315	10.2	0	2.3
59126_at			AI660548	10.2	4.2	8
	ADP-ribosylation factor-like 1	ARL1	L28997	10.1	1.4	0.1
	KIAA0833 protein		AB020640	10.1	0.5	1.8
	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	ITGB3	M35999	10.1	1.4	1.8
	spermine synthase	SWS	AD001528	10	1.2	1.1
74478_at			A1808640	6.6	1.8	0.7
<u></u>			R05809	6.6	0.4	0
	PCTAIRE protein kinase 1	PCTK1	X66363	8.6	8.0	0.2
37203_at carboxyl	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	CES1	L07765	9.6	2.2	0.3
58404_at			AA487503	8.6	6.0	18
85610_at			AI913562	8.6	2.4	1.5
at			AI686521	8.6	1.4	1.5
at hypothet	hypothetical protein FLJ11336		R51067	8.6	3.1	1
_s_at RAB9, m	RAB9, member RAS oncogene family	RAB9	A1934576	8.6	4	2
at hypothet	hypothetical protein LOC57333		AI797684	8.6	0	0.7
	- 1		AA281494	9.6	0	2
	small protein effector 1 of Cdc42		H10816	9.7	4.8	4.9
			F36583	9.7	2.1	2.9
ᇹ			AA442301	6.7	6.0	0
_	secretory leukocyte protease inhibitor (antileukoproteinase)	SLPI	X04470	9.6	9.0	2.1
ig.	ets homologous factor	EHF	AI554809	9.6	0.3	0
	protein tyrosine phosphatase, non-receptor type 1	PTPN1	M33684	9.5	2.1	3.5

69629_at			AI/44/11	9.5)	1.4
70377_at			AI753158	9.5	1.4	1.9
38942 r at	AD024 protein		W28610	9.4	9.0	1.8
39976 at	hypothetical protein from EUROIMAGE 783647		AL050087	9.4	4.1	5.9
77831_at	phosphodiesterase 4D, cAMP-specific (dunce (Drosophila)-	PDE40	AI093171	9.4	1	0
	homolog phosphodiesterase E3)					
50932 at			AI745136	9.4	1.6	2.9
54146 at			AA167624	9.4	1.1	2.7
40919 at	somatostatin receptor 2	SSTR2	M81830	9.3	1.5	2.9
34800 at	DKF2P58601624 protein		AL039458	9.3	0	0.1
91992 at	novel Ras family protein		AI382139	9.3	1.2	
53398 at			AA127950	9.3	2.3	0
76024 at			AI052586	9.3	2.2	1.7
47069 at	hypothetical protein FLJ20185		AA533284	9.3	1.3	1.6
46303 at			AA524250	9.3	9.0	1.7
47943 at			AI916838	9.5	0.3	1.6
61263 at			A1568596	9.5	3.5	0
46260 at	claudin 1	CLDN1	AI452474	9.2	6.7	2.4
90218 at			N50080	9.5	1.5	0
33452 at	plasminogen activator, tissue	PLAT	M15518	9.1	0	3.2
37338_at	phosphoribosyl pyrophosphate synthetase associated protein 1	PRPSAP1	D61391	6	1.4	0
63357_at			AI290954	6	0.2	0.4
47414 at			W91949	σ	0.1	9.0
41202_s_at	conserved gene amplified in osteosarcoma		AF000152	6.8	1.5	0
86806_at			AA962815	8.9	2	1.4
56372_at			AI078177	8.9	0.4	1
39878_at	protocadherin 9	РСДН9	AI524125	8.8	0.4	1.8
40458_at	signal transducer and activator of transcription 5A	STAT5A	U43185	8.8	6.5	1.9
33377_at		Z :>	X03168	8.8	1.7	2.8
83381_at	artemin	ARTN	AI695822	8.8	0	2
59830_at			AA995120	8.7	2.3	1.3
72917 at			W19971	8.7	0.1	0
45564 s at			AI290237	8.7	1.4	0

Figure 12P

intors:

tumor associated calcium signal transducer 2 at hypothetical protein FLJ20173 at adaptor-related protein complex 3, sigma 2 subunit at adaptor-related protein complex 3, sigma 2 subunit at adaptor-related protein complex 3, sigma 2 subunit beroxisome biogenesis factor 13 at peroxisome biogenesis factor 13 BCL3 at DKFZP566D133 protein Sat Breell CLL/lymphoma 3 at Cyclin dependent kinase inhibitor 2A (melanoma, p16, inhibits CDKN2A CDKN2A at caspase recruitment domain 4 at hypothetical protein at hypothetical protein at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7	AKHU LZ508	700		
Apporthetical protein FLJ20173 Complement component Last		J04152 8.6		
Appothetical protein FLJ20173	NT ALOS	AL080213 R 6	6	0
at interleukin 7 at peroxisome biogenesis factor 13 at peroxisome biogenesis factor 13 at peroxisome biogenesis factor 13 at peroxisome biogenesis factor 13 at peroxisome biogenesis factor 13 at peroxisome biogenesis factor 13 at DKFZP566D133 protein B.cell CLL/Iymphoma 3 at Z.:3-cyclic nucleotide 3' phosphodiesterase CDK4) at CDK4) at caspase recruitment domain 4 at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at twor necrosis factor (ligand) superfamily, member 7 at twor necrosis factor (ligand) superfamily, member 7 at two necrosis factor (ligand) superfamily, member	AA5	ά	.7	1.9
at interleukin 7 at interleukin 7 at interleukin 7 at peroxisome biogenesis factor 13 at peroxisome biogenesis factor 13 at DKF2P566D133 protein S_at B cell CLL/lymphoma 3 at Z;3·cyclic nucleotide 3' phosphodiesterase CDK2) at caspase recruitment domain 4 at hypothetical protein at hypothetical protein FLJ10450 B_at tumor necrosis factor (ligand) superfamily, member 7 at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at thypothetical protein at hypothetical protein at thypothetical protein at thypothetical protein at thypothetical protein at KIAA0635 gene product at trinucleotide repeat containing 3		o o		0
at interleukin 7 PEX13 at peroxisome biogenesis factor 13 at CLL/lymphoma 3 at 2'.3'cyclic nucleotide 3 phosphodiesterase CNP Cop(A4) at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at kiAA0635 gene product at kiAA0635 gene product at kiAA0635 gene product at kiAA0635 gene product at kiAA1181 protein at kiAA1181 protein at at kiAA1181 protein at at kiAA1181 protein at at kiAA1181 protein at at kiAA1181 protein at at kiAA1181 protein at at kiAA1181 protein at at kiAA1181 protein at at kiAA1181 protein at at kiAA1181 protein at kiAA1181 protein at at kiAA1181 protein	<u> </u>			0.0
at DKZPS66D133 protein at DKZPS66D133 protein at DKZPS66D133 protein BCL3 at Exell CLL/lymphoma 3 at CoDK4) at Caspase recruitment domain 4 at hypothetical protein at hypothetical protein at hypothetical protein at Hypothetical protein at Hypothetical protein at Hypothetical protein at Hypothetical protein at Hypothetical protein at Hypothetical protein at Hypothetical protein at Hypothetical protein at Hypothetical protein at Hypothetical protein at KIAA1181 protein at KIAA1181 protein at KIAA1181 protein at KIAA1181 protein at Alain	1_	0		1.1
peroxisome biogenesis factor 13 at DKFZP566D133 protein s_at Bcell CLL/lymphoma 3 at 2,3°cyclic nucleotide 3' phosphodiesterase CDK4) at caspase recruitment domain 4 at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at hypothetical protein at thypothetical protein at thypothetical protein at thypothetical protein at thypothetical protein at KIAA0635 gene product at KIAA0635 gene product at trinucleotide repeat containing 3 at KIAA1181 protein at trinucleotide repeat containing 3 at thypothetical protein at thypothetical protein at thypothetical protein at thypothetical protein at thypothetical protein at thypothetical protein at thypothetical protein at thinucleotide repeat containing 3 at thinucleotide repea		0		7.0
Sat Brcell CLL/lymphoma 3 Sat Brcell CLL/lymphoma 3 BCL3 at 2,3°cyclic nucleotide 3' phosphodiesterase Lat CDK4) at caspase recruitment domain 4 at hypothetical protein at hypothetical protein at hypothetical protein at thypothetical protein at KIAA0635 gene product at KIAA0635 gene product at KIAA1181 protein at KIAA1181 protein at thinucleotide repeat containing 3 at thinucleotide repeat containin	1	ο	0.1	4.4
Saf Brcell CLL/lymphoma 3 Sat Brcell CLL/lymphoma 3 BCL3 at Cyclic nucleotide 3' phosphodiesterase CNP CDKA2 at caspase recruitment domain 4 at hypothetical protein at hypothetical protein FLJ10450 Sat throughout the cyclase 1' soluble, beta 3 At KIAA0635 gene product at kinucleotide repeat containing 3 at KIAA1181 protein at KIAA1181 protein at A KIAA1181 protein at at KIAA1181 protein at at KIAA1181 protein at at KIAA1181 protein at at KIAA1181 protein at at A BOL (S. Cerevisiae) I soluble, beta 3 at at KIAA0635 gene product at at KIAA0635 gene product at at KIAA1181 protein at at A BOL (S. Cerevisiae) I soluble, beta 3 at at A BOL (S. Cerevisiae) I	1			20.0
at Core continued and an interesting at Core continued at Core core core core core core core core c		α		7 0
2'3'cyclic nucleotide 3' phosphodiesterase CNP -r_at cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDKN2A at caspase recruitment domain 4 at caspase recruitment domain 4 at hypothetical protein at hypothetical protein at thronor necrosis factor (ligand) superfamily, member 7 TNFSE7 at ERO1 (S. cerevisiae)-like at guanylate cyclase 1, soluble, beta 3 GUCY1B3 at KIAA0635 gene product at trinucleotide repeat containing 3 TNRC3 at trinucleotide repeat containing 3 TNRC3 at trinucleotide repeat containing 3 TNRC3 at at KIAA1181 protein at at All All B protein		0 0		6.0
at cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDKN2A CDK4) at caspase recruitment domain 4 at hypothetical protein at hypothetical protein FLJ10450 at tumor necrosis factor (ligand) superfamily, member 7 at EROI (S. cerevisiae)-like at guanylate cyclase 1, soluble, beta 3 at KIAA0635 gene product at kinucleotide repeat containing 3 at kinucleotide repeat containing 3 at kinucleotide repeat containing 3 at trinucleotide repeat containing 3 at at KIAA1181 protein at at kinucleotide repeat containing 3 at at trinucleotide repeat containing 3 at at at at at at at at at at at at at a	1		0.7	1.0
at caspase recruitment domain 4 at hypothetical protein at hypothetical protein at hypothetical protein at ERO1 (S. cerevisiae)-like at hypothetical protein at KIAA0635 gene product at KIAA0635 gene product at KIAA1181 protein at KIAA1181 protein at AI Innucleotide repeat containing 3 at AI Innucleotide repeat Containing 3 at AI Innucleotide repeat Containing 3 at AI Innucleotide repeat Containing 3 at AI Innucleotide repeat Containing 3 at AI Innucleotide repeat Containing 3 at AI Innucleotide repeat Containing 3 at AI Innucleotide repeat Containing 3 at AI Innucleotide repeat Containing 4 at AI Innucleotide repeat Containing 4 at AI	S CANCO	Ö		5.2
at caspase recruitment domain 4 at hypothetical protein at thypothetical protein at thypothetical protein at ERO1 (S. cerevisiae)-like at hypothetical protein at ERO1 (S. cerevisiae)-like at hypothetical protein at ROA40635 gene product at KIAA0635 gene product at trinucleotide repeat containing 3 at KIAA1181 protein at at KIAA1181 protein at at trinucleotide repeat containing 3 at at AAA1181 protein at at KIAA1181 protein at at KIAA1181 protein at at KIAA1181 protein	COKINA	AA909181 8.3		1.1
at hypothetical protein at hypothetical protein g_at hypothetical protein FLJ10450 g_at at EROI (S. crevisiae)-like at EROI (S. crevisiae)-like at hypothetical protein at hypothetical protein at KIAA0635 gene product at trinucleotide repeat containing 3 at trinucleotide repeat containing 3 at KIAA1181 protein at Alian brotein at trinucleotide repeat containing 3 at trinucleotide repeat containing 3 at at hypothetical protein at at rinucleotide repeat containing 3 at at rinucleotide repeat containing 3 at at rinucleotide repeat containing 3 at at rinucleotide repeat containing 3 at at rinucleotide repeat containing 3 at at rinucleotide repeat containing 3 at at rinucleotide repeat containing 3 at at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3 at rinucleotide repeat containing 3	0714	41797917		
at hypothetical protein at hypothetical protein FLJ10450 g_at at tumor necrosis factor (ligand) superfamily, member 7 at ERO1 (S. cerevisiae)-like at hypothetical protein at guanylate cyclase 1, soluble, beta 3 at KIAA0635 gene product at trinucleotide repeat containing 3 at trinucleotide repeat containing 3 at AIAA1181 protein at at AIAA1181 protein at at AIAA1181 protein	6/10		9.0	0
### Appointment of the protein FLJ10450 ##################################	AAO		1	1.6
8 at inported by Oten Publication (ligand) superfamily, member 7 TNFSF7 at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at EROI (S. cerevisiae)-like at hypothetical protein at guanylate cyclase 1, soluble, beta 3 GUCY1B3 at KIAA0635 gene product at trinucleotide repeat containing 3 TNRC3 at KIAA1181 protein at KIAA1181 protein at at KIAA1181 protein	AA53	AA534272 8.3	0.1	9.0
at tumor necrosis factor (ligand) superfamily, member 7 TNFSF7 at ERO1 (S. cerevisiae)-like at hypothetical protein at guanylate cyclase 1, soluble, beta 3 at KIAA0635 gene product at trinucleotide repeat containing 3 at KIAA1181 protein at KIAA1181 protein at AIAA1181 protein at AIAA1181 protein at AIAA1181 protein	AA62	AA626176 8.3	1.7	0.8
tumor necrosis factor (ligand) superfamily, member 7 at EROI (S. cerevisiae)-like at hypothetical protein at guanylate cyclase 1, soluble, beta 3 at KIAA0635 gene product at trinucleotide repeat containing 3 at KIAA1181 protein at KIAA1181 protein at at KIAA1181 protein at at AIAA1181 protein	AWOC	AW007803 8.3	1.1	17
at EMD recross factor (ligand) superfamily, member 7 TNFSF7 at EMOL (S. cerevisiae)-like TNFSF7 at EMOL (S. cerevisiae)-like All Record (S. cerevisiae)-like at guanylate cyclase 1, soluble, beta 3 GUCY1B3 at KIAA0635 gene product All KIAA0635 gene product at trinucleotide repeat containing 3 TNRC3 at KIAA1181 protein All All All Brotein at at All All Brotein All All All Brotein	88X X83	X83492 8.3	1 1	1
at EROI (S. cerevisiae)-like at Inypothetical protein at guanylate cyclase 1, soluble, beta 3 at KIAA0635 gene product at trinucleotide repeat containing 3 at KIAA1181 protein at KIAA1181 protein at at A1181 protein at A1181 protein at A1181 protein	12	α	1 8	1 4
at guanylate cyclase 1, soluble, beta 3 GUCY1B3 at guanylate cyclase 1, soluble, beta 3 GUCY1B3 at KlAA0635 gene product At trinucleotide repeat containing 3 TNRC3 at KIAA1181 protein At at at At	AL04	000		2.6
at RIAA0635 gene product at KIAA0635 gene product at trinucleotide repeat containing 3 at KIAA1181 protein at AIAA1181 protein	AA66	000	C	200
at KIAA0635 gene product at trinucleotide repeat containing 3 at KIAA1181 protein at Alax Alax Alax Alax Alax Alax Alax Alax				2.0
at KIAA0635 gene product at trinucleotide repeat containing 3 TNRC3 at KIAA1181 protein at at at at at at at at at at at at at a	A192		1.2	7.4
at KIAA1181 protein at KIAA1181 protein at All All All All All All All All All Al	AI37722		0.5	0.8
at KIAA1181 protein at KIAA1181 protein at at at at at at at at at at at at at a	_	AB014535 8		2.4
at KIAA1181 protein at at at at at at at at at at at at at a	_	AI743134 8		2.1
at himitor protein	AIS7	AI571525 8		O
at at	AA19	AA196096	0.8	C
at at	A107	AI076335 7.9		000
٩	86N	9.7 79789N		
	A101	AI016213 7.8		· C
45551_dt AV	AWOZ	AW022176 7.8		7.0

miventors:

65088_at	hypothetical protein FLJ21313		AI378584	7.8	2.1	2.9
51247_at			AI264314	7.8	0	0.3
77899_at			N30618	7.8	0.8	0.4
35410_at	small inducible cytokine subfamily B (Cys.X.Cys), member 6 (granulocyte chemotactic protein 2)	SCYB6	U81234	7.7	0	2.2
41971_at	proline-serine-threonine phosphatase interacting protein 2	PSTPIP2	AA102566	7.7	6.0	0.7
63360 at	membrane spanning 4-domains, subfamily A, member 7	MS4A7	AI829939	7.6	6.0	0
51242_at			A1123826	7.6	0.8	1.4
54916_at			AI459123	7.6	0	0.3
38748_at	adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)	ADARBI	U76421	7.5	0	0
51208_at	metal-regulatory transcription factor 1	MTF1	N46867	7.5	2.1	1.2
77081_at			AI792789	7.4	0	0
85493_at			AI553724	7.4	0.5	0.5
76387_at			AA772692	7.3	1	1.6
90462_at			AA806207	7.3	2.2	3.1
54413_at			W72267	7.3		1.1
79207 r_at			A1939637	7.2	3	2.2
43697_at			AA504249	7.2	3.3	3.4
70204_at			R70880	7.2	0	0
49811_s_at	mitochondrial solute carrier		AA906314	7.2	0.8	1.3
82344_at			AI373048	7.1	0	0
82114_at			AA745458	7.1	0.8	0
51807_r_at			R38998	7	1.5	1.9
54016_s_at	uncharacterized hypothalamus protein HT011		AI248306	7	0.7	0
62125_at			N31710	7	0	0
46665_at			A1949392	7	0.2	0
91124_i_at	leukemia-associated phosphoprotein p18 (stathmin)	LAP18	AA156060	7	0	0
85911_r_at			AI285486	7	0.7	2.7
41402_at	DKFZP56400823 protein		AL080121	8.9	0	0
73989_at	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5	CLECSF5	A1653660	8.9	0	O
86814_at			A1620731	6.8	9.0	0.8
72050 at			AI147202	6.8	0.5	0
44827_s_at	_s_at hypothetical protein STRAIT11499		AW016331	6.8	0	0

Figure 12R

1979 at integrin, alpha 6 1266 at integrin, alpha 6 1266 at integrin, alpha 6 12140 at 1210 at 1210 at 1220 at 1233 at 1233 at 1223 at 1233 at	d protein kinase 8	MAPK8	AI052039	6.8	1 9	7.0
	aining protein		AF054589	8.9	C	ò
			AA877462	8 9	2 1	
		ITGA6	X53586	6.2	1 7	4.0
			AA765781	6.7	0.0	000
			AI820621	6.7	0	3.0
			AI267607	9.9		37
			W18190	9.9	0.8	0 6
	a)	TPM2	M12125	6.5	С	0 0
			AL042362	6.5	1.7	800
			AI984040	6.4		0 0
			AI476732	6.4	0.3	5
	glutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	X66435	6.3	0	7.0
	-activated, alpha 1 catalytic subunit	PRKAA1	AB022017	6.3	0.3	27
			AI217191	6.3	0.1	
	- 1		AA923345	6.3	0.8	
	1 FLJ20139		AI860687	6.3	С	
	nase 17b (apoptosis-inducing)	STK17B	AB011421	6.2		1 4
	group IVC (cytosolic, calcium-independent)	PLA2G4C	AF058921	6.2	1	
			AA420590	6.2	0.3	0.6
		- 1	AI204439	6.2	3.7	1.4
		INS	AW007778	6.2	1.2	2.1
	-1		AB024705	6.1	0	0.9
	El 110000	CDYL	AL050164	6.1	0.8	0.4
	FI 120630		AI765280	6.1	0	0
	arminal orthograph 12 (this it it it		AI749464	6.1	1	0
oxidoreductase UCPA chromosome 11 open reading frame 1 porcupine small nuclear ribonucleoprotein polypeptide hynothetical protein El 12438	eininal esterase L3 (ubiquitin thiolesterase)	NCHL3	AA746355	9	0.3	0
chromosome 11 open reading frame 1 porcupine small nuclear ribonucleoprotein polypeptide hynothetical protein El 12438	AG.		400000			
porcupine small nuclear ribonucleoprotein polypeptide lynonthetical protein El 11 24 38	en reading frame 1	100010	A1360294	٥	9.0	0
small nuclear ribonucleoprotein polypeptide		CI SURF4	W60695	9	0.2	0
hynothetical protein FI 112438	O - Fitnessian minimum	_	AA206621	9	-1	0.8
	El 113/30	SNRPG	AA234175	9	0.8	0.5
יין שמייים איים איים	11212400		AI979240	9	6.0	0
19.CZCO+			AL120741	9	0.7	C

Figure 12S

35,000,00		SCN1B	L10338	5.9	С	~
32330 at			4B007947	5.9		je
30034 at	B15 ramily, member 2	BTG2	U72649	5.9	00	0.00
5/364 at			AA031731			000
			AF052169			
30081_s_at	chromosome 21 open reading frame 18	C210RF18 /	AB004848	5.8		ò
09001 at			AI872476	5.8	0	
38038 at	lumican	LUM	U21128	5.7	0	C
3305 - 1			AA701259	5.7	C	
43390 s at	Unau (HSp4U) homolog, subtamily B, member 5	DNAJB5 A	AW006148	5.7	0.1	2.5
1856 at	Wra swip ration foodstall constant		W07089	5.7	2.1	
63251 c at	Vici avian i cuculoci idoni ellosis viral oncogene nomolog	REL	X75042	5.6	4.1	5
46727 at		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	AA904828	5.6	1.3	9.0
57000 f at	u	_	AI146850	5.6	6.0	
35182 f at		MGEA5	AI453779	5.6	0.1	
74006 at	האסמונים אוסופון ברסדוסטאה		W25874	5.5	O	
55280 at	District NG DNA math. disc.		AI984623	5.5	0.7	
73601 at	Parative No. Dividing International Parative Internative Internative Internative Internative Internative Internati		AI016585	5.5	5.1	10.4
71516 r at			AI885677	5.5	0	0.2
31633 0 24	aine finance protein JEO and James James		240202	5.5	0.3	2
41275 at	11 233,	ZNF259P	295118	5.4	0	0.2
2045 s at	hemocoletic cell kinger	E2F5	U31556	5.4	0	0.7
48436 at	Herriopoletic cell kinase	HCK	M16592	5.4	0.8	9.0
75064 at	MODS protein		AI922968	5.4	0.1	2.4
51151 i at	hynothetical protein	4	AA910520	5.4	0.7	1.1
ı ``			AI983052	5.4	1	0.3
54799 at	plutaminase	- 1.	N71632	5.4	0.3	4.4
57042 at	Similar to Caenorhabditis alegans protein 04201 0	GLS	W72090	5.4	0	
49298 at			W74749	5.4	1.6	
86004 at		V	AW021968	5.3	9.0	0.1
830 at	Tax1 (himan Tidell leijkemia viris tuos I) bindina	4	AA767895		0.5	0.7
39950 at	acid sohingomyelinase like abosabadisatassa.	IAXIBP2	U25801	5.2	0.8	3.6
119 at	realization protein 42 (32kD)		Y08136	5.2	0	0.9
38397 34	polymorase (DNA disorted) della 4	RPA2	J05249	5.2	0.5	9.0
יייייייייייייייייייייייייייייייייייייי	* C. C. C. C. C. C.	27	201001	C		

Figure 12T

04300 at			AI004417	2.5	0.5	0.0
8/493_at			AL042667	5.2		
47430_at			165857	5.5		
ä	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	COX7A2	L	5.2	0 0	
Т	KIAA0931 protein		4	5.1		
at	glutamınase	GLS	AB020645	5.1	0	
Ţ	IIDUIIN I	FBLN1	X53742	5.1	6.0	0.50
at			AA100654	5.1		
jar.	HZB histone family, member B	H2BFB	AI125923	5.1	0	0.6
T			AI590115	5.1	9.0	
at	absent in melanoma 1	AIMI	U83115	5	2.4	
	KIAA0170 gene product		AL041663	2	0	
T	hypothetical protein		AI889499	5	0	
ar	otein FLJ10521		AI913628	5	9.0	0
T	ancient conserved domain protein 4		A1655884	5	6.9	5.7
9 2			AI884621	2		0.5
, d	non-kinase cac4z effector protein SPEC2		AI825880	2	2.2	2.4
T	1000 to 1000 t		AA187437	2	0	0.5
100	Hornolog of yeast SPB1		AJ005892	4.9	1.3	0
T	אואאטטבש טרטנפווו		D21852	4.9	6.0	0
04360 at			AI691077	4.9	2.9	4
81083 at			AA019641	4.9	0.2	0.4
46668 at			AI248920	4.9	1.3	0.2
+	thyroid hormone recentor constitution		AA479835	4.9	0.8	6.0
┪~	insulin induced gene 1		X87613	4.8	1.1	0.9
Γ		INSIGI	9/8960	4.8	2.6	
64152 at			AI377910	4.8	9.0	0.4
76989 at			AA703523	4.8	0	0.4
64577 at			AI333655	4.8	0	0.3
T	adreneraic heta 2 recentor curioss		H60064	4.8	2.1	2.9
<u>+</u>	acid consume A lines	ADRB2	M15169	4.7	6.0	2
T	Schain fath coelleying A ligase 3		AA514342	4.7	0.8	
89955 at			AI280818	4.7	9.0	0.5
76610 at			AW020975	4.7	1	0
0010_at			A1 04 3934	7. 1		ľ

	binder of Arl Two		AA206524	46		
bbb9U at			H92909		0 4	
4/4/1_at			AAQ16868	2 4		1.0
44643_at			A162272A		0.4	0.9
55264 at hy	hypothetical protein SBBI67		A10337.34	4.0	0	0
			W/9937	4.6	0.5	0
80778 at			AA887112	4.6	0	6.0
T	ال مؤمرا المارية		AA179496	4.6	0	C
1	١.	ARRB2	AF106941	4.5	ας	
ā	tumor necrosis factor receptor superfamily, member 6	TNFRSF6	Z70519	4.5		
٦			A1243147	2 7	100	1.0
Ī	ras homolog gene family, member C	ARHC	A1860379	2 4	5 .	4.0
_	karyopherin beta 2b, transportin	2	A100003/3	4.0	-1	0.3
			AI8858/3	4.5	0	9.0
87673 at			AI652445	4.5	9.0	0.4
84407 r at			AI982610	4.5	9.0	00
54067 24			AI032906	4.5	9.0	
57700 at			AI982669	4.5	0.3	
1			AA433928	4.5	300	
1	monoamine oxidase A	MAOA	AA420624	4.4		0.0
35007_at			AC004940	4.4	0.5	
04991 at			AI762686	4.4	200	0.5
823/2 at			AA907150	4 4	0	
70379 at			AI744361	4.4	1.0	0.0
/404/ Lat			AW023188	4 4	2.0	0.7
48696 at			H48142			5.0
ij			A1031837	1 0	5 0	O
\neg	follistatin-like 3 (secreted glycoprotein)	FSTI 3	1176702	4.4	5 0	0.8
Ħ	mitogen-activated protein kinase 8	MAPKR	126318	5.4		5.7
39975_at Kl.	KIAA1080 protein; Golgi-associated, gamma-adaptin ear		AC002400	4.3	6.0	0.0
91181 at un	uncharacterized hematonoietic stem/progenitor collegation					
			AW044698	4.3	0	0
57414_at			AA878480	8		(
78392_at			H12966	0.0		2
85068_at			AI032972	7 7	0.2	0.3
80554_s_at			7,000,000	3 0		0
			AW004040	4.3	<u>σ</u>	2

Figure 12V

85293 2						
70202			AI468014	4.3	ō	0
10002 at			AI222295	4.3	1.6	0.3
43246 at			N66550	4.3	C	1 3
42700_i_at			T86284	4.2	0	1.3
338_at	activating transcription factor 6	ATF6	ļ۷	4.2	0,5	0.0
40813_at	solute carrier family 5 (inositol transporters), member 3	SICSAR	1_	7	1.4	0.1
35245_at	coagulation factor V (proaccelerin, labile factor)	FF	_1_	4.6	0 0	O
38005 at			_l_	4.6		0.4
56231 at	A Section of the sect		AJUUSSEE		0.5	0.5
33777 24			AA151678	4.2	-	0.2
33///at	uriornooxane A synthase 1 (platelet, cytochrome P450, subfamily V)	TBXAS1	D34625	4.2	-	0
73576_at			AIDRRODG	0 7	0	
91474_at	hypothetical protein FLJ10339		T77538	1:0	0.0	
63369_at			A192000F	4.6	0.0	0
53933 at			AIGSTONS	4.2	0.7	0.4
72960 c at			A12C2CIA	4.2	Ö	0.3
20627			AA199856	4.2	6.0	0
39027 dt	early endosome antigen 1, 162kD	EEA1	L40157	4.1	0	0.6
64298_r_at		ARRBZ	ARRB2 AW002000	4.1	0	
52656 s at	AIP-binding cassette, sub-family A (ABC1), member 1	ABCA1	AW019972	4.1	70	20
46122 at	NY-KEN-58 antigen		W52480	4.1	20	
46/36_at	ring finger protein 3	RNF3	AI301953	4 1	5	
77905_r_at			A1287423		1	0.6
33004 g at	NCK adaptor protein 2	NCKO	A1276502	1.1	0 0	0
41447 at	KIAA0990 protein	70004417	•	1	0.5	0.3
34823 at	dinentidylnentidase IV (CD26 adenosina desacrimana)	NIAAUSSU	4Ι	4	0.8	0.7
	protein 2)	4440	X60708	4	0.4	9.0
56854_f_at			A1742034			
90417_at	ribosomal protein S6 kinase, 90kD, polypeptide 5	RPSGKAF	A1382181			7.0
74763_at	cold shock domain protein A	AUSU	AI081577	\$ \		0
77232 at			//0000014	4	0.5	
63270 at			A1683999	4	0	0.2
85864 at			AA027103	4	0	2.6
73460 i at			AW023438	4	0.5	0.3
2000			H52268	4	0.2	0.8
30000 at			R12560	4	,	C
62876_at			AI393573	4	C	

Figure 12W

46316_at	hap0256 protein		AI494647	4	190	(
44675 at	xylosyltransferase II		AA043495	4		
46378_at			AA019557	4	0 6	
45597_at	intracellular membrane associated calcium-independent		AI093502	4		0.9
	phospholipase A2 gamma		1	+	<u></u>	0.
44809 at	hypothetical protein FLJ10803		AW008368	4	90	0
31516 f at	basic transcription factor 3, like 1	BTF3L1	M90354	3.9		
33/48 at	minor histocompatibility antigen HA·1		D86976			100
37912_at	TNF receptor associated factor 4	TRAF4	X80200	3.9	200	0
53790_at	actin-related protein 3-beta		AA772242	3.9	0 1	0
53358_at			AI279946	3.9	7.0	5 -
90173_at			AA203229	3.9	0.0	α (
54842 at			AI758780	3.9	0.7	οα
63069 at			AA521016	3.9	0 1	9
. 4			R10311	3,9	500	0 0
/31/1_at			AI953346	3.9	10	200
58913_at			AI916598	3.9	0 1	
			AA115471	6.6	α ς	
851// at	HZB histone family, member R	H2BFR	AI336982	3.9	0.4	C
48589 s at			N98652	3.9	0.3	1.0
46/32 at			AA075666	3.9	0 6	P. C
55289_at			W86056	3.9	0 3	000
3/929_at	immunoglobulin superfamily, member 4	IGSF4	AB017563	3.9	0.0	4.0
3/611_at	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	TNFRSF11B	AB008822	3.9	0	
			AI808755	30	2.0	
78611_at			AI378890	9.0	ά	
32/81 t at	KIAAU/28 prote		AA058762	38	900	1 0
33541_s_at	leukocyte-associated lg-like receptor 2	LAIR2	AA133246	888		0 -
28106 at			AA496024	3.8	0 3	100
			AI675886	3.8		9
45191 at		PPP1R6	AI680750	3.8	286	5
33261_at	laminin, gamma z (nicein (100kD), kalinin (105kD), BM600 (100kD), Herlitz junctional epidermolysis bullosa))	LAMC2	U31201	8. 8.		1.8
54049_at			AI652991	3.8	5.9	C
	!					3

Figure 12X

80967_at			AA703048	3.7		0.8	~
75265_at			AI821772	3.7	0.2	0.3	ī~
83640_at			AI948598	3.7		9.0	1.0
88805_at			AI761186	3.7	0.3	9.0	116
43120_at	myeloid/lymphoid or mixed-lineage leukemia3	MLL3	AI640514	3.7	1	0.8	. ~
34397_at	acid-inducible phosphoprotein		AF069250	3.6	6.0		1~
59119_at			AL038787	3.6	ō		T
68570_at			AA496390	3.6	0.3	0.2	Io.
81370_r_at			AA578920	3.6	0.7	0.7	I.
43383_s_at	hypothetical protein FLJ20727		AW000901	3.6	1.1	0.5	1.5
53354_at			AI668938	3.6	0		10
61314_at	KIAA0203 gene product		AL043152	3.6	9.0		<u> </u>
51817_at			AI991014	3.6	0.2	0.3	I~
53573_f_at			AA573272	3.6	2.7	3.9	<u></u>
41233_at	DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	AB014888	3.5	0.5		<u> </u>
37688 f at	Fc fragment of IgG, low affinity IIa, receptor for (CD32)	FCGR2A	M31932	3.5	0		10
74390_at			AI740774	3.5	0.5	9.0	<u>م</u> ا
76759_r_at			AI224653	3.5	1.1		<u>. </u>
58371 g at	hypothetical protein DKFZp761A052		AW003291	3.5	-		
69337_at			AI925894	3.5	9.0		
59619 at			AW007238	3.5	0.1	0.5	ייו
78473_at			AW051926	3.5	0.7	9.0	lιο
87678_at			A1270326	3.5	6.0		<u> </u>
75923_at			AI356228	3.5	-		\overline{a}
68633_s_at	hypothetical protein		A1650829	3.5	6.0	0.3	īm
33510_s_at	33510_s_at glutamate receptor, metabotropic 1	GRM1	U31216	3.4	0.5	0.9	٦٥
37956_at	aldehyde dehydrogenase 8	ALDH8	U37519	3.4	0	2.1	<u>_</u>
78618_at			AI889955	3.4	0.3	0.5	जा
54720_at			AA493420	3.4	10.4		N.
56662_at			AI627666	3.4	0.2		റ
67593_at			AI033153	3.4	0.5	9.0	ı.o
65662_at			AA019910	3.4	1.6	0.2	\sim
87481_at	hypothetical protein FLJ10698		AI951927	3.4	0	0	ري ا
45751 g at			AA528592	3.4	0.8)	ত
72954 at			AA883059	3.4	0.7	8.0	m

37819_at	hypothetical protein		AF007130 I	3.3	10	
40069_at		IIAS	AF051850	3 3	0 0	
41523_at	RAB32, member RAS oncogene family	RAB32	1159878	3.3	000	1
38037_at	diphtheria toxin receptor (heparin-binding epidermal growth factor)	DTR	1	(N)		1.3
80698_at			41051390	2.3		
81813_at			AI732902	3.3		
77275_at			A1693524		0 4	5 0
84163_at			AIR02667		0.0	0
48527_at			Al394438	5 6	0 0	1
64083_at			AL044092	3.3		
46126_at			AI498592	3.3	C	0
39004_at	hypothetical protein FLJ22512		AI432190	3.2	0.0	
32249_at	H factor (complement)-like 1	HFL1	M65292	3.2	60	0
40034_r_at	acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells.		D86864	3.2	0.8	0
84187_s_at	KIAA0729 protein		AI952956	3.2	α	C
63106_at			AA521504	3.2	0 0	
59594_r_at			A1632101	32	16	10
61697_at	ankyrin repeat, family A (RFXANK-like), 2	ANKRAZ	A1829903	3.5	0,00	
aţ	hypothetical protein FLJ12389 similar to acetoacetyi.CoA synthetase		AA640793	3.2	0.4	0.1
51995_at	cysteine knot superfamily 1, BMP antagonist 1	CKTSF1B1	AA912445	32		90
46583_at			A1640524	3.5	0	0.0
46652_at			AA524036	32		0.00
76844_at	hypothetical protein FLJ20608		AI797782	3.2	7 0	000
37274_at		BTD	AF018631	3.2		0.0
44801 s at	hypothetical protein FLJ21080		AI769154	3.2	0.3	0.8
/8889_at			H53956	3.2	0.6	
31884_at	hypothetical protein		L40399	3.1	200	00
40049_at		DAPK1	X76104	3.1	0.7	
452_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	SMARCC1	U66615	3.1	6.0	0
35703 at	platelet-derived growth factor alpha polypeptide	PDGFA	X06374	3.1	12	80
362_at	protein kinase C, zeta	PRKCZ	Z15108	3.1	C	0.0

Figure 12Z

81672 at			W38444	3.1	16 0	0
82436_at			AI242023	3.1	0	0.5
86391_at			W90335	3.1	1	0
68575_at			AA993965	3.1	0.2	0.1
89640_f_at			AI422384	3.1	0.4	0.7
72876_at			AI970209	3.1	0.3	0.7
45334_at	hypothetical protein, clone		AI628609	3.1	0	0
	Telethon(Italy_B41)_Strait02270_FL142					
44027_at			AI472026	3.1	0.7	0.2
62168_at	caspase 4, apoptosis related cysteine protease	CASP4	AI246018	3.1	6.0	0.2
57230_at			N98637	3.1	1	0.3
55067_at	KIAA1450 protein		N32192	3.1	2.5	0.7
35218_at	programmed cell death 10	PDCD10	•	m	6.0	0
34827_at	unc-51 (C. elegans)-like kinase 1	ULKI		m	0.3	0.5
33167_r_at	33167_r_at adenylosuccinate synthase	ADSS	ı	m	0.1	0.2
52207_at	protein phosphatase 4 regulatory subunit 2		W87465	m	0.8	-
88879_at			A1378857	m	0	0.8
67251_at			AI379741	m	0.2	0.5
70798_at			AI400344	m	0	0.4
85190_at			AA737437	m	0.7	0
86047_at			AA689588	m	0.3	6.0
46229_at			H23103	m	0.8	0
86346 at			44528523	č	60	0

Figure 12AA

affyID	Gene Name	Gene Symbol	GBA	Score_Ecoli	Score_Candida	Score_Influenza
38549_at			AF026941	484.1	612.	9 1149.5
35061_at	small inducible cytokine subfamily B (Cys. X.Cys), member 11	SCYB11	AF030514	655.1	844.8	3 729.7
909 g at	interferon induced protein with tetratricopeptide repeats 2	IFIT2	M14660	320.5		
431_at	small inducible cytokine subfamily B (Cys-X-Cys), member 10	SCYB10	X02530	152	390	
1214_s_at	interferon, beta 1, fibroblast	IFNB1	V00535	433.9	0.1	
61371_at	cyclin-E binding protein 1		AA555023	204	148	3 479.5
1715 at	tumor necrosis factor (ligand) superfamily, member 10	TNFSF10	U37518	8.99	179.7	
49148_at			AA947472	182.2	52	
425_at	interferon, alpha-inducible protein 27	1F127	X67325	565.9	7	
41048_at	phorbol 12 myristate 13 acetate induced protein 1	PMAIP1	D90070	159.8	8.6	3 408.5
908_at	interferon induced protein with tetratricopeptide repeats 2	IFIT2	M14660	22.9	34	
39945_at	fibroblast activation protein, alpha	FAP	009278	1.1		279.2
38299_at	interleukin 6 (interferon, beta 2)	11.6	X04430	1566.4	101	3 227.7
51972_at	ubiquitin specific protease 18	USP18	AA143794	114.4	158.3	3 218
1107_s_at	interferon-stimulated protein, 15 kDa		M13755	159	.98	3 213.8
1403_s_at	small inducible cytokine A5 (RANTES)	SCYA5	M21121	232.1	9.06	
1666_at	interferon, type 1, cluster	IFN1@	J00210	2.7		
37219_at	monokine induced by gamma interferon	MIG	X72755	261.6	704.2	182.7
675 at	interferon induced transmembrane protein 1 (9.27)	IFITM1	J04164	112.7	140.9	9 173.6
37944_at	GTP cyclohydrolase 1 (dopa-responsive dystonia)	GCH1	U19523	505.4	330.9	9 169
84893_at			AI446168	83.4	119.5	
91313_at			AA131041	84	77.5	5 157.1
38584_at	interferon induced protein with tetratricopeptide repeats 4	IFIT4	AF026939	179.4	153.2	
48864_at		1F127	A1991845	216.4	274	141.4
40159_r_at	neutrophil cytosol	NCF1	M55067	160.7	16	1 140.3
	disease, autosomal 1)					
70458 i at			AI654525	120.3	174.	3 127.2
1369_s_at	interleukin 8	IL8	M28130	2300.5	32.6	5 122.1
62330_at			AI075407	185.9	169.	121.9
269_at	2'-5'oligoadenylate synthetase-like	OASL	L40387	19.8	9	119.4
71174 r_at	KIAA1682 protein		AI921158	67.8	81.9	9 115.6
1520_s_at	endothelin 1	EDN1	105008	4444	283.5	5 113.7
41677_at	linterleukin 15 receptor, alpha	IL15RA	AF035279	278	99.5	5 111.4
41384_at	receptor-interacting serine-threonine kinase 2	RIPK2	AF117829	46.7		8 104.9

Figure 13A

1736_at	insulin-like growth factor binding protein 6	IGFBP6	IM62402	L 03		0.00
33304_at	interferon stimulated gene (20kD)	115620	1188967	207.0	0 000	104.8
38388_at	2',5'.oligoadenylate synthetase 1 (40.46 kD)	OACT	100000	327.2	7007	103./
52615_at		1000	M11810	38.7	54	103.7
39081 at	metallothionein 24		AA948319	425	188.4	94.9
33705 24		MIZA	AI547258	92.5	37.3	94.1
3	prospinates as 4b, camir-specific (dunce (Drosophila). homolog phosphodiesterase E4).	PDE4B	ר20971	232.3	51.8	92.7
36892 at	lintegrin, alpha 7	14 O H				
1097 s at	Chemokine (C.C motif) recentor 7	11GA/	AF032108	0.5	0	92.6
47013 at		ראין	L31584	276.6	100.6	88.3
36927 at	hynothetical protein expressed is set-elisa-		AA121732	0.1	3.2	86.3
71839 at	Special process, expressed in osteopiasi		AB000115	53.4	60.4	83.5
89884 24	metallothionoin 34		AA251131	111.4	76.5	82.8
62493 24	יויפנפווסנוווסופוון לא	MT2A	AI991852	138	45.1	82.3
50591 24			W68034	1.7	0	ν 1 2
17637			N95225	42.1	4 1	808
14034 01			AW052044	0	C	79.8
20014 4	pentaxin related gene, rapidly induced by IL-1 beta	PTX3	M31166	827.3	σ	2007
32614 at	Interferon-induced protein with tetratricopeptide repeats 1	IFIT1	M24594	50 5	70.7	0 24
70460 r at			AI654525	48.9	06	787
44399 at			H11732	1 6	20.5	7.0.7
13/2 at	tumor necrosis factor, alpha induced protein 6	TNFAIP6	M31165	5720	27.7	/5.4
63335_at	sorting nexin 10		A1285531	10.7	0.77	75.1
51546_at			41400001	127.4	22.8	74.2
49117 at	Interferon-induced protein 75, 52kD	11111	A1438301	113.1	77.9	73.9
89899 at	myxovinis (inflienza) resistance 2 homolog of	111/5	AI743445	26.5	24.4	71
2002 s at	RCI 2, related protein A1	MXZ	AW001846	54	64.3	70.9
1914 at	Cyclin A1	BCL2A1	U27467	547.8	65.2	70.5
41745 24	oci loci	CCNA1	U66838	57.6	16	70.3
36776 24	line leton Induced transmembrane protein 3 (1-8U)	IFITM3	X57352	49.6	74	60 09
2201 / O at	lymprocyte-activation gene 3	LAG3	X51985	132	1487	200
3/014_at	myxovirus (intluenza) resistance 1, homolog of murine (interferon. MX1 inducible protein p78)	MX1	M33882	53.6	82.5	69.2
879_at	myxovirus (influenza) resistance 2, homolog of murine	MX2	M20010		;	
48856_at	plastin 3 (T isoform)	55 10	0100014	1.10	19	69
57699 at			A1983923	42.8	2.1	68.4
87002 at			AA133285	12.1	31.2	65.3
			AI270476	14.8	28.7	63.7

Figure 13B

plactin 2 (Ticoform)	RBBPb	X85133	16.5	2.8	615
	PLS3	M22299	37	C	60.4
growth factor receptor-bound protein 10	GRB10	D86962	19	3.9	60.3
		AI825713	36.1	32.1	60.3
		T93893	3.6	10.2	50
		AI692445	15.4	6.3	2,000
0	HZAFO	L19779	64.6	21	57.1
mile lieutosis lactor (TNF Superfamily, member 2)	TNF	X02910	201.2	47.5	57
		AI733197	16.5	11.6	56.6
		AI742057	87.7	54.8	56
	PELI1	AL043980	85.4	6.2	54 5
	IRF7	U53831	49.2	41.5	54 1
Confide Subjectify A (Cys-Cys), member 20	SCYA20	U64197	943.4	28.3	53.8
		AI470600	0.7	0.1	53.5
Prostagrandin-enloperoxide synthase Z (prostagrandin G/H Synthase and cyclooxygenase)	PTGS2	004636	495.3	26.7	53.1
		AW008790	85.4	4.8	523
		Al161358	45.6	13.2	52.1
precessum nominology domain-containing, family A (phosphoinositide binding specific) member 4	PLEKHA4	AA521373	23.6	0.2	49.9
, interferon inducible, 67kD	GBP1	M55542	72.1	49.4	70.0
	MT1A	K01383	160.3	22.3	49.7
		AI936516	93.7	6	49.7
nbed tetratricopeptide repeat gene, X	XLO	AF000993	10.2	4.6	48.9
		AI823649	65	717	707
ement modulator	CREM	568134	7.7	8.5	40.7
0,1		AI040220	0.8	6	47.3
sinan inductione cytokine subramily A (Cys-Cys), member 8 (monocyte chemotactic protein 2)	SCYA8	Y16645	17.3	63.9	47.1
		N47894	2.2	14.6	47
		S62138	11.6	25	46.1
27 10 /=67 1/1=0)		AI566481	10.4	12.6	45.7
surthetase	CDKN1C	U22398	0.3	5.2	45.6
	WAKK	00000	0 0 0		

75093 at			A1807000	1.5	1	45.1
04/1/at			AI307804	0.5	0.7	45.1
60103 at			AI347618	15.7	26.5	44.6
24703 4 24	1		AI916948	46.9	13.9	44.2
50746 24	endogenous retroviral protease		M27826	4.3	0	43.9
100740 at			AA897516	71	20.1	43.9
37641 2t	_	AKAP2	AA101125	95.8	38.5	43.7
3/041_d1	interieron-induced, nepatitis C-associated microtubular aggregate protein (44kD)		D28915	68.5	51.1	43.6
			AA580047	37.3	200	000
870 f at	3 (growth inhibitory factor (neurotrophic))	MT3	M93311	90.7	15.1	43.2
90048 at	H3 histone, family 3B (H3.3B)	H3F3B	AA609509	0.4	C	7 27
20420 at			AI743005	15.4	14.3	42.7
39420 at			562138	11.6	20.2	42 5
34000 at	Jtase 2, mitochondrial	S0D2	X07834	141.3	63.1	42.3
50777 24	macrophage mynstoylated alanine-rich C kinase substrate		X70326	119.6	44.8	42
70777 at			AA766831	98.3	63.3	41 1
35763 24	ette, sub-ramily B (MDK/TAP), member 2	ABCB2	X57522	34.3	33	40.6
18885 at	Horrigo Doy (expressed in ES cells) I	HESX1	AF059734	19.4	20.3	40.2
62130 at	28th interference account of the		R61847	2.1	17.1	40
70097 at	esponsive protein		AA651720	37.5	34	40
84909 at	ore 2,3 dioxygenase	NDO	AI302268	99.2	29.8	39.9
33352 24			AA902134	29.7	55.3	39.5
37623 at	ily, internoer Q	HZAFQ	X57985	8.1	11.8	37.7
36804 at	Subjecting 4, group A, member 2	NR4A2	X75918	0.7	0.4	37.7
42048 at		NDO	M34455	91.3	36.9	37.7
35254 at	FI NOQ gene product		AA897644	4.4	2.5	37.2
44513 at			AB007447	31.4	36.2	36.8
82094 : 21			AI760613	68.8	81.5	36.6
1021 at	interferon gamma		AI810266	12.4	6.4	36.3
59215 at		FNG	J00219	289.9	58.8	36.2
649 s at	X.C motify recentor 4 (finite)		AI807018	151.1	63	36.2
32182 at	mount, receptor 4 (nasin)	CXCR4	L06797	53.5	40.7	36
J6104 at	ווואטרטטט אוטופווו		AB023182	3.6	C	35.9

Figure 13D

36085_at	guanine nucleotide binding protein (G protein), alpha transducing GNAT1 activity polypeptide 1	GNAT1	X63749	9	2.4	35.8
74402_at			A1924226	0	6.0	35.7
78482_at			AA705165	62.7	3.6	35.7
56608_at	endogenous retroviral protease		AW007800	2.7	1.6	35.5
56922_at			AA211158	32.7	18.2	35.1
36488_at	multiple 5	EGFL5	AB011542	0	0	35
38389_at	ite synthetase 1 (40-46 kD)	OAS1	X04371	36.5	71.8	35
39263_at	e synthetase 2	OAS2	M87434	26.7	28	34.8
56879_at	glucosamine) 3-0-sulfotransferase 3B1	HS3ST3B1	AA780067	67.6	2.5	34.8
58918_at			AA210892	176.1	24	34.8
35302_at	nuclear RNA export factor 1	NXF1	AJ132712	6.9	8.3	34.6
55625_at			N21579	2.2	3.6	34.4
63347_at	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related)		AA745981	8	1.7	33.9
81887_at			AI766826	27.8	10.9	33.8
86168_at			AA745606	2.2	99	33.8
57761_at			AI313253	161	50.6	33.7
45256_at	pre-B-cell colony-enhancing factor		A1271460	35.1	7.1	33,4
37406_at	microtubule associated protein, RP/EB family, member 2	MAPRE2	X94232	0	0.1	33.3
53588_at			AI967984	29.5	4.3	33.3
1580 f_at	interferon, alpha 4	IFNA4	M27318	0.5	0	33.1
32775_r_at	phospholipid scramblase 1	PLSCR1	AB006746	81.8	68.4	32.6
31622_f_at	metallothionein 1F (functional)	MT1F	M10943	101.8	13.1	32.6
72808_at			A1640523	16.1	6.1	32.6
45164_at	19A24 protein		W74027	189.7	74.5	32.5
31850_at	cysteine ligase, catalytic subunit	CCLC	M90656	1.3	7.4	32.4
35937_at	MHC class I polypeptide related sequence B	MICB	U65416	16.3	17.2	32.3
35682_at			A1133727	17.4	1.4	32.1
68328_at			AI475514	5.5	10.2	32.1
53809_at	lation initiation factor 5	EIF5	AA831658	1.4	2	31.5
54594_at	KIAA0668 protein		AA009571	78.6	23.3	31.3
39070_at	iila)-like (sea urchin fascin homolog like)	SNL	U03057	36.9	23.6	31
84661_at	protein 1; HQ0024c protein		AI436109	0	0	30.9
44825_at	RAD50 (S. cerevisiae) homolog	RAD50	AA126482	27.8	17.5	30.9

52878 at			141632502	0.3	127	0.06
1007			2005000	5	15./	30.3
50061_at			AI742085	0	3.5	30.8
52085_at			AA210833	33.1	21	30.6
40639_at	SCO (cytochrome oxidase deficient, yeast) homolog 2	SC02	AL021683	7.1	5.2	30.4
38908_s_at	REV3 (yeast homolog) like, catalytic subunit of DNA polymerase	REV3L	AL096744	0.3	0.2	30.2
	zeta					
38649_at	KIAA0970 protein		AB023187	14.2	7	30.1
38570_at	major histocompatibility complex, class II, DO beta	HLA.DOB	990E0X	84.2	55.5	30.1
37643_at	ımily, member 6	TNFRSF6	X63717	69	17.4	30
40852 at	tudor repeat associator with PCTAIRE 2		AB025254	20.7	18.9	29.9
52831_at			AI160811	14.7	0	29.8
53010_at			AI809925	28.6	4.2	29.8
73236 g at	guanylate binding protein 1, interferon inducible, 67kD	GBP1	AW014593	63.9	55.8	29.8
36094_at		TNNT3	M21984	11.6	0.2	29.6
2072_at		CDH12	L34057	20.9	3.1	29.5
56169_at			W55852	35	2.2	29.4
46187_at			AI344122	2.1	3.1	28.9
36223_at	splicing factor proline/glutamine rich (polypyrimidine tract- binding protein-associated)	SFPQ	AI827895	-	0	28.7
39114_at	decidual protein induced by progesterone		AB022718	68.6	26.6	28.6
44815_s_at			AA733119	92	11.1	28.6
36296_at	lymphotoxin alpha (TNF superfamily, member 1)	LTA	D12614	154	62.8	28.5
58957_at	hypothetical protein FLJ20637		AI620475	108.9	42.7	28.3
65867_at	FXYD domain containing ion transport regulator 6	FXYD6	AL043089	103.8	73.3	28.2
62495_f_at			AI433785	4.4	17.4	28.1
32114_s_at		ADORA2A	S46950	137.9	31	27.9
38111_at	chondroitin sulfate proteoglycan 2 (versican)	CSPG2	X15998	71.2	4.1	27.4
92145 at			AI703103	21.9	13.4	27.4
43848 s at			A1968465	9.1	8.8	27.3
669_s_at	interferon regulatory factor 1	IRF1	105072	50.6	35.4	27.2
53508_at			AI247103	124.7	84.6	27.2
39643_at	IA directed), gamma 2, accessory subunit	POLG2	U94703	1.2	0.1	27
595 at	tumor necrosis factor, alpha induced protein 3	TNFA1P3	M59465	65.1	11.4	26.6
42456_at			AA758732	1.3	2.2	26.6
63780_at	hypothetical protein FLJ11259		AA814195	51.4	19.6	26.4

10000						
الم	_	DNAJB4	AI741503	18.5	4.6	26.4
	metallothionein 1H	MT1H	R93527	91.6	9.4	26.1
37187_at	GRO2 oncogene	GR02	M36820	785	32	26.1
74689_at	lymphocyte-activation gene 3	LAG3	AW003135	77	77.5	26.1
36398_at			W28729	16.1	5 - 1	250.1
33413_at	protein tyrosine phosphatase type IVA, member 1	PTP4A1	AF051160	α	6	25.0
190_at	_	NR4A3	1112767	20.5	2 1/0	25.0
33113_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	U65093	5.8	0.47	25.7
40301_at			A1703188	3.2		2 30
64293_at			A1971000	7.6	0 0	25.0
41472_at	phorbolin-like protein MDS019		AL078641	22.9	41.0	25.0
427_f_at	interferon, alpha 10	IFNA10	V00551	4 6	- C	25.7
1370_at	Interleukin 7 receptor	IL7R	M29696	100 3	808	4.02
61368_at			N22849	6.0	0.00	25.3
48873_at	Gene 33/Mig-6		AI571452	5.2	3.4	25.3
44921_at			R42823	7.0		20.5
40004_at	sine oculis homeobox (Drosophila) homolog 1	SIXI	X91868	6.0	0 7	0 70
41992_at			A1002966	3.1	4 9	27.0
33236_at	retinoic acid receptor responder (tazarotene induced) 3	RARRES3	AF060228	00	55.0	24.2
35985_at		AKAP2	AB023137	40	20.5	2 4.0
37078_at	CD3Z antigen, zeta polypeptide (TiT3 complex)	CD3Z	J04132	99	1 7	24.0
81966_at			AI199418	31.2	19.8	24.5
45289_at	novel Ras family protein		AA133248	617	0.01	1.1.7
35669_at	KIAA0633 protein		AB014533	3.2	200	24.3
40757_at	granzyme A (granzyme 1, cytotoxic T·lymphocyte-associated	GZMA	M18737	5.6	100	23.0
	serine esterase 3)))	3
81908_at			A1650444		o c	0.60
62214_at	hypothetical protein FLJ11354		A1583960	35.5	28.7	23.9
39726_at	glucagon	909	104040	2 -		20.0
61738_at			A1475680	7.0	0 - 0	23.0
77244_at	bHLH factor Hes4		000000	1100	7.7	23.0
56023_at			A1041EE6	7.40	10.4	23.6
39168 at	Ac-like transposable element	AITE	AB011930	0.3	200	23.6
63342 at		ML I L	ABU10320	7	11.8	23.5
00045 at		hypoprotein	AA150254	31.6	2 4	23.4

48167 r at			1 4 4 7 4 9 7 7 4 4			
34759_at			1159404		1.5	23.4
76364 at			000434		7.7	23.3
63607 at	hypothetical protein El 190360		AA643507	6.4	17.1	23.3
50/51 2+			AI923841	0	0.7	23.3
			A1800640	5.3	6.2	23.2
440E7 at	himself at 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		AA843533	3.2	0.8	22.9
74403/-at	riybomerical protein rujiobaa		AA708740	0	0	22.9
07040 dt			AI217382	4.8	9.0	22.9
4319/ at			AA863064	6.0	6.0	22.8
53509 at			C14904	39.3	13	22.8
51104 at			AI937446	37.7	10.5	22.6
51550 at			AI681179	34	13.3	22.5
29020 at			AA160474	7.2	2.8	22.5
33587 at	entiation associated protein-5		AA134958	61.8	41.7	22.4
97425 at	butyrate response factor 2 (EGF-response factor 2)	BRF2	U07802	2	0	22.2
1036 24			A1239840	8.2	0.5	22.2
1030 at	Therieukin 13	L15	U14407	64.7	16.6	22.1
02049 at			N35156	1.3	4.3	22.1
40920 at	0.000		R61533	0	0.5	22
03/49 at	NIAA151U protein		AA411556	2	ō	22
03300 at			W81119	0	4 8	200
40419 at	ibrane protein band 7.2 (stomatin)	EPB72	X85116	42.8	19	21.9
41440 al	RIVA nelicase-rel		H68340	71.4	101	210
39821 s at	growth arrest and DNA-damage-inducible, beta	GADD45B	N95168	11.8	7.1	21.5
55940 at			N49940	0.8	3.2	21.4
50210 24			AI701480	0	5.2	21.4
71370 # 2+			AA429326	5.8	19.9	21.3
7174 of			T55845	0	0	21.2
41/44-41	turior recrosis ractor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcrption factor IIIA-interacting protein		AF070533	26	45.9	21.1
35849_at	phosphatidylserine receptor		AR011157	0		
63628_at	interleukin 7 receptor	1 7R	A1655791	122	ייני	77
62246_at			T97947	163.1	41.5	5.02
53489_at			A1928764	0 0 0	υ. Υ. α.	2008
				7.0	ī.	

Figure 13H

34214 at	KIAA0644 gene product		10001000		,	
2010			AB014344	6.2	5.7	70.7
35844_at	syndecan 4 (amphiglycan, ryudocan)	SDC4	D79206	77.4	5.8	20.7
64683 at			AI681906	1.3	0.1	20.7
47643_at			H10322	0.5	0	20.7
35606_at	histidine decarboxylase	HDC	D16583	5.7	26	20.5
51141_at	protein kinase domains containing protein similar to		A1949781	1.3	7.1	20.5
	phosphoprotein C8FW			1))
37060_at			079289	1.5	6.0	20.4
51161_at	ras homolog gene family, member A	ARHA	AI743085	20.9	5.2	20.3
86293_at			AI439642	7.4	2.3	203
1717_s_at	baculoviral IAP repeat containing 3	BIRC3	U45878	63.1	47.7	202
58867_s_at	immunoglobulin	1GL@	AI872510	33	2.9	20.2
1005_at		DUSP1	X68277	44.6	0.2	20.1
36139_at			AL050289	28.5	1.5	20.1
609_f_at	metallothionein 1B (functional)	MT1B	M13485	116.3	11.1	20.1
40505_at	ubiquitin-conjugating enzyme E2L 6	UBE2L6	AA883502	29.7	38.7	20
33380_at	topoisomerase related function protein 4·1		AB005754	6.9	6.7	20
34595 at		MYHL	AF105424	10.9	1.8	20
58391_at	testis zinc finger protein		AI798147	55.2	2.9	20
60812_at	pyruvate dehydrogenase phosphatase		A1625803	O	1	19.9
48076_at	hypothetical protein		A1949434	24.1	7.5	19.9
55362_at			AI653767	4.6	18.2	19.8
33273 f_at	$\overline{}$	1 CL @	X57809	0.5	1.5	19.7
52905_at	Rag C protein		AI279898	26.9	14.5	19.7
41582 at	advillin		AF041449	1.7	0	19.5
31540_at		TNFRSF9	U03397	72.2	7.8	19.5
47090_at			A1004667	37.2	45.7	19.5
41544 at	serum-inducible kinase		AF059617	24.6	0.2	19.4
1173 g at				26.2	15.6	19.2
65031_at			A1142111	0.7	1.1	191
40700_at	nuclear body protein Sp140		U36500	3.7	13.3	19
34460_at	peripheral benzodiazepine receptor associated protein 1		AB014512	1.9	0.2	19
90662_at	2'-5'oligoadenylate synthetase 2	OAS2	A1340262	25.2	27.3	19
38787_at	promyelocytic leukemia	JMH	X63131	17.9	49.4	18.9
39755_at	X-box binding protein 1	XBP1	Z93930	15.7	2.1	18.8

Figure 131

52183 at			AI350977	2.1	2.8	18.8
43373 s at			AA243659	33.5	15.4	18.8
1737 c 2+	المناسبة المناسبة المناسبة المناسبة		AA176915	ō	0.1	187
111	actor-binding protein 4	IGFBP4	M62403	26.2	72	186
40323 at	945)	CD38	D84276	160.1	102.8	200
56060 + 2+	lighterical protein		AA618602	296.2	15.3	186
37701 at			AI658703	8.2	3.1	186
48416 at	hypothetical protein signalling 2, 24KU	RGS2	L13463	9.2	1.3	18.5
56103 at			AA082707	0	0	18.5
56244 at			H48444	0.3	9.0	18.5
36227 at			H64595	9.0	9.0	18.5
38631 at			AF043129	63.4	21.8	18.5
41635 at	1. seconsting profession	TNFAIP2	M92357	63.8	17.8	18.4
36019 at	r associating protein		D14661	31.6	6.1	18.4
38369 at	(00)	SIK19	L26260	25.5	9.0	18.4
62512 at	ration printery response gene (66)	MYD88	U70451	5.1	15	184
40447 at	linin 2		AI927692	9.7	7.3	18.4
48357 at	nal protein Coo	LPIN2	D87436	20.2	47.2	182
83734 at	320	RPS28	AA968694	0.2	2	18.1
91655 f at			AI381435	5.6	12	18.1
39224 at	KIAA0580 protein		Al419764	3.1	3.5	18.1
33106 at	subfamily 1 group H member 2		AB011152	71.4	27.4	18
1377 at	kanna light polynontide gone on the	NR1H3	U22662	13.2	18.1	18
	happa ngin polypeptide gette enhancer in B-cells	NFKB1	M58603	54.5	18.3	18
42106 at			AA868517	22.9	1 1	01
51725 at			AA394226	7.3	4 1	α
3030 21			AA521246	129.3	35.4	α[
30221 24			AI590710	44.5	9.7	18
2661_dl	reukcyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	LILRB2	AF004231	62.6	6.1	17.8
86419_f_at			AA837767		0	
55776_at			W20092	4,50	0.3	17.8
45237_at		SOD2	AA142976	10.8	26.9	17.7
59403_at	coatomer protein complex, subunit beta	COPR	AAAAA14	1.	32.0	17.7
		2	#1#70#UU	T	1.6	17.71

74567 at			AI424832	7.5	0.4	17.0
79341 at			AA084622	7	12	17.6
. 1	interferon, alpha 16	IFNA16	M28585	1.2	0.5	17.5
52591 s at	Infutamate-cysteine ligase, catalytic subunit	CCLC	AI971137	0	5.6	17.5
50049 f at	1		AA045236	0.7	9.0	17.5
35817 at	myelin basic protein	MBP	M13577	2.1	2	17.4
49459 at		APOL1	AA156784	25.2	18.2	17.4
35822 at	nib	BF	L15702	1635.7	287.1	17.3
87415 at			W73083	22.7	4.8	17.3
44060 at	selenoprotein W, 1	SEPW1	AA625451	4.6	1.9	17.2
90375 at			N25135	0	0	17.2
52989 at			3143817	0.3	0.1	17.2
33499 s at	immunoglobulin heavy constant gamma 3 (G3m marker)	IGHG3	AF067420	5.9	3.8	17.1
39775_at	serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor),	SERPING1	X54486	41.5	67.8	17.1
	member 1					
58161_at			AA813728	9.7	1.5	17.1
49496 at			AA521168	1.1	7.4	17.1
58889 at			R45627	0.2	0	17
39517 at	hypothetical protein 23851		AF035313	20.5	14.3	16.9
39412 at		ZNF173	009825	4.3	5	16.9
40390 at	serine dehydratase	SDS	105037	3.7	5.2	16.9
40686 at	neuromedin B	NMB	A1985272	2.9	3.2	16.9
38342 at	KIAA0239 protein		D87076	4.2	10.8	16.9
60001 at			AA405241	9.0	2.4	16.9
51672 f at			AI161358	14.7	5.7	16.9
35408 i at	zinc finger protein 44 (KOX 7)	ZNF44	X16281	3.8	1.5	16.8
35224 at			AF070569	7.9	1.9	16.8
50310 at			2805207	0	1.9	16.8
41475 at	ninjurin 1	NIN)1	U91512	65.2	35.7	16.7
35868 at	advanced glycosylation end product specific receptor	AGER	M91211	3.2	1	16.7
34445 at	KIAA0471 gene product		AB007940	1.2	6.4	16.7
36575 at	regulator of G-protein signalling 1	RGS1	S59049	31	46.9	16.7
61148 at			AA884400	1.5	1.5	16.7
37531 at	KIAA0210 gene product		086965	1.6	0.7	16.6

Figure 13K

32026_s_at	32026_s_at PDZ domain containing guanine nucleotide exchange factor(GFF)		AB002311	68.3	25.1	16.6
49875_at			AI733353	6.3	5.9	16.6
56525_at	integral membrane protein 2B	ITM2B	N73873	7.7	9.0	16.6
48767_at	ALEX1 protein		AI693923	3.8	5.8	16.6
77840_f_at			AI720888	4.4	8.1	16.6
32595_at	Grich RNA sequence binding factor 1	GRSF1	U07231	7.8	22.7	16.5
32253_at	acid dipeptide (RE) repeats	RERE	AB007927	0	3.9	16.4
39132_at	d, actin dependent regulator of	SMARCA5	AB010882	7.1	3.9	16.4
	ımily a, member 5					
35099_at		APOL1	AF019225	8.3	7	16.3
32088_at	per nuclear factor 1 (JEM-1)	BLZF1	U79751	6.7	6.4	16.3
33849_at	pre-B-cell colony-enhancing factor		002020	41	8.3	16.3
35337_at	F-box only protein 7	FBX07	AL050254	8.6	8.5	16.3
33969_at	interferon, omega 1	IFNW1	X58822	3.6	1.5	16.3
38450_at	e antigen B (autoantigen La)	SSB	X69804	1.4	7.7	16.2
44126_at			W28501	73.5	28.6	16.2
46867_at			AI659243	0	0.7	16.2
64692_at			W30810	10.8	3.6	16.2
83553 f at			AA703100	9.9	1.9	16.2
37168_at			AB013924	6.06	9.05	16.1
33035_at	n L34 pseudogene 1	RPL34P1	AL021397	7.5	0.1	16.1
38576_at	ily, member B	H2BFB	AJ223353	37.4	13.7	16.1
34439_at	oma 2	AIM2	AF024714	40.9	18.1	16
1326_at	caspase 10, apoptosis-related cysteine protease	CASP10	U60519	7.2	18.6	15.9
81061_at			AI978710	0.5	6.0	15.9
59052_at	similar to aspartate beta hydroxylase (ASPH)		T83087	0	1.5	15.9
55915_r_at	hypothetical protein LOC54149		AI922520	5.2	13.7	15.9
69458_f_at			AI693465	9.6	2.1	15.9
62217_at			T81422	23.7	7.2	15.8
49438_at			A1535730	68.4	21	15.8
31345_at	e protease		AB002134	4.6	2.7	15.7
35015_at	CD80 antigen (CD28 antigen ligand 1, B7·1 antigen)	CD80	M27533	61	26.5	15.7
42893_at			R16983	3.1	3.7	15.7
54398_at			AA679287	4.1	1.6	15.7

Figure 13L

88629_at			AI337136	42	18.5	15.7
36423_at	p8 protein (candidate of metastasis 1)		W47047	3.1	1	15.6
56307_at			AI862477	0	2.3	15.6
49241_at			AI376957	3.6	4.6	15.6
61074_at			AI817642	0.4	0	15.4
37137_at	anzyme 2, cytotoxic T-lymphocyte-associated	GZMB	M17016	52.3	9.1	15.3
36760 at	Sernie esterase 1)		7760711	6		C
65008 g at	splicing factor (CC1.3)		A1539492	2.1	6.0	15.3
60190 at			A1668659	α.	1 7	15.3
51032_at	proteasome (prosome, macropain) 26S subunit, ATPase, 2	PSMC2	AI754675	0	0	15.3
287_at	activating transcription factor 3	ATF3	L19871	9.2	4.8	15.2
36097_at	immediate early protein		M62831	6.2	1.6	15.2
33814_at	protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs		AF005046	3.5	2.3	15.1
39660_at		DEFB1	AI309115	21.1	7.8	15.1
70682_at	YME1 (S.cerevisiae)-like 1	YME1L1	AI832869	0.4	e	15.1
32344_r_at	channel, shaker-related subfamily,	KCNA4	M55514	0.3	0.8	15
50205_at		LEPR	N46838	5.2	5.1	15
44594_at	CGI-112 protein		AA570477	1	2.2	15
40434_at	podocalyxin-like	PODXL	U97519	3.7	1.4	14.9
45234_at			AA648522	7.8	11.3	14.9
1008_f_at	protein kinase, interferon-inducible double stranded RNA dependent	PRKR	U50648	2.6	1.7	14.9
49634_at			N51441	0	3.2	14.9
90424 r at			AI122603	11.7	1.2	14.9
38678_at	small nuclear ribonucleoprotein polypeptide E	SNRPE	AA733050	1.2	0.4	14.8
37064_at			U66048	3.4	2.8	14.8
73776_at			AI554044	18.6	13.5	14.8
53016_at	hypothetical protein FLJ20654		AL121389	1.2	1.8	14.8
920_at	natural killer tumor recognition sequence	NKTR	L04288	6.4	0	14.7
54769_at			AA203416	33.9	10.8	14.7
52111_at			H47347	1.3	1.5	14.7
48259_at			AI123757	3.7	2.4	14.7

Figure 13M

natural killer cell stimulatory factor 1, cytotoxic 1112A
TAC3
IFIA1
7
Small inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotactic and inducible cytokine 42 (monocyte chemotacyte chemotacyte and inducible cytokine 42 (monocyte chemotacyte cytokine 42 (monocyte chemotacyte cytokine 42 (monocyte cytokine
otein 1, SCYA2
IGFBP3
J
ScryA2 homologous to mouse Sig-je)
PPP1R5
ZNF173
IGFBP4
LRP4

35488_at	small nuclear RNA activating complex, polypeptide 1, 43kD	SNAPC1	1044754	3.4	180	130
823_at	-	SCYD1	U84487	9.8	1:1	
40755_at	MHC class I polypeptide related sequence A	MICA	X92841	15.4	α	0.01
80773_at			H15073		σ	13.3
46526 at	hypothetical protein MGC5242		A1434025	14.2	13.0	13.9
56619_at			A1808330	200	10.1	13.0
1089_i_at			M64936	1.0	† (m	13.9
48431_at	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid- specific)	FUT4	AI970292	9	14.7	13.8
47032_at			A1885390	1		
36934_at	hypothetical protein LOC57158		AI 035/47	7.0	0.4	13.8
37049 g at	translocase of outer mitochondrial membrane 34		1158970	2,00	200	13.6
38750_at	Notch (Drosophila) homolog 3	NOTCH3	097669	233	2/1	13.6
56019_f_at			44992380	20	1 -	13.0
32693_at	KIAA1040 protein		AR028963	0 2	1.7	13.6
36578_at	baculoviral IAP repeat-containing 2	BIRC2	1137547	1 2 2	0.7	13.5
37249_at	phosphodiesterase 8B	PDFAR	AE070520	2.7	n c	13.3
38017_at	(CD79A antigen (immunoglobulin-associated alpha)	CD79A	1105259	1.1		13.5
143_s_at	ng protein (TBP) associated factor, RNA	TAFON	1175200	0.0	0.0	13.5
	, 100kD		60000	£.1	5 .	13.5
58182_r_at			AA814034	c	0 -	100
51450 s at			AA121544	26	0 0	13.3
32533_s_at	vesicle-associated	VAMP5	AF054825	14.5	30.7	13.0
41052_s_at	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	CACNA1A	999620	0.3	(F)	13.4
47899_at			44056755	0 00		
84064_at			A1365033	0.07	10.9	13.4
64194 at	hypothetical protein FL 110903		11 4000	0 0	1.3	13.4
63746 i at			114920	٥	0.2	13.4
	adrenardic alpha. 10 recontor		AA2/99//	2.3	0	13.4
36677 24	small industrial authors (Authors)	AUKA10	M/6446	6.0	2.6	13.3
74720 at	ytokille A4 (floritologous to mouse Mip-1b)	SCYA4	J04130	30.3	13.4	13.3
51105 at	elli ruuskaa		AI027524	28.8	10.5	13.3
101 IO2 AT	IKNO guanine nucleotide exchange factor (GEF) 3	ARHGEF3	N57933	0	5.7	13.3

inventors.	rair Haconen, et u	į

34308 21	epithelial sodium channel regulator		880/00av	N		13.2
3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	H2A histone family, member L	HZAFL	1190551	121	0	, ;
33527_at	OI	KCNJ3	U39196	90		13.0
846 s at	BCLZ-antagonist/killer 1	BAK1	U16811	1 4	2.5	13.6
45306 at			AA742560	12	0 4	13.6
89589_t_at			R05527	3:1	† F	13.6
36214_at	Kruppel-like factor 4 (gut)	KLF4	1170663		0.1	13.4
48919_at	potassium inwardly rectifying channel, subfamily J, member 2	KCN 12	AA393850		5 6	13.1
68002_at			AA503803	130	11.2	13.1
88861_at			AA303003	21.9		13.1
42116_at			AID80122		6.0	13.1
40113 at	GS3955 protein		AA398118	2.4	0	13.1
34227 at	profession 4		D87119	0	4.7	13
		7754 4577	070136	5.8	0.7	13
32233_at	torsin family 1, member B (torsin B)	TOBIE	0.5050074			
47371 at		GIVIO	AF00/8/2	5	6.9	13
48062 at			AA017037	3.9	7	13
45178 at	RAP1A member of BAS oncomes family		AA418490	13.8	0.1	13
39857 at	of the original artiflity	RAP1A	AI476340	0	0.1	13
46.4 5.24	indicated according of	STX11	AF044309	12.7	5.6	129
36450 at	protein 35	IF135	U72882	24.3	35.4	120
18-00-to	function)	ENPP4	AB020686	10.3	1.2	129
88714 at	ימויניוטון			-		
47447 at			AA873008	94.5	63.3	12.9
49237 at			AI262829	3.6	3.6	12.9
44200 at	process, A cirornosome	RBMX	AI971694	4.9	2.5	12.8
72290 r at			AI420959	0	3.3	12.8
			AA814901	9.1	10.9	12.8
80045 at			AI953847	25.7	8.6	12.8
90850 f at			AI989871	29.1	26.8	12.8
38004 24	3 - 37		AI522161	2	C	12.8
-ac	visic aviali sarconia (Schmidt-Kuppin A.2) viral oncogene homolog	SRC	AF077754	4.6	1.9	12.7
34898_at	amphiregulin (schwannoma-derived growth factor)	AREG	M30704	4.4	0	197
85409 at					1.0	7.71

Figure 13P

\neg			1 A 1 A 4 A 1 A	7	0 0	100
	Ac-like transposable element	AL TE	A1979194	7	2.0	12.7
34476_r_at_le	epiregulin	FDEC	207050	1 200	0.0	12./
	MyoD family inhibitor	MOFI	170212	36.5	8.0	12.6
	melan.A	MINA	0/0313	4.0	5 (12.6
Γ	Tat-interacting protein (30kD)	ייוראואא	000432	4.2	0.3	12.6
			AF039103	5.1	5.8	12.6
Γ	aminolevillinate delta cyathaca 1		WbUZb3	34.8	34.9	12.6
T		ALAS1	Y00451	9.6	3.7	12.5
50008			N36284	20.1	12.7	12.5
22050 1 at			AI815758	7	4.2	12.5
T			T93073	1.4	3.2	12.5
T	INA nomeobox (Urosophila), family 3, A	NKX3A	AI557413	63.8	2.8	12.5
			L27065	0.5	0.4	12.5
	protein priospnatase z (formerly ZA), regulatory subunit B (PR 52), alpha isoform	PPP2R2A	M64929	5.3	7.5	12.4
s_at	dual specificity phosphatase 4	DUSP4	U48807	10.8	35.6	12.4
			AW006742	13.4	2 2	101
	v-jun avian sarcoma virus 17 oncogene homolog	NOr	J04111	2.1	2.3	12.4
30022_at			W23499	3.5	2.8	12.4
51200 at			AL045781	2.4	1.3	12.4
52228 24			AA827683	0	0	12.4
32220 at			AI242476	0.2	1.6	12.4
ğ ;			AA005281	14.7	16.7	12.4
ğ ;	interieron, alpha 21	IFNA21	V00540	0	0.5	12.3
i t	MAGGOT Protein		AA916905	1.6	0	12.3
a			AL079289	11.6	0.5	12.3
÷	redripter associated testis-expressed 1-like 1	TCTEL1	D50663	22.1	20.3	12.3
49136 at			AI871408	13.7	6.9	12.3
5 6	myosin FC		W56900	1.1	7.4	12.3
T		MYOSC	AA195002	0.9	3.8	12.3
58550 at			AI126206	4.6	1.9	12.3
76160 at			AA081874	0.9	0.2	12.3
53567 at			AI745624	5	4.5	12.3
- F			AW003119	0	0.2	12.3
4/128_at			AI341820	2	3.3	12.3

Figure 13Q

3R
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gure
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	7		2	0.00	12.6
inditial ittiitiuuodeliciency virus type I ennancer-binding protein 1	HIVEP1	X51435	5.6	6.4	12.2
IGF-II mRNA binding protein 3		1197188	2,5	5	
		AA810864		11.9	12.4
		4110110004	0.7	1.0	12.2
	-4-	Alfelli	0.4	2.8	12.2
		AI624103	2.5	0.2	12.2
neuropentide FE amide pentido accominado		AI625805	5	6.2	12.2
KIAAAAAA	NPFF	AI936758	1.9	1.2	12.1
		AB014550	3.7	m	12.1
		R71414	0.8	m	12.1
		AI033014	3.6	5.8	121
apolipoprotein L, 3	APOL3	T63428	20	24.4	121
reucilies itcli, giloria iliactivated 1	LGI1	AF055636	1.1	0.1	12
carboxypeptidase 62 (plasma)	CPB2	M75106	3.1		121
Neil blood group precursor (McLeod phenotype)	XX	232684	2.3	187	121
NAMORUS gene product		AI948512	17.5	187	100
		N57875	8.6	4 9	12
		AI916641	0		12
		AW000885	2		
en reading frame	C60RF32	AB002384	0.2	0	11 9
TOTALP HOTHOLOG		AB020631	0	0.1	11.0
		AL079294	0.7	0.8	119
		AA741304	10.6	26.4	119
protoin photosphot		AI219734	7.3	2.6	119
protein priospiratase 15 (iornierly 20), magnesium-dependent, beta isoform	PPM1B	AW020971	10.6	7.4	11.9
		AI 050378	276	L	
carbonyl reductase 1	CBR1	AB003151	1,0		11.8
		AA004879	29	4 4	11.0
nive less to the second		A1769692	1.2	4.7	211.0
Similar to rat myomegaiin		A1659612	71.1	8.6	11.8
		T92908	0	1.6	11.8
		AA055179	2.2	4.6	
		AA282811	1.5	9.0	11.8
	neuropeptide FF-amide peptide precursor KIAA0650 protein apolipoprotein L, 3 leucine-rich, glioma inactivated 1 carboxypeptidase B2 (plasma) Kell blood group precursor (McLeod phenotype) KIAA0603 gene product Chromosome 6 open reading frame 32 PCF11p homolog protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform carbonyl reductase 1 similar to rat myomegalin	amide peptide precursor 3 3 3 a inactivated 1 B2 (plasma) orecursor (McLeod phenotype) coduct ben reading frame 32 see 1B (formerly 2C), magnesium-dependent, e 1 megalin	amide peptide precursor 3 3 3 APOL3 a inactivated 1 B2 (plasma) Ordect coduct ise 1B (formerly 2C), magnesium-dependent, PPM1B e.1 CBR1 CBR1 CBR1 CBR1 CBR1 CBR1	Al161111	Al161111 0.4 2 Al624103 2.5 0 Al624103 2.5 0 Al624103 2.5 0 Al624103 2.5 0 Al624103 2.5 6 Al624103 2.5 6 Al624103 2.5 6 Al624103 2.5 2.4 Al033014 0.8 2.5 Al033014 0.8 2.5 Al033014 0.8 2.5 Al033014 0.8 2.1 Al033014 0.8 2.1 Al0348512 17.5 18 Al0402034 0.7 2 Al0402034 0.7 2 Al0402031 0.6 2 Al056303 0.7 0 Al056303 0.7 0 Al056303 0.7 0 Al05631 0.7 0 Al05631 0.7 0 Al05631 0.6 0 Al05631 0.6 0 Al05631 0.6 0 Al05631 0.6 0 Al06631 0.7 0 Al06631 0.8 0 Al06631 0.1 0 Al066

73420_at			A1858360	6.8	7 6	0
33328_at			W28612	17	ο (φ	11.0
1105_s_at	eta locus	TRB@	M12886	5.2	7	11.7
3/228_at	polo (Drosophia)-like kinase	PLK	U01038	0.3	C	117
/80/2 at			AI743607	13.5	1.1	117
64260 at			N54523	1.1	2	117
5216/ at			AA151346	13.5	12.1	117
64029 ot			AI808804	1.3	4.3	11.7
24020 at			AL048962	2.5	6.1	11.7
47,420 41			166087	0	2.4	11.6
56141 24			T86276	1.1	1.5	11.6
51627 24			AI566128	2.3	0.4	11.6
1004 at			T62959	20.8	2.6	116
3692E 2+	la receptor 1, GTP-binding protein	BLR1	X68149	92	0.2	11.5
3670E at	Is-acting factor (50 KDa)		X82200	18.3	22.2	11.5
30703	protein kinase, AMP-activated, beta 2 non-catalytic subunit	PRKAB2	AJ224538	1.8	2.4	11.7
500410-1-at			N24659	6.9	1.1	11.5
01057 24	priospirationiserine-specific phospholipase Alaipha		AI765967	28.1	24.1	11.5
51037 at			AA085091	4.2	1.3	11.5
51022 at			AI377043	0	2.3	115
30517 at			AA780058	1.5	1.1	11.5
3031/ dl	lated transcription factor 3, gamma (48kD)	ISGF3G	M87503	10	6.3	11.4
25000 ct	base C, epsilon 2	PLCE2	AB029015	1.7	3.6	11.4
1623 C of		PPL	AF001691	3.4	5.6	114
27000 St		PIM2	U77735	32	15.7	11 4
3/ 309_a1	(150kD), epilegrin)	LAMA3	L34155	9.0	1.2	11.4
63332_at			AA127696	α οι	11.7	
59283_at	hypothetical protein FLJ20035		AI 042790	27.0	11.7	11.4
43463_at	neuropilin 2	NRPO	NIO0777	0.70	24.0	11.4
71530_at		7 (1)	A1936520	0,0	2./	11.4
59941_at	phosphoprotein associated with GEMs		0700000	7.0	1.3	11.4
42933_at			AI/69545	21.2	7.6	11.4
77297 at			193101	15.3	4.8	11.4
			ALU46564	4.6	6.9	11.4
			- 77	-	•	-

Figure 13S

150 01			AWOOS696	c		7
106_at	runt-related transcription factor 3	RUNX3	73527R	200	2 -	4.1.
40930_at	sulfortranferase family 4A, member 1	SIII TAA1	WOEDEO	100	,,,,	11.3
39008_at	ι.Ψ	0000	W23530	3.0		11.3
38056 at		5	M13699	5.9	2	11.3
30053	STORES OF THE STORES		D83779	1.8	0.3	11.3
	Т		AB014528	1.2	0.1	11.3
4000/ at	CUb antigen	CD6	X60992	1.5	23	11.5
78498 at			AI374686	1.3	90	11.3
42/20_at			A1393727	0	000	2 .
62837_at			A12A02E0	2.0	3.6	11.3
43084_at			A 404011	Σ.Ο.	4.2	11.3
60514 at	LATS (large tumor suppressor Drosophila) homologio	COLV	1120250	4.4	4.8	11.3
56246 at	6-phosphofricto. 2-kinase /frictose 2 & highscapates 2	LAI 32	069566	3.3	0.4	11.3
80915 at	transcription factor ats	PrKrB3	AI765775	91	6.2	11.3
53978 at			AI347001	38.2	44.7	11.3
20000			AW024692	4.5	1.2	113
30000 at		DUSP10	AB026436	18.8	7.8	11.0
34200 at	Dreast carcinoma amplified sequence 2	BCAS2	AB020623	0.7	α ο	11.0
2241 at	mitogen-activated protein kinase kinase 8	MAP3K8	D14497	53.8	4.5	11.0
32413 at	Interieron, alpha 5	IFNA5	V00541	0.4	24	11.2
47020 -t	selectin L (iymphocyte adhesion molecule 1)	SELL	M25280	5.8	25	11.2
7240F 21			AA102788	0	171	11.2
/ 3403_dl	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	DYRK2	AI990466	3.1	5.8	11.2
53773_at	tumor necrosis factor (ligand) superfamily, member 13h	TNECE13D	70000			
74361 at		00 10 IVI	AA002490	16.9	17.6	11.2
73536 f at			AI015/72	1.2	0	11.2
35955 at	cytochrome c-like antigen		AA737775	1.8	0	11.2
1061 at			580864	0.7	0.2	11.1
37678 at	Dutative transmembrane protein	ILIUKA	U00672	9.6	5.1	11.1
37961 at	phosphoinositide. 3 kinasa ramulatan ministration		U23070	8.7	2.6	11.1
	(p55, gamma)	PIK3R3	106060	2.1	2.1	11.1
58452_at		SPAG9	AL079765	4.7	0.0	-
48893_at			AI452715	7		11.1
40091_at	B-cell CLL/lymphoma 6 (zinc finger protein 51)	BCL6	1000115	10	0.1	11.1
32606_at	brain acid-soluble protein 1	RASP1	44125602	2 0		
		1 1000	UNT 22000	20.9	17.8	111

Figure 13T

15057 at			AA131894	3.1	3.1	11
63692 at			167687	9	1.8	-
03003 at			N56920	7	7	
50652 at			N53764		0.0	1 1
63032 at			A1653152		200	
48587_at	Kruppel·like factor 4 (gut)	V1 CV	A1000014	14.7	3.1	11
55631 at	KIAA1414 protein	NLF4	A1290876	3.5	0	11
33859 at	sin 3.2550ciated not montide 10.0		A1499339	0.3	0	11
53773 24	and associated polypeptine, toku	SAP18	U96915	8	12.8	10.9
78701 + 2+			AI033021	2.2	6.0	10.9
40700 -1			AA609601	1.7	1	10.01
30876 at			AA102395	0.3	1 9	10.9
710E4 00	cattleballt F	CTSF	AF071748	0.1	171	α O1
33110 24		MYB	M13666	0.8	C	10.8
35720 at	Milerieroni related developmental regulator 2	IFRD2	U73167	0	0.6	10.8
36766 04	ייביייין אינייין		AB020700	4.9	22	0.01
20,700_41	nbundclease, Kivase A family, 2 (liver, eosinophil-derived neurotoxin)	RNASE2	X55988	3.5		10.8
56213_i_at			100000			
85344_f_at			AA04000/	1.4	1.4	10.8
62207 at			AW024994	0	0	10.8
64450 at	2:5 oligoadenvlate synthetase 3		AA058770	1.1	9.0	10.8
42229 r at	25,000	UAS3	AA135525	25.2	30.3	10.8
35545 at	solite carrier family 1 andime to		AA453357	6.6	10.2	10.8
70-000	member 8	SLC4A8	AB018282	0.3	1.5	10.7
1575 at	ATP-binding cassette, sub-family B (MDR/TAP), member 1	ABCB1	M14758	C		
36041_at	UDP-N-acetyl alpha-D-galactosamine: polypeptide N- acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1	U41514	0	6:0	10.7
50666 at			1011072	0		
57642_at			4,007,000	3.0	9.0	10.7
59220_at			AAU05336	1.6	0.9	10.7
60896_at	integrin, beta 8	TOBO	AA922861	9.0	1.6	10.7
48672 at		ogpi	AID34852	137.5	31.7	10.7
52985 at			AI817153	1.2	0.2	10.7
	Singren syndrome antigen A1 (52k) ribonizione	, , ,	3075759	0.1	9.0	10.7
	Joseph Sylvatoric angles of Joseph Hamiltonian (Joseph Hamiltonian Sylvatoric	SSAI	M62800	8.6	8.2	10.6

37163_at	DKFZP586C1619 protein		AI 050374	56.3	9.11	10.6
32082_at			AL049229	4.5	1.8	10.6
31443_at			S76346	2.4	1.5	10.6
90878_at			179248	1.1	1.9	10.6
56889_at	phosphatase 10	DUSP10	N36770	14.2	4.1	10.6
43592_at	chondroitin 4-0-sulfotransferase 2		AA449104	0.5	6.1	10.6
88354_at			H18944	2.5	1.6	10.6
40097_at	eukaryotic translation initiation factor 1A, Y chromosome	EIF1AY	AF000987	1.6	3.2	10.5
529_at	dual specificity phosphatase 5	DUSP5	U15932	45	12.1	10.5
35340_at	mel transforming oncogene (derived from cell line NK14). RAB8 M	MEL	AI819948	0	6.9	10.5
39119_s_at	_		AA631972	22.5	34.2	10.5
44895_at			H00995	111	2 0	10.5
50829_at			AA706818	4 8	10.8	10.5
78020_at			AI470127		0.7	10.5
58222_at	neural precursor cell expressed, developmentally down-regulated N	NEDD1	R71348	1:1	1.3	10.5
59516_at	KIAA1268 protein		AA210695	14.1	11.3	10.5
65531_at	hypothetical protein FLJ22794		AA948676	1.9	5.2	10.5
45453 at			AW000995	1.6		10.5
46317_at	lagen type I receptor, thrombospondin sosomal integral membrane protein II)	CD36L2	W07476	8.0	8.8	10.5
40492_at	KIAA0826 protein		AB020633	0.2	1.7	104
32820_at	cription complex, subunit 4	CNOT4	U71267	4.7	4	104
	91	IFNA6	X02958	0.4	0	10.4
36315 i at	KIAA0919 protein		AB023136	0.5	0.4	10.4
	3, RNase A family, 3 (eosinophil cationic protein)	RNASE3	X55990	3.8	0	10.4
36914_at		CTSO	X77383	8.0	1.4	10.4
41045_at	secreted and transmembrane 1	SECTM1	U77643	37.2	67.4	10.4
61150_at			AA894558	0.5	0.3	10.4
43363 s_at			AI978590	5.1	1.9	10.4
65331_at			AW009884	1.9	2.5	10.4
43269 at	KIAA1554 protein		AA424170	7.6	12.5	10.4
119/3 r at			AI089044	9.3	5.3	10.4
86326 g at			AA488988	13.1	0	10.4

71701 24			OONTACIA			
11,21 01			AI34/400	5	0.3	10.4
32882_at	sterol O acyltransferase 2	SOAT2	AF059203	1.2	0	10.3
33828_at	SWI/SNF related, matrix associated, actin dependent regulator of SMARCE1 chromatin, subfamily e, member 1	SMARCE1	AF035262	0	1.4	10.3
40696_at	receptor (TNFRSF) interacting serine threonine kinase 1	RIPK1	U50062	10.9	2.9	10.3
31590 g at	gamma-aminobutyric acid (GABA) B receptor, 1	GABBR1	AL031983	4.9	6.0	10.3
37921_at	neuronal pentraxin l	NPTX1	U61849	1.3	3.6	10.3
55551_at			AI766561	10.6	7.1	10.3
90167 at			AI684439	æ	2.3	10.3
62528 at	hypothetical protein FLJ20073		AA741307	51.4	23.4	10.3
54565 at			AA149736	45.6	8.7	10.3
1203_at			017357	17.8	5.2	10.3
35096_at	igh affinity aspartate/glutamate	SLC1A6	U18244	7.7	4.1	10.2
	transporter), member 6					
41784_at	DKFZP564B0769 protein		AL080186	0	0.3	10.2
39802 at	small inducible cytokine A7 (monocyte chemotactic protein 3)	SCYA7	X72308	1.8	15	10.2
37275_at		GABPB1	U13045	6.5	3.9	10.2
602_s_at		HSD17B1	M29037	0	0.7	10.2
38782_at		GTF2H1	M95809	0.4	2.1	10.2
66524_at			AA830101	0.4	0.5	10.2
62288_at			AI336854	6.4	3.1	10.2
76762_at			AI246590	53.8	8.9	10.2
44947_at			AA047365	1.7	2.3	10.2
53595_at	AD:015 protein		6006EN	9.0	3.4	10.2
78732_f_at			A1094933	4.2	9.3	10.2
78728 g at			AA425815	1.1	0.4	10.2
35113_at	in transporter), member 1	SLC22A1	X98332	16.2	1.8	10.1
40457_at	splicing factor, arginine/serine-rich 3	SFRS3	AF038250	0.4	0.7	10.1
1449 at	pain) subunit, alpha type, 4	PSMA4	D00763	8.3	6.2	10.1
37018_at		H1F2	A1189287	26.1	2.3	10.1
53720_at	hypothetical protein FLJ11286		AI862559	9.5	10.4	10.1
61181_at			AA063523	2.9	3.1	10.1
43131_at			R00030	2.1	5.6	10.1
65678_at			AA461084	8.4	9	10.1
76802_at	core promoter element binding protein	COPEB	A1355637	m	0.3	10.1

			AI741209	5.6	4.3	101
64694_at			AI799784	2.7	0.6	101
42083_at			AI247356	9 2	0.50	101
70252_f_at			AA825923	200	2.0	10.1
	ubiquitin-conjugating enzyme E2L 3	UBF213	A 1000519	3 0	7.70	10.1
ţ	interferon, alpha-inducible protein (clone IFI-6-16)	G1P3	0752211	1 2 0	4.4	01.
	KIAA0615 gene product		AR014515	12.5	0.0	
	hypothetical protein FLJ11149		AF038172		1.7	
g at	nuclear antigen Sp100	SP100	MEDETA	7 0 0	1.0	100
-	myeloid cell leukemia sequence 1 (BCL2-related)	MCL1	108246	5.2	3.0	10
7			AW006763	10.01	000	
7	hypothetical protein FLJ11264		AI692513	4.7	6.4	
68194_at			AA291194	3.1	8 4	101
/2862_at			AW026509	11.9	15.3	
			AA194980	40.7	35.3	101
	KIAA0442 protein		AB007902	0.7	5.6	66
at	heat shock transcription factor 4	HSF4	D87673	4.1	-	66
1		TAGEN	M95787	0	2.4	00
┰	trefoil factor 3 (intestinal)	TFF3	AI474125	2.3	0.1	66
_			AA682849	2.9	1.8	99
_		CTNND1	A1863000	5.3	4.5	5 6
Т	hypothetical protein FLJ13171		AW001604	6.4	13.8	6 6
			AI066588	3.5	2.5	00
at	serine (or cysteine) proteinase inhibitor, clade A (alpha·1 antiproteinase, antitrypsin), member 8	SERPINA8	AI208913	23.9	15.5	9.6
ji	RAB9-like protein		AI334284	80	3.7	00
			AL042923	9.7	200	0.0
ă	tumor necrosis factor (ligand) superfamily, member 8	TNFSF8	L09753	0.5	C	86
		TLL2	AB023149	2.5	0.7	86
	BCL2-associated X protein	BAX	L22474	4.1	4.6	86
1	exostoses (multiple) 1	EXT1	879639	50.9	5	9.6
T	growth arrest and UNA-damage-inducible 34		U83981	23.2	1.9	9.6
T		RAB5B	X54871	2.8	2.5	9.6
Ja.	CU4& antigen (B-cell membrane protein)	CD48	M37766	15.4	21.6	9.6
54/50 at			AAEOSEOC	C		

,

20000			AI740855	1.7	1.2	9.8
030/0 at			W04199	C	0.8	8.6
/1984_at	Humothatical protein El 120647		AI478759	7		8.6
01617 1 01	Cytotoxic T.lymphocyte-associated protein 4	CTLA4	AI733018	0	19.5	9.8
77310 at			AA521497	0.4	2.6	9.8
51839 at			AA284279	1.6	3.3	8.6
63982 at	Inhiminal extochrome c reductase (6.4kD) subunit		AI480328	29.8	9.8	8.6
87258 at			N53015	4.1	14.9	8.6
39541 at	KIAA1237 protein		W52003	2.7	7.1	9.7
	hypothetical protein P15-2		AL031387	8.2	4.5	9.7
37638 r at	12	ADH1	M12963	1.8	0.2	9.7
34030 - at			N67059	0.2	0.1	9.7
42707 at			R08912	2.6	3.3	9.7
45/27 at			R51079	0.4	6.0	9.7
13760 at			AA397579	1.4	9:0	9.7
£1207 at			N54899	4.3	3.4	9.7
46712 at			W63773	13.2	2.4	9.7
51508 i at			T92882	13.7	7.2	9.7
32053 at	cyclin T2	CCNT2	AF048731	4.2	6.0	9.6
33841 at			R48209	0.1	1.8	9.6
34376 at	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	PKIG	AB019517	5.4	2.2	9.6
37729 at	exportin 1 (CRM1, veast, homolog)	XP01	Y08614	1.5	2.4	9.6
45379 at	٠I		AI659019	6.4	5.8	9.6
59479 at			W44692	1.2	0.8	9.6
63066 at			AA001735	113	12.6	9.6
44055 at			AA133979	0	6.8	9.6
54025 at			H16294	6.6	2.6	9.6
58459 s at			AA150805	0	6.0	9.6
46961 r at			191186	6.9	8.3	9.6
58457 f at			AI819225	0.2	0	9.6
31523 f at	H2B histone family, member H	Н2ВГН	280780	8.6	0.3	9.5
32206 at	KIAA0451 gene p		AB007920	2.4	1.4	9.5
36866 at	testis-specific ankyrin motif containing protein		D78334	2.1	2.4	9.5
33823_at	CD36 antigen (collagen type I receptor, thrombospondin	CD36L2	012676	16.8	30.9	9.5

56373_at	UDP-Gal:betaGlcNAc beta 1,4 galactosyltransferase, polypeptide B4GALT5	B4GALT5	AA133969	42.2	ю. б	9.5
+0 + 00022	Ω		AI638850	0.8	1.9	9.5
1/032 41			T59016	0	2.4	9.5
48189 at			AW002600	8.6	2	9.5
74034 at	CHMD1 5 profein		AI368368	1.8	1.7	9.5
	in 281	ZNF281	AA121673	5.1	5.9	9.5
43101 at			AI253196	0	0	9.5
50016 at			AI400414	15.6	6	9.5
57722 at			AI492902	0.2	5.8	9.5
37027 at	AHNAK nucleoprotein (desmoyokin)	AHNAK	66808W	7.7	4.7	9.5
35298_at	lation initiation factor 3, subunit 7 (zeta,	EIF3S7	U54558	ф. ф.	5.6	9.5
35537 at	KIAA0514 gene product		AB011086	2.7	0.2	9.4
33063 at	(platelet), alpha polypeptide	GP1BA	J02940	30.9	9.1	9.4
40200		ICAM5	U72671	2.7	1.3	9.4
32137 24	testin		AL050162	2.8	1	9.4
30650 6 21	_		AB007895	1.6	1.9	9.4
36053 at	ryclin-denender	CDKN2C	AF041248	0	0	9.4
36814 at	KIAA1109 profein		AB029032	0.3	2.9	9.4
20014 890 at	Libiquitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A	M74524	1.2	4.2	9.4
61191 2			AI539443	3.9	14.2	9.4
	transcriptional regulator protein		AI074024	2.4	2.7	9.4
46065 at	. 1		N23366	0	2.3	9.4
48039 at			AI634580	15	16.9	9.4
58605_at	DNA segment on chromosome X (unique) 9928 expressed	DXS9928E	AI697939	21.5	20.6	9.6
	sednence		44216639	17	0 1	9.4
32163 t at			AA167191	40	0	9.4
44212 at			2884969	111	1.3	9.4
40062 at	auclear domain 10 profein		U22897	7.9	5.1	9.3
32725 at	ıاa	DIB	AF042083	9.9	4.2	9.3
1222 at	in kinase 2	PCTK2	X66360	0.4	0.1	9.3
34304 c at	spermidine/sp	SAT	AL050290	17.7	12	9.3
32193 at	plexin C1	PLXNC1	AF030339	18.3	38	9.3

1797_at	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDk4)	CDKN2D	U40343	5.9	11	0 2
796 i at	cyclin-dependent kinase-like 1 (CDC2-related kinase)	CDKL1	X66358		100	0.0
37005 at	neuroblastoma, suppression of tumorigenicity 1	ZBI 1	D28124	711	0 0	0.0
48018_at			AA700227	19.1	31.1	5.0
68493_r_at			R43774	17.7	31.1	0.0
59434_r_at			R43805	100	0.1	0.0
48245_at			AA180163	7.7	4.7	200
57785_at	H4 histone family, member H	H4FH	N32748			0.0
47330 at			W81697			3 0
56469_at	hypothetical protein		W44483		4 4	0.0
46304_at	hypothetical protein, clone 2746033		AA126461			0.0
1951_at	angiopoietin 2	ANGPT2	AF004327			0.0
31924_at			AL035122	1 7	0	2.0
32648_at	delta-like homolog (Drosophila)	DLK1	1115979	400		3.6
39317_at	: acid hydroxylase	СМАН	D86324		1.7	9.2
33362 24	Can receive and minate monooxygenase)					
33302 dt	Cuc4z enector protein 3		AF094521	5.5	2.1	9.2
5/658 at			U55989	1	0	9.2
83245 at			AI300111	7.7	4.9	9.2
50640_at			N32169	1.3	2.4	0 0
43105_at			T98171	3.6	3.7	9.5
63984 f at			AA535914	15	16.4	9.0
44235_at			H82526	23.6	6	9.0
51609_r_at			AW051767	0		000
55629_at			AL040635	16.7	9.7	9.0
485_at	desert hedgehog (Drosophila) homolog	DHH	U59748	0.9	4.4	9.2
43/89 r at			AA226513	0.2	1.5	0.6
34469_at	ABU blood group (transferase A, alpha 1.3.N. acetylgalactosaminyltransferase; transferase B, alpha 1.3. galactosyltransferase)	ABO	X84746	3.6	e.0	9.1
39733_at	homocysteine inducible, endoplasmic reticulum stress inducible, ubiquitin-like domain member 1	HERPUD1	AF055001	1.4	3.4	9.1
34594_at	terminus of tre		D13644	0.2	0.8	9.1
3/650 at	ger protein, 1	MKRN1	U41315	2.1	4.2	9.1
4102/_at	forkhead box C1	FOXC1	AF078096	2.9	0.7	9.1

Figure 13AA

11001 6 24		0000	4 . 4 . 4			
41021 3 41	niate deriyurogenase Z (mitochondriat)	GPUZ	U36310	16	10.7	9.1
5810/ at			AA984220	1.5	1.1	9.1
89202_at			AI347361	28.3	30.4	9.1
48374 at			W87470	5.1	1.4	9.1
63968_at			AI979124	1.3	c	6
83253_i_at			H11766	1.4	1 4	100
47343_at			AI655198	2.4	2	9.1
53670_at			AA664156	4.7	17.4	9 1
64794_at			AA120764	2.6	2.9	9 1
42056_at			AA282541	1.8	1.6	9.1
48964_at			AI629027	24.2	17.2	9.1
41455_at	KIAA0712 gene product		AB018255	0.7	0.1	6
31847_at	highly charged protein		X59131	2	2.4	σ
32319_at	ly, member 4 (tax-	TNFSF4	AL022310	1.2	1.4	6
36000	activated Riycopioteill I,					
30202 at			AF054994	1.4	6.4	6
1452 at		LM04	U24576	5.7	1.5	6
33952_at			U71601	0.4	0.8	6
1512_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	DYRK1A	D86550	6.9	2.9	6
37578_at	actin filament associated protein		D25248	0.7	7.0	σ
51307_at			AI589165	00	10	0
48417_r_at	hypothetical protein PRO2849		AA636101	0	0.2	10
74628 g at	NICE-5 protein		AI986085	0	2.5	6
65626_at			AA059458	96.4	20.4	σ
46172_at			AI142832	9.7	6.8	0
47823_r_at			AI452659	0	0	O
43640_at	sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 5	SIRT5	N55168	1.1	3.2	6
61789_i_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	PSMD11	H05559	0.3	0.2	0
58560_f_at			AA810101	1.7	1.1	δ
31722_at	in L3	RPL3	AL022326	4.9	3.9	0
38546_at	ssory protein	IL1RAP	AB006537	2.5	1.5	8.9
1754_at	death-associated protein 6	DAXX	AF006041	3.1	3.1	8.9

33365_at	KIAA0945 protein		AB023162	0.0	0.0	σ
1354_at	neurotrophic tyrosine kinase, receptor, type 2	NTRK2	U12140	1.7	90	
465_at	HIV-1 Tat interactive protein, 60 kDa	HTATIP	U74667	9	2.8	0
33135_at	solute carrier family 19 (folate transporter), member 1	SLC19A1	U17566	1.6	5,3	0.00
45748_at	SAR1 protein		A1143121	15.6	1.9	6.8
59870_at			A1003552	2.3	1.1	6.8
91329_at			AI669284	0	0	6.8
59548_at			AI732248	3.3	4	8
32156_at	poliovirus receptor-related 2 (herpesvirus entry mediator B)	PVRL2	AF044968	23.4	5.9	6.8
80897_at			R63836	1.8	1.7	8.9
74908_at	interferon-induced protein 35	IF135	AW026462	19.7	35.8	6.8
53157_at			AI092930	1.2	1.1	8
35310_at			D45288	9.4	5.5	8.9
38227_at	microphthalmia-associated transcription factor	MITF	AB006909	8.9	2.2	88
34057_at	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	SLC28A2	U84392	2	0	8.8
34066_at	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	Н6РД	AJ012590	m	1.3	8.8
39210_at	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	FUT4	M58597	2.8	6.2	8.8
1048_at	retinoid X receptor, gamma	RXRG	U38480	1.7	0.8	8
56968_at	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)	MEF2D	AL118605	3.4	5.6	8 8
56459_at			AI821762	6.0	9.0	888
77121_at			AI733322	2.4	2.1	88
59865_at			AI003502	8	2.5	8.8
47484 at			H17489	32.5	22.9	8.8
61149_at			AA88887	2.2	2	8.8
46069_at			W45330	5.2	3.8	8.8
65262 <u>r</u> at			H29209	0.5	1.8	8.8
			N71364	2.3	4.1	88
82421 i at			AI554417	4.1	6.2	8.8
85192 r at			AI351062	9	2.5	8.8
45326_at	hypothetical protein PRO2577		N21414	0.1	2.2	8.8
52425_at	KIAA1376 protein		AA164405	1.4	0	8.8

50804_at	L-kynurenine/alpha-aminoadipate aminotransferase		AIZGRAN	0 0	13 6	0
45099_at			N92526	0 0		0.00
55830_at			700000	1.0		X.X
47870 r at	hypothetical protein DKFZp761C169		AMODODO	19	13.5	8.8
54940 at			AW003245	22.9	4	8.8
38786 24			R49669	2.9	3.2	8.8
72130 at	promiserocytic reakernia	PML	M82827	25.1	20.3	8.8
42130 at			AA400680	1.4	4.7	88
40102 at			T91299	5.9	0	8.8
04403 - 41			AI459092	1.7	6.0	8
30493 at	lymphocyte specific protein 1	LSP1	M33552	4.7		0 00
44688 at	KelA associated inhibitor		AA614049	7.7	6.7	000
41432 at		RPS6KA5	AF090421	5.5	3.3	87
33016 at	replication factor C (activator 1) 3 (38kD)	RFC3	L07541	2.1	0	8.7
33010 at			AI052224	2.4	1.4	2 2
39710 at	r311 protein		U30521	9.9	35	2 0
32254 at	vesicle associated membrane protein 2 (synaptobrevin 2)	VAMP2	AL050223	1.8	1.7	8.7
34/45 at			AF070570	38.1	14.3	78
356/5 at			AF037261	4 8	0	7.8
36469_at	dystrobrevin, alpha	DTNA	U46744		7 0	0.7
36780_at	clusterin (complement lysis inhibitor, SP-40,40, sulfated	CLU	M25915	32.0	2	000
	2,			6:36	n e	xi Xi
38286_at	KIAA1071 protein		700000			
694 at	mucin 5, subtype B, tracheohronchial	0.00	AB028994	2.5	1:1	8.7
64989 r at		MOCOR	X/4955	1.3	0.4	8.7
53410 at	tumor susceptibility gene 101	70,0101	AA482282	3.2	2.8	8.7
61896 at		190101	AA553646	0	2.3	8.7
75031 at			AL038511	3.6	4.4	8.7
57847 at			AW051699	7	0.4	8.7
63288 at			R48461	2.9	2.6	8.7
51155 at			R12689	2.9	4.2	8.7
11713 at			AL043669	19.8	6.2	8.7
41/46_5_41	ruffor flectosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; Iranscrntion factor IIIA-interacting protein		AF061034	24.3	28.1	8.7
57739 at	hynothetical protein FI 120105					
12 10 10	Inflormence protein Lagarda		A1949010	4	3 7	7 8

Figure 13DD

45855_at			AI872417	3.4	3.3	8.7
45889_at			AW024527	0	0	8.7
57194_at			157670	0	2.6	8.7
64344_at	lysosomal-associated membrane protein 1	LAMP1	AI984264	1.8	0.8	8.7
44093_at	hypothetical protein FLJ13441		W28327	5	8.8	8.7
39917_at	gamma-tubulin complex protein 2		A1961040	2	9.0	8.6
40552 s at			AL049987	0	0	8.6
33439_at	transcription factor 8 (represses interleukin 2 expression)	TCF8	D15050	4.1	2	8.6
37026_at	core promoter element binding protein	COPEB	AF001461	6.9	5.7	8.6
41503_at	KIAA0854 protein		AB020661	23.1	10.5	8.6
36472_at	N-myc (and STAT) interactor	IMN	U32849	7.8	12.1	8.6
36130_f_at	metallothionein 1E (functional)	MT1E	R92331	78.7	4.6	8.6
237_s_at	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha	PPP2CA	M60483	7.6	D.	8.6
	11.000					
59414 at			AI480103	0.8	0	8.6
47510 r at			AI924696	1.9	1.9	8.6
62256_at			R50614	0	1.8	8.6
90421_at	conserved gene amplified in osteosarcoma		AA633203	36.5	35.1	8.6
70516_at	leucine-rich protein mRNA		AI817736	14.2	6.4	8.6
59630 g at			AA143009	1.2	0.5	8.6
69142_at			AI635522	72.4	7.89	8.6
43958_at			AI499157	O	6.0	8,6
47655_at			AI022328	6.4	6.5	8.6
43031_at			AL045916	0	1.8	8.6
60116_r_at			N59866	1.8	1.1	8.6
55412_at			AI768697	3.1	1.6	8.6
49792_at			AI298555	2.7	2.4	8.6
55423_f_at	- 1		AA001367	1.1	6.0	8.6
39013_at	APG5 (autophagy 5, S. cerevisiae) like	APG5L	Y11588	1.6	1.2	8.5
36734_at		SPRR2A	M21302	1.2	0.8	8.5
39744_at	DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 3	DDX3	AF000982	33	1.5	8.5
40088_at	nuclear receptor interacting protein 1	NRIP1	X84373	15.6	6.6	8.5
31522 f at	\neg	H2BFG	622082	5.4	2.5	8.5
34709 r at	stromal antigen	STAG2	275331	7.4	1.8	8.5
1241_at	protein tyrosine phosphatase type IVA, member 2	PTP4A2	U14603	0	0.5	8.5

89894 2			1 50110014		7	0
1			A1331103	† . 1	5.4	0.0
59266_at			AI272654	1.2	1.7	8.5
79512_at			AI248270	m	2.5	8.5
70238_at			AA521399	3.9	2.3	8.5
64176_at			AI650542	10.3	6.9	8
51092_at	putative zinc finger protein NY-REN-34 antigen		AI950095	21.1	14.6	8.5
73455 fat			H72723	70.4	8.2	8.5
55974_at			AI732621	0.8	6.0	8.5
56435_at			AA573749	6.7	5.9	8,5
64508_s_at	KIAA0430 gene pr		A1968969	7.4	6.4	8.5
64739_at	docking protein 2, 56kD	DOK2	AI828929	8.8	8.3	8.5
41374_at	ise, 70kD, polypeptide 2	RPS6KB2	AB016869	1.5	0.4	8.4
39084_at	muscle)		X56832	1.2	3.2	8.4
40621_at	gulator		608890	0.2	1.1	8.4
40641_at			AF038362	0	0	8 4
33455_at	Đ	ALDOB	X02747	0		8 4
36484_at		GALNT3	AI935146	12.9	5.5	8.4
						;
41283_at	tein H3 (2H9)	HNRPH3	AF052131	1.3	0.4	8.4
32629_f_at	, subfamily 3, member A1	BTN3A1	U90552	10.8	6.6	8.4
34318_at	JM4 protein		AJ005896	2.9	2.7	8.4
40738_at	CD2 antigen (p50), sheep red blood cell receptor	CD2	M16336	8.0	1	8.4
566_at	promyelocytic leukemia	PML	M79462	6.1	9.9	8.4
66442 f at			AA774820	1.1	0.2	8.4
60305_at			AI015280	4.3	3	8.4
60723_at			AA744550	1	6.0	8.4
61140_at			AI768092	1.1	0.2	8.4
47215 r at			AA129058	4.9	2.9	8.4
84319_at			AI684171	0	0	8.4
44640 at			W30985	40.2	11.6	8.4
33489_at	trefoil factor 2 (spasmolytic protein 1)	TFF2	U47292	1	0	8.4
44602_at			AA156238	0.3		8.4
45922_at			AI560775	2.6	4.6	8.4
45225 at	ATPase, Class I, type 8B, member 2	ATP8B2	AA142939	9.1	1.6	8.4
52750_at		!	A1632711	1.6	0.4	8 4

40907 at			AA043502	6.4	6.5	8.3
31970_r_at	protein phosphatase, EF hand calcium binding domain 2	PPEF2	AF023456	0.7	9.0	8.3
32480_at	homeo box C4	HOXC4	X07495	16.6	2.1	8.3
1783_at	ras association (RalGDS/AF-6) domain containing protein JC265		M37190	1.7	0.5	8.3
37360_at	lymphocyte antigen 6 complex, locus E	LYGE	U66711	13.4	13.6	8.3
38740_at	factor 1 (EGF response factor 1)	BRF1	X79067	2.5	0.8	8.3
39230_at	similar to APOBEC1		AL022318	4.4	11.8	8.3
46806_at			R66690	3.8	0.4	8.3
76551_at			AI125848	1.6	1.1	8.3
45486_s_at			AW021213	1.4	0.8	8.3
59347_at			R25153	0	1.5	8.3
67975_at			AA934126	8.0	6:0	8.3
52535_s_at		CDKN1B	AI680672	9.1	3.9	8.3
51084_at	SUMO-1 activating enzyme subunit 1		AI339364	2.5	1.2	8.3
49943_at			AI681558	11.3	3.8	8.3
44051_at	SMC4 (structural maintenance of chromosomes 4, yeast)-like 1	SMC4L1	AI338462	1	1.6	8.3
55361_at			AI821565	4.3	6.5	8.3
56080_at			AI703473	13.1	12.8	8.3
56697_r_at			AI791520	7.1	8.2	8.3
85630_at			AI086384	0	0.3	8.3
1357_at	ubiquitin specific protease 4 (proto oncogene)	USP4	U20657	5.7	3.4	8.3
32859_at	signal transducer and activator of transcription 1, 91kD	STAT1	M97935	3.2	18	8.2
33847_s_at		CDKN18	AI304854	6.6	5	8.2
36860_at	KIAA1064 protein		AB028987	1.1	1.2	8.2
77757_f_at			AA806526	3.2	2.3	8.2
42764_at			AI459108	0.1	0.1	8.2
58370_at	hypothetical protein DKFZp761A052		AW003291	0.2	0.4	8.2
87874_at			T69727	4.7	4.4	8.2
54990_at	hypothetical protein		AW009586	16.3	9	8.2
53468_at			AI149508	0.2	0.3	8.2
64394_at	cadherin 12, type 2 (N-cadherin 2)	CDH12	AI476284	0.4	9.0	8.2
45074_at			N69656	3.6	2.2	8.2

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48081_at	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)	MACS	AA131320	18.7	7.3	8.2
53756_f_at			AA709471	11.3	0.7	8.2
88927_at			AA889052	3.8	2.2	8.2
2055_s_at			M34189	2.8	1.5	8
33538_at	myelin gene expression factor 2		H96671	1.1	0.5	8.1
39995_s_at	WW domain-containing oxidoreductase	WWOX	U13395	2.8	1.9	8
1909_at		BCL2	M14745	12	6.6	8
33997_at			AL049449	1.6	0.7	8
82887_at			AI760827	0.5	5.7	8.1
81659_at			AI928037	0.3	1.8	8.1
65364_at			W56309	6.3	9.2	8.1
	leucine aminopeptidase		AF034175	10.1	15	8.1
63921_at			AI683528	1.4	1	8.1
64804_r_at			T40707	6.3	3.1	8.1
73574_at			AI290214	4.8	3.7	8
50365_at			AI760821	1.1	3.5	8,1
49939_at	KIAA1201 protein		AL042980	2.3	3.4	8.1
52355 g at			AW003924	1.6	3.8	8.1
84963_r_at			R42423	4.9	2.9	8.1
36954_at	KIAA0218 gene product		D86972	7.4		8
65827_at	STIP1 homology and U-Box containing protein 1	STUB1	A1630895	7.2	6.3	8
214_at	msh (Drosophila) homeo box homolog 1 (formerly homeo box 7)	MSX1	M97676	1.2		8
34981_at	potassium voltage gated channel, shaker related subfamily, member 5	KCNA5	M55513	1.8	1.3	Ø
31418_at	ity group (nonhistone chromosomal) protein 17-like 1	HMG17L1	Z97055	3.4	4.3	∞
1826_at	family, member B	ARHB	M12174	0	0	00
32940_at	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	AMMECR1	AJ007014	8.4	1.1	0
32288_r_at	ce receptor subfamily C, member 3	KLRC3	AJ001685	9.0	0.5	000
34699_at	CD2-associated protein	CD2AP	AL050105	20.4	12.9	80
259 s at	in alpha (TNF superfamily, member 1)	LTA	M16441	13.8	2.9	8
34573_at	ephrin-A3	EFNA3	U14187	9.0	O	00

41 300 at	Indrodiast growth factor 18	FGF18	AA022949	1.6	C	α
37294_at	B-cell translocation gene 1, anti-proliferative	BTG1	X61123	34.3	15.2	α
37980_at	CBF1 interacting corepressor		1103644	4 1	19.5	0 0
66332_at			R43566	1 6	101	٥
79145_at			W72060	12.5	ά	ο
79520_at			AW022213	18.4	οα	٥
63382_at	interferon consensus sequence binding protein 1	ICSBP1	A1073984	53.5	35.7	Σ
72361_at			AIRREDER			
87585_at			AA565209	29	1 -	
61745_r_at			N76044	5.1	2.7	
44422 r at			D59337	σ	33	
65898_at			AI743396	2.1		
59454_at	serine/threonine kinase 17a (apoptosis-inducing)	STK17A	AI806790	2.1	2.3	0
63663_at			AA649208	1.1	C	~
80940_f_at			A1147061	0	00	
37684_at	solute carrier family 21 (organic anion transporter), member 9	SLC21A9	AB020687	8.4		
1084_at	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	ABL2	M35296	11.3	1	7.9
32137_at	jagged 2	JAG2	AF029778	90	6	7.0
40496_at	complement component 1, s subcomponent	C1S	104080	26.3	T U	0.7
629_at	interleukin 9 receptor	IL9R	L39064	0.2	0.0	7.0
35328_at			AF055023		1 P C	6.7
1885_at	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xenderma nigmentation group B	ERCC3	M31899	10	1.7	7.9
38301_at	adenosine kinase	ADK	U50196	4.1	-	7.9
57406_at			AI240813	1.4	2.3	7.9
50546 at			AA761629	2.8	2.4	7.9
42582 at			N22508	1.2	2.3	7.9
44 / 18 at			AA577672	9.9	5.7	7.9
82992_r_at			AI565735	1.3	1	7.9
			AA904435	2.3	1.1	7.9
55002 4 24			AA995447	2.6	1.2	7.9
2000 I at			H14337	0	3.5	7.9
89024 at			A1720099	000	S ()	7

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10 C1010			AI668557	3.5	2.4	7
45541_s_at			AW015697	1.7	3.6	7
46198 at			AI356548	2.5	3.2	7.9
T			U55967			7.9
at	brefeldin A.inhibited guanine nucleotide exchange protein 2		AI741843	5.1	2.9	7.9
at			AA581878	6.4	9	7.9
t_at	ribosomal protein, large, PO	RPLP0	AA588862	4.4	4.1	7.9
gat	runt-related transcription factor 2	RUNX2	L40992	0	C	7 8
-	SH3-containing protein SH3GLB1		AB007960	0	0.7	7.8
Ħ	metastasis-associated 1-like 1	MTA1L1	W26677	1.3		7.8
at	TNF-induced protein		AF099935	19.9	2 6	7.8
at	Duffy blood group	FY	X85785	0.5	0.3	7.8
T	protease, serine, 8 (prostasin)	PRSS8	L41351	1.5		7.8
_at	KIAA0211 gene product		996980	0.5	0.8	7.8
56927_at			W49628	4.3	4.5	7.8
1	- [AA641972	493	59	7.8
T	2,3'cyclic nucleotide 3' phosphodiesterase	CNP	D13146	23.7	6.6	7.8
63202_at			AI218553	0	2.8	7.8
83013_1_at			AI400387	1.1	0.8	7.8
60460_at			N95430	1.6	0.8	7.8
86261_at			AA017070	15.5	12.3	7.8
69/08 at			AI689617	1.6	1.6	7.8
46207 at			AI640326	1.5	0	7.8
63124_at			AA631399	3.6	1.7	7.8
<u></u>			AI679413	2.6	6.0	7.8
41190_at tum (tra	tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein)	TNFRSF12	U83598	0.7	0	7.7
at		H3F3B	748950	ď	1 3	
_	chromosome 14 open reading frame 3	C140RF3	AJ243310	0.4	5 -	7
뉽	aining 4	BRD4	Y12059	32	c	7
	JAK binding protein		AB000734	4.9		7
넒		TDGF3	M96956	1.2	0.3	7
	hydroxy delta 5 steroid dehydrogenase, 3 beta- and steroid delta- isomerase 2	HSD3B2	M77144	1.6	1.1	7.7
38278 at Imor	modulator recognition factor					

entors:	7-411	naconen,	6

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5056/ r at			AA780080	9.0	1.7	7.7
49458_at			AA921835	4.5	1.1	7.7
47206_at			AA984304	0	2.8	7.7
62857_at			AI784540	1.3	0.4	7.7
71584_at	X-box binding protein 1	XBP1	AA503434	2.5	0	7.7
83201_at			A1984360	1.4	3.2	7.7
82126_at			AA831700	0.8	0.1	7.7
64460_at	M-phase phosphoprotein homolog		AI823360	6.0		7.7
45298_at			N66638	9	2.8	7.7
44808_at			AA455864	2.5	3.9	7.7
87497_f_at			AI832016	27	21.1	7.7
47018_at			Al168404	0	0.8	7.7
56668_at			AI806747	0.4	2.3	7.7
36050_at	zinc finger protein 313	ZNF313	AL031685	9.0	0.5	7.6
39041_at	Itransferase (E2 component of pyruvate	DLAT	Y00978	0	3.7	7.6
	dehydrogenase complex)					'
32217_at			AF052105	12.6	6.3	7.6
33754_at	thyroid transcription factor 1	TITF1	U43203	2.3	0.3	7.6
34312_at		NCOA2	AI040324	4.5	œ	7.6
1562 g at	losphatase 8	DUSP8	U27193	2.9	3.7	7.6
36066_at	KIAA0828 protein		AB020635	5.7	2.4	7.6
36103_at	small inducible cytokine A3 (homologous to mouse Mip-1a)	SCYA3	D90144	13.1	6.1	7.6
36943 <u>r_at</u>	pleiomorphic aden	PLAGL1	U81992	8.1	5.8	7.6
37195_at	cytochrome P450, subfamily XIA (cholesterol side chain cleavage) CYP11A	CYP11A	M14565	2.9	1.1	7.6
40681_at	integrin, beta-like 1 (with EGF-like repeat domains)	ITGBL1	AB008375		0.4	7.6
47202 at			AA116061	-	1.2	7.6
53862_at			AA447888	0.1	0.7	7.6
62431_at			AI197909	7.1	7.9	7.6
62866_at			AI274114	1.4	1.8	7.6
55217 i at			AA886955	2.2	0	7.6
81583_f_at			AI243475	38.1	2.1	7.6
44920_at			AI914925	12.7	4.8	7.6
43312_at			R10159	2.8	2.6	7.6
68447_at			AI809257	0	1.4	7.6

EDEAG 2+	himothotical arctain Fl 100F00					
32340 at	hypometical protein reachago		AA747316	2.1	2.5	7.6
50853 at			AI299719	0.8	0.4	7 6
45893 at			H24387	7.5	Ľ	7.6
38831_f_at	erythropoietin	EPO	AF053356	ας	0 0	2 7
52107 g at	CGI-90 protein		A1800674	i r	6.5	7.0
35009_at	low density lipoprotein related protein 2	LRP2	1133837	, - C R	4.0	7.5
35386_at	acetylcholinesterase (YT blood group)	ACHE	41825097	ο α	0.7	7.7
32294 g at		LHCGR	M63108	000	2.0	7.5
1338_s_at	0, subfamily IIA (phenobarbital inducible),	CYP2A6	X13930	0.0	2.0	7.5
		!		?	7.0	Ü.
32353_at	ma (Fletcher factor) 1	KLKB1	M13143	1.2	10	7.5
37162_at	DNA segment, single copy, probe pH4 (transforming sequence,	D10S170	872869	1 4	000	7.7
				•	3:1	<u>;</u>
1317_at	shage stimulating 1 receptor (c-met-related tyrosine	MST1R	X70040	8.0	2	7.5
38735_at			AB011085	0.3	1.5	7.5
35638_at	or, runt domain, alpha subunit 2; translocated	CBFA2T1	D43638	2.4	0	7.5
	Dicialed					
40344_at		NLGN1	AB028993	1.3	2.3	7.5
37535_at	element binding protein 1	CREB1	M27691	13	1 6	7.5
38436_at	u		D87440	0.0	2 2 2	7.7
38485_at	drogenase (ubiquinone) 1, subcomplex unknown, 1	NDUFC1	AA760866	1.2	0.7	7.5
	(6KU, KFYI)		_			
38772_at	giogenic inducer, 61	CYR61	Y11307	0.4	-	7 5
38319_at	CD3D antigen, delta polypeptide (TiT3 complex)	CD3D	AA919102	9.0	40	7 7
66366_at			AI695056	0	90	7.5
/3703_at			AA777616	7	4.7	7 5
51193_at			R14888	2	c	7 5
82251_at			AI819034	0.5	0.7	7.5
44833_s_at	heat shock 70kD protein 8	HSPA8	AI986374	2.2	2 1	7.5
48210_r_at			AA251543	5.1	2.0	7.5
72313_at			AI041279	3.2	2	7.5
/2092_f_at			AA677864	4.9	3.4	7.5
46033_at			AA063037	2.1		7.5
42007_at			AA210684	1.9	3.1	7.5

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27161 24			W28948	0.7	0.4	7.5
3/101 41			3038358	0.3	0.5	7.5
54125 at			0.00000		1 / 1	7 5
72546_at			A1033943	1.0	1	5 7
40074_at	methylene tetrahydrofolate dehydrogenase (NAD+ dependent),	MTHFD2	X16396	ɔ ·-	5	C.,
1705 24	retinoblectoms.hinding protein 2	RBBP2	S66431	5.9	2.4	7.5
1/05 41			A1982669	3.1	8.9	7.5
38688 24	KIAA0461 protein		AB007930	3.1	3.3	7.4
30050 at	KIAAOK10 protein		AB011182	2.2	5.1	7.4
40053 at	KIAA0573 profein		AB011145	0.1	3.1	7.4
38187 at	N.acetyltransferase 1 (arylamine N.acetyltransferase)	NAT1	D90041	0.5	0.5	7.4
32321 at	major histocompatibility complex, class 1, E	HLA.E	X56841	2.6	2.5	7.4
31524 fat		HZBFK	280782	4.5	1.4	7.4
33879 at			U79528	3	0	7.4
33454 at			AF016903	2.2	3.1	7.4
3/333 at	KIAA0063 gene product		AL021707	2.3	1	7.4
32530_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	YWHAQ	X56468	4.8	2.9	7.4
	activation protein, theta polypeptide	3			c	7 7
36176 at	tubulin-specific chaperone c	TBCC	U61234	5.6	3.0	4
37681 i at		MATR3	AB018266	1.4	0.3	7.4
41107 at	svntaphilin		AB002372	0.8	0	7.4
٠.	Charot Leyden crystal protein	CLC	L01664	0	1.7	7.4
61757 at	4		AI273692	8	3.3	7.4
48238 at			AA421131	3.9	1.1	7.4
67068 at			AI298437	0.3	2.4	7.4
49312 at	CGI-102 protein		AA747303	4.4	3.2	7.4
51474 at			AA127641	58.7	2.4	7.4
44306 at			AA707318	3.8	8	7.4
69439 at	Ihynothetical protein MGC5356		AI655792	7.9	4.2	7.4
88792 at			AI681436	0.4	1.8	7.4
71/83 24			AI937154	0.1	0.8	7.4
74482 at			AW025586	1.2	8.3	7.4
13738 at			AA565834	3.6	2.9	7.4
50228 at	hemnolohin gamma G	HBG2	AA992592	0	4.3	7.4
77703 24	2		AI016311	0	4.2	7.4
4/475 01						

144331 at			AI922892	8.1	12	7.0
44050 at	_		AW016801	1.7		1
	CGI-34 protein		AA528059	129		1,1
45011 at			N48679	90	7 -	1.1
			N21600		1.7	7.7
61867_at	ribosomal protein S20	BPC20	20077040	‡ 6	1.4	4.7
57251_at	Ť	050	AA4/942/	6.2	2	7.4
55720 at			AA394228	4.6	3.3	7.4
62052 f at			W37770	0.7	3.9	7.4
41295 at	GTT1 protein		H60827	2	0.5	7.4
44120 at			AL041780	5.9	2.9	7.4
50297 f at	anolinoprotein 1-3		AI879381	6.9	6.9	7.4
38691 s at	Surfactant pulmonany accordated	APOL3		10	17.1	7.3
41474 at	T -	SFTPC	J03553	2.2	2	7.3
39901 at	FOR like repeate and discitled in the second se	KIF2	Y08319	13.3	24.6	7.3
41208 24	mostocides allu discolulii i-like domains 3	EDIL3	U70312	2.3	0.0	7.3
27757 24	ingiliosidase, alpila, class 1A, member 2	MAN1A2	AF027156		C	5,7
0// 04_at	iectini, galactoside-binding, soluble, 3 binding protein (galectin 6 Ibinding profein)	LGALS3BP	L13210		19.8	7.3
37587 at	recoverin					
37996 c 34	0,000	RCV1	S43855	1.1		7.3
2021 5 25	Systematical protein carprotein Kinase	DMPK	L08835	0		7.3
73789 24	Cycliil E.I	CCNE1	M73812	0.4	0 0	5.7
19756 at			AA706942	22	200	5.7
49230 at	peptidyiprolyi isomerase A (cyclophilin A)	PPIA	A1952127	1 ×	7.0	, r
Segue at			R01845	0.0	0 0	5.7
88833 r at			H68862	7.7	0.7	5.7
45/10_at	UNA segment, single copy, probe pH4 (transforming sequence, thyroid-1,	D10S170	H15313	0	0.5	7.3
47324_at	heat shock 90kD protein 1, alpha	ИЗВСА	100001			
92101 s at	ubiquitin A-52 residue ribosomal protein fusion product 1		AA139881	3.7	2	7.3
51842 at	T connoid library was a second and a second	UBASZ	AI802408	0	9.0	7.3
49837 at			AI570531	15	2.9	7.3
			AI209180	3.4	2	7.3
٦, ۱	Orotoin photostate 10 mm		AA525067	1.4	0.2	7.3
	provent prospiratase 1.0 magnesium-dependent, delta isotorm	PPM1D	078305	1.1	0.1	7.2
31985 at			AL049228	43	7.6	0 1
				>	7:/-	

1411 Fiaconen, or ar.

34931 at	KIAA0940 protein		AB023157	0.8	6.0	7.2
39920_r_at	C1q-related factor		AF095154	1.8	0.1	7.2
317_at	ле, 1 (legumain)	PRSC1	D55696	2.5	8.6	7.2
32779_s_at	inositol 1,4,5-triphosphate receptor, type 1	ITPR1	U23850	2.2	2.1	7.2
40428 i at			AW043812	0	0.3	7.2
1065_at	fms-related tyrosine kinase 3	FLT3	U02687	2.2	1.8	7.2
32628_at	zinc finger protein 161	ZNF161	D28118	3.7	3.5	7.2
1953_at	lial growth factor	VEGF	AF024710	28.4	6.2	7.2
1106_s_at	alpha locus	TRA@	M12959	6.0	1.2	7.2
37994_at	retardation 1	FMR1	X69962	00.	CI	7.2
63350_at	hypothetical protein FLJ20707		N66569	1.7	0.4	7.2
81276_at			N63894	3.5	5.5	7.2
81726 at			AI885498	15.1	10.7	7.2
77922_at			AA884304	17.6	0.5	7.2
50868_at			AW021051	1.2	11.4	7.2
43524_at	KIAA1170 protein		C14031	42.1	18.4	7.2
82383_r_at			AI215733	0.5	0	7.2
44000_at			AA534378	2.8	2.8	7.2
63142_at	hypothetical protein FLJ14033 similar to hypoxia inducible factor 3, alpha subunit		C16964	4.0	1.5	7.2
50146_at			AI819320	1.9	3.1	7.2
44567_at			A1992275	1.4	0	7.2
51024_at			AI400509	13.3	17.3	7.2
45220_at			AA150501	9.0	2.2	7.2
45608_at			AI202327	11.7	4.7	7.2
84373_at	fragile X mental retardation, autosomal homolog 2	FXR2	AI703341	2.2	1.1	7.2
47844_at			AA131302	1.7	2.5	7.2
58848_at	d protein kinase kinase 2	MAP2K2	AI809489	2.8	2.8	7.2
64267_f_at	ated protein interacting protein (duo)	HAPIP	AI962617	9.0	2.7	7.2
47113_at)	KLF5	AI815057	31.5	41.2	7.2
52860_at	hypothetical protein FLJ20279		AA039793	0	8	7.2
55521_at			AI201082	1.9	0.2	7.2
1280 i at			Z25424	0.1	0	7.2
1937_at			M26460	8.0	0	7.2
60690_at			AA203328	4.2	4.4	7.2

40285_at adenylate 32854_at f-box and 45509_g_at NADH det coenzyme 39422_at KIAA04377 1252_at DNA segn 37925_r_at apolipopri 33922_at apolipopri 33922_at netrin G1 33429_at adrenome 34777_at adrenome 36535_at microfibril 844_at GR01 onc		ADCY7	D25538	7.2	5.5	
at g at t t t at at at at at at at at at at				7./		-
g at t t at at at at at at at at at at at			ADO14506	,	2.1	7.5
t t at at at at at at at at at at at	e) Fe-S protein 4 (18kD) (NADH.		H45672	6.4	2.5	7.2
t at at at at at at at at at at at at	KIAA0477 gene product					
at at at at at at at at at			AB007923	23.8	11.2	7.1
g at at at at at at at at at at	segment, single copy probe this califers. Call (deleted in osis		M73547	0	0.7	7.1
at at at at at	apolipoprotein M		A 12/15/13/			
at at	PR domain containing 2, with ZNF domain	PROMO	111 70 20	5 0	0.8	7.1
at at		7,110,11	01/030	5	0	7.1
at			A114085/	2.6	9.0	7.1
at	adrenomedullin		AI624840	4.7	1.8	7.1
	sociated protein 1	AUM	D14874	27.2	8.5	7.1
	A Cinhibitory and a feet a	MFAP1	U04209	5.8	5.1	7.1
	melanoma growth of military	PPPIRIA	U48707	9.0	0.5	7.1
	Concinua grown sunnalaning activity, alpha)	GR01	X54489	486.7	11.5	7.1
39476_at			7/0005		,	
	basic transcription factor 3	PTE2	25500514	0.0	0.6	7.1
76768_at			A1788775	0.5	1.2	7.1
62375_at			A179226/	3.1	0.3	7.1
53959 at			A1521162	1.4	9.0	7.1
Γ	natural killer cell recentor 284		AW009031	1	1.1	7.1
at	1		AI871467	2.3	3.8	7.1
at	ancient conserved domain profein 4		AA534572	3.1	1.6	7.1
at			AI636759	9.6	æ	7.1
			AA481181	3.5	5.5	7.1
44265 at			AA460146	0.7	1.1	7.1
			H10709	1.9	3.9	7.1
54166 at			R97957	4.3	2.7	7.1
41985 at			AI082750	4.3	1.9	7.1
48940 at			AA143802	2.6	1.6	7.1
53155 at			AA773807	0	4.3	7.1
Π	GPI anchored metactasis associated protein hamela		AA608559	5.7	4.4	7.1
1	tastasis associated profess normolog		AJ223603	1.6	0	7
10507_6 at 121110 111	וואפ ז	ZFPL1	AF001891	2.5	17	7

Figure 13PP

80	
gure 13	
丘	

40109_at	ctor (c-fos serum response element-binding	SRF	J03161	0	1.7	7
	∵ 1.					
1478_at	IL2-inducible T-cell kinase	ITK	L10717	9.7	4	7
34776_at	Cdc42 effector protein 4; binder of Rho GTPases 4		W27541	8.6	0	7
36116_at	thyroid hormone receptor interactor 10	TRIP10	AJ000414	215.9	26.7	7
1052_s_at	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	M83667	15.2	c	7
38127_at	syndecan 1	SDC1	248199	0.1	0.1	7
75868_r_at			AI791208	41.5	10.4	7
50855_at			AA789332	0	8.4	7
59187_at			AA970451	1.6	1.9	7
60417_r_at			AI081821	5.7	3.3	7
75201_f_at			AI688900	5.5	11	7
77231_at			AI761622	4	3.1	7
59299_at			Н98190	3.3	3.3	7
91636_at			AI652725	886.7	27.7	7
83074_at			AI817967	2.3	6.0	7
62624_at			AL043110	ō	1	7
86090_at			T69814	3.3	1.9	7
68084_at			AI916367	2.7	1.1	7
59627_at	hypothetical protein FLJ10628		AA885169	2	5.5	7
70209_at			AI761629	6.4	1.3	7
49600_at			AI936984	3.5	3.9	7
49485_at	PR domain containing 4	PRDM4	W22625	3.5	1.7	7
42867_at			AI701798	2.4	2.3	7
64174_at			A1127460	11	8.6	7
83561_at			W26087	8.2	2.8	7
56273_at	hypothetical protein FLJ20514		AA534400	3	0	7
72462 f at			H40456	1.4	0.4	7
78727 at			AA425815	0	0	7
38712_at	membrane protein CH1		AL035291	6.7	6.1	6.9
34966_at	T brachyury (mouse) homolog	T	AJ001699	1.1	0	6.9
32755_at	actin, alpha 2, smooth muscle, aorta	ACTA2	X13839	3	4.3	6.9
34175_r_at			AL049242	9.0	0	6.9
678_at		ALPP	104948	3.4	1.1	6.9
32429 f at	32429_f_at zinc finger protein 33b (KOX 31)	ZNF33B	D11958	0	1.4	6.9

mventors:

	AI934552	.13
	AA129377	2.
	A1968249	2.
	W63595	2.
	190987	
	AI311917	5.
	F02458	4
	AI817760	29.
	AA425402	0
	AI242202	0
	۹.	1.
	AA280886	G
	AI963771	2.
	AI475473	53.6
	AI821408	4
	H12612	3.
	AI692654	1.9
	AI523569	2.7
	\Box	1.8
	AA639553	1.6
	AA024934	0.0
	AI810946	2.4
	AI146850	3.8
	AA513748	5.3
	W22908	2.6
	AA928996	
	U37352	
	AF039843	0.4
×		

CGI-141 protein

47159_at 56683_i_at

54060_at

61180_f_at

89276_at

46727_at

PRKAG2

protein kinase, AMP-activated, gamma 2 non-catalytic subunit

80665_r_at

57101_at 46697_at 44763_at

47287 at 62582 at 53334 at 64490 at

49339_s at reticulocalbin 1, EF-hand calcium binding domain 67857_at

hypothetical protein FLJ10675

57619_at 58549_at

47818_at

85019_at

59341_at

RCN1

0.8

6.9

6.9 6.8

3.1

6.9 6.9 6.9

0.8

0.1

7.6

D87078 AB020648 X80754 AF038954

ATP6J

NCK2

DRG2

developmentally regulated GTP-binding protein 2 ATPase, H+ transporting, lysosomal (vacuolar proton pump),

T-box 19 KIAA0235 protein KIAA0841 protein

36702 at 35359 at 36888 at

37664_at 38814_at

member J NCK adaptor protein 2

48025_at 46778_at

AJ010277

TBX19

3.8

51.7

0.1

PPP2R5C

protein phosphatase 2, regulatory subunit B (B56), gamma

sprouty (Drosophila) homolog 2

33700_at

isoform

hypothetical protein FLJ20173 DKFZp564J157 protein hypothetical protein LOC57187

46093_at 46218_at

32125_at

176_at

SPRY2

	indical localization signal defered in velocardiolacial syndrome	NLVCF	AF034091	2.4	16.3	8.9
33881_at	fatty-acid-Coenzyme A ligase, long-chain 3	FACI 3	44977580	0.0		
35568_at	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	ADCYAP1R1	D17516	1.7	2.1	6.8
32529_at	transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment		X69910	21.7	23.9	6.8
36949_at	casein kinase 1, delta	CSNK1D	17100111		ľ	
37736_at	artate (D.aspartate) O.methyltransferase	PCMT1	013003	0 0	0.7	9.9
38284_at		1	0.13692	0.5	2	6.8
50545_at			AAAA74E0	7.7	/ .	6.8
50807_at			AA128061	7.7	9.1	6.8
76062 i at			AA020898	0.0	1.7	8.9
50864_at			R94508		7,00	0.0
60903_s_at	T-cell lymphoma invasion and metastasis 2	TIAM2	A1126294	416	25.5	0.8
79795 at			AI361218	0.8	2.9	9.0
76700 at			AI091533	1.6	2.7	89
55239 at			AI221251	1	1.9	8.9
59357 at			AA233120	6.1	7.4	6.8
52667 at			AI433468	0	0	8.9
58473 at			Н09073	3.2	2.9	6.8
48085 at			AA020010	1.2	2.7	6.8
49645 r at			199531	0	2	8.9
46673 at			N66472	4.9	4.3	8.9
44884 at			H18113	0	1.4	8.9
61409 at			AA039908	4.1	7.3	8.9
78387 at			AA442889	4.4	2.3	8.9
39561 at	dynein axonemal light polypeptide /		AI244757	9	3.9	6.8
33198 at	t postadad for the first of the	UNAL4	AL008583	4.2	1	6.8
51251 at			AA206524	4.8	2.3	8.9
40218 at	7		AI189200	9.9	2	6.8
18-01-01	or synthiase (phosphatidate cytidylyltransferase)	CDS1	060808	0.1	6.8	6.7
40448_at	n homologous to Zfp.36 in mouse	ZFP36	M92843	4.9	0.5	6.7
	Uriau (HSD40) nomolog, subtamily (), member 4	DAIA	10000000			

Figure 13SS

34295_at	ubiquitin specific protease 15	USP15	AB011101	0.4	17	7 7
36600_at	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	PSME1	L07633	15.9	191	6.7
37230_at	KIAA0469 gene product	KIAA0469	AB007938	13.3	1-	
37368_at		NFATC4	AA292277	3.6	1.6	6.7
38091_at	lectin, galactoside binding, soluble, 9 (galectin 9)	LGALS9	749107	3.2	7.7	
37941_at	myosin-binding protein C, fast-type	MYBPC2	X73113	2.0	, ,	7.0
38254_at	KIAA0882 protein		ABOZOGRA		2.1	0.7
66311_r_at			H56152	α	0.0	0.7
66515_at			AA707328	6.0	0 00	6.7
28890 at			T89102	8.8	3.5	6.7
49388 at	chromosome & open reading frame 2	C80RF2	W23473	0.3	1.3	6.7
01022 at			AI743880	0	2	6.7
91032 at			AI791640	0.3	0	6.7
06222 24			AA643238	9.0	0	6.7
55031 at			AI523641	1	0.1	6.7
13300 g gt			AI819394	9.0	1.9	6.7
43300 s at	paired infinitional section of the receptor beta		AI990273	2.7	3.8	6.7
51796 at	ilypoinetical protein FLJZ3445		N30264	9.0	2.5	6.7
15018 r at			R63923	2.6	1.5	6.7
53576 24			R98767	4.6	4.1	6.7
51053 at			AI168683	4.8	3.7	6.7
45661 at			AI122787	3.8	4.8	6.7
46237 at			N90348	4.5	5.5	6.7
65715 at	no particular continued a		AW001342	4.8	2.5	6.7
13/10 24	יימינים וככלונים כספרוואסום ד	NCOA1	AL079440	2.5	2	6.7
31680 24			AA082768	0.5	0.2	6.7
61321 f at			M55630	14.3	5.5	6.7
			AA534354	0	0.8	6.7
3313/ 24	and on the second of the secon		3147616	3.1	0	6.7
45578 c at	מתבוז ומוכ כארומאם כ	ADCY3	AB011083	5.8	0	6.7
39061 at	book marrow etramal as less than		N26243	5.5	1.8	6.7
33001 at	Journa High ow Strollia cell allitten 2	BST2	D28137	5.5	9.7	9.9

Figure 13TT

37880_at	alanine glyoxylate aminotransferase (oxalosis I: hyperoxaluria i:	ALTXT	V52414	2.2		
1		, VPV	V23414	2.3	1.2	9.9
37883_i_at	hypothetical protein		A1375033	ř	1 6	
31508_at	upregulated by 1,25-dihydroxyvitamin D.3		573501	ס כ	0 -	0.0
1044_s_at	n factor 5, p130-binding	F2F5	1131556	0 0	0.1	9 0
33872_at			AR018329	1.5	4.0	9.0
37240_at	histidyl-tRNA synthetase like	HARSI	1118937	2.1		9 0
793_at	placental growth factor, vascular endothelial growth factor related PGF protein	PGF	X54936		2.9	9.9
40299_at	G-protein coupled receptor		AF091890	α		
35335_at	Rho-associated, coiled-coil containing protein kinase 2	ROCK2	AR014519	1.0	0.0	0.0
35219_at				2.8	0.3	0.0
36899_at	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)	SATB1	M97287	4.3	4.8	9.9
36573_at	J-Ala-Asp/His) box binding protein 1	DDXBP1	U78524	3.7	α	0
1217 g at		PRKCR1	X07109	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		0.0
1779_s_at	pim·1 oncogene	PIM1	1116760	100	0.0	0.0
40691 at	in 274	7NE274	171500	23	3.5	9.9
34060 g at		417 714	0/1398		m	9.9
38805 at	TG.interacting factor (TALE family homochay)	1.01	AA586695	5.8	1.1	9.9
50713 at	CONTRACTOR INCLIENCE AND A STATE OF THE CONTRACTOR AND A STATE OF	1611	X89750	6.2	4.4	9.9
60685 at			H73401	5.8	4.1	9.9
47521 at			AA292534	8	1.9	9.9
51389 at			AA621958	0.7	2.9	9.9
75652 at			AI392609	1.9	1.6	9.9
67262 at			AI983437	24.3	2.9	9.9
82961 at			AI378639	0.5	0	9.9
			AI286142	1.1	2.6	9.9
20000 at	1		AA548518	1.2	0	9.9
02140_41	Orlype (carcium dependent, carbonydrate-recognition domain) lectin, superfamily member 9	CLECSF9	AI968491	7.5	4.9	9.9
50352_at	hypothetical protein FLJ10652		4415170G		1	
61328_at	C-terminal binding protein 1	CTBP1	A1970615	0 0	2.0	0.0
87416_r_at			T91504	1.0		0.0
48098_at	glucose regulated protein, 58kD	GRP58	AA478520	2.6	0.0	0.0
84995_at			AA769482	1174	100	5
			1)	F	7.51	5

64672 at			A1339915	2	0.6	9
48573_at	zinc finger protein 161	ZNF161	AA452188) m	15.5	9'9
44972_at			AA999894	18.1	2.5	9.9
55673_at	RAB-8b protein		AI807023	16	13.1	9.9
48960_at			AI191934	1.4	1.5	99
63037 s at			AI653002	2.4	1.1	9.9
46454 at			AA401446	0.1	0.4	9.9
49843_at			A1082569	2.2	3.3	9.9
59805_f_at			A1636743	98.2	2.6	9.9
51938_at			N33202	4.0	0	9.9
44110_at			AI762752	2.9	9.9	9.9
44127 at			AA604375	4.3	2.8	9.9
31559_at	solute carrier family 13 (sodium-dependent dicarboxylate	SLC13A2	U26209	0.8	0	6.5
40082 at	fattv-acid-Coenzyme A ligase, long-chain 2	FACI 2	010040	991	11.5	7
1118 at	prostaglandin E receptor 4 (subtype EP4)	PTGER4	128175	27	200	200
34237 at	HBS1 (S. cerevisiae)-like	HBS1L	AB028961	60	0.0	9 2
38660_at	cytochrome c oxidase subunit VIa polypeptide 2	COX6A2	F27891	0.4		6.5
34708_at	ficolin (collagen/fibrinogen domain-containing) 3 (Hakata	FCN3	D88587	0.7	9.0	6.5
	antigen)					
37218_at	BTG family, member 3	BTG3	D64110	9.7	8.7	6.5
40698_at	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)	CLECSF2	X96719	0.3	8.4	6.5
38326_at	te G0/G1		M69199	64.6	20.8	6.5
58024_at			N32301	0	1.2	6.5
82892_at	hypothetical protein FLJ12567		AA192481	2.9	2.3	6.5
56894_at	RAB38, member RAS oncogene family	RAB38	N29070	2.6	5.1	6.5
56930_at	integrin beta 1 binding protein (melusin) 2	ITGB18P2	AI568769	1.1	1.1	6.5
56991_at			AI927199	4.7	1.2	6.5
42486_at			AI004422	3.4	4.1	6.5
66819_at			AA984073	3.4	1.6	6.5
67223 at			AI003757	6.9	7.8	6.5
51643_at			AL036254	5.9	3.9	6.5
49903 at	KIAA1404 protein		W72798	7.5	3.2	6.5
89178_at			AI741934	0	7.2	6.5

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60815_at			AA601208	0.4	1.2	6.5
65544 at	hypothetical protein FLJ12799		AA524503	1.2	2.5	6.5
71661_at			Al174651	9.1	5.4	6.5
59273_at	hypothetical protein FLJ11729		AI681511	2.3	2.4	6.5
46767_f_at			N95476	1.4	3.2	6.5
50083_at			A1669535	0	2.2	6.5
43190_at	mel transforming oncogene (derived from cell line NK14). RAB8 Nomolog	MEL	AA211355	8.0	1.1	6.5
55342_at			AA010697	1.1	4.7	6.5
55873_at			AI674683	0.1	13	6.5
54077_at	hypothetical protein FLJ10430		W18181	14.2	6.0	6.5
57543_at	bromodomain adjacent to zinc finger domain, 1A	BAZ1A	AA112166	8.3	6.2	6.5
42109 at			AA435715	1.5	4.3	6.5
55540_at			A1806973	2.8	1.2	6.5
42245 r at			AA461492	1.6	2.2	6.5
55542_at			AI735416	0	0.2	6.5
60022_f_at			AA584560	2.2	0.7	6.5
52341_at			3052895	0.5	1.3	6.5
75000 at			AI735440	25.9	12.1	6.5
7657_f_at			AI371706	0.2	0.4	6.5
37037_at	t-dioxygenase (proline 4.	P4HA1	M24486	2.1	1	6.5
48810_at	hypothetical protein DKFZp761H221		AI547243	4.6	3.7	7.
58954_at	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH NDUFS8 coenzyme Q reductase)	NDUFS8	AW021179	6.4	5.3	6.5
1373_at	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3	M31523	0	0.3	6.4
32474_at	7	PAX7	X96744	2.8	0.2	6.4
39415_at	heterogeneous nuclear ribonucleoprotein K	HNRPK	X72727	1.7	0.3	6.4
31756_at			AL049328	2.6	0.5	6.4
36347_f_at		H2BFD	AA873858	4.4	1.4	6.4
32681_at	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 S (antiporter, Na+/H+, amiloride sensitive)	SLC9A1	S68616	0	6:0	6.4
40576_f_at	iclear ribonucleoprotein D-like	HNRPDL	D89678	0	0	6.4
31628_at	solute carrier family 15 (oligopeptide transporter), member 1	SLC15A1	AB001328	1.5	0.4	6.4

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33886_at	spectrin SH3 domain binding protein 1	SSH3BP1	AF006516	12.4	4 4	6.4
32776_at	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	RALB	M35416	11.3		9
41288_at	matrix Gla protein	MGP	AI 036744	1	13	7
35223_at	alpha integrin binding protein 63		AB023234		1.3	0.4
36008_at	protein tyrosine phosphatase type IVA, member 3	PTP4A3	AF041434	77	2.4	0.4
41584_at	nudix (nucleoside diphosphate linked moiety X) type motif 3	NUDT3	AF062529	7.0	4.7	0.4
40041_at	highly expressed in cancer, rich in leucine heptad repeats		AF017790	i C	0.0	0.4
1102 s at	nuclear receptor subfamily 3, group C, member 1	NR3C1	M10901	7		0.4
37971_at	bromodomain adjacent to zinc finger domain, 1A	BAZ1A	AI 050089	2 4	1.1	0.4
156 s at	G protein-coupled receptor 19	GPR19	U64871	1.9	1.0	6.4
56192_at			H15097		1 5	100
64733 <u>_r_</u> at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9	SERPINB9	AA156247	526	12	6.4
48078_at			W04245	c		
59967_at			R37678) m		6.4
599/5_at			A1808778	3.6	0	5
78742 at			A1939581	0.0	1 2	0.4
G.	lung type-I cell membrane associated glycoprotein		AA149854	5.2	3.5	6.4
51067 r at			AA470798	4.2	3.7	64
51965 at			AI024309	6.0	1.8	6.4
r Lo			AI289185	2.9	3.5	6.4
			AI220443	4.1	5.4	6.4
67701 24			AI807856	2.4	3.1	6.4
44734 at			A1434675	16.7	16.1	6.4
67470 at			R60867	8.2	1.2	6.4
88916 24			AI928355	7.8	4.5	6.4
80391 at	kinesin like 2		AI703450	0	0	6.4
74508 at	AILCOLLING C	KNSL2	AI953141	4.1	3.8	6.4
65506 at	TIAI outotoxic granula acceptation Dala Elitain		AW015038	0.4	1.4	6.4
43965 at	The growing grainie associated Mix-Dinding protein	IIAI	AL046419	1.3	1.7	6.4
44294 at			AA115111	1.2	1.7	6.4
68369 at			T91110	2.6	2.5	6.4
00000 at			T89659	1.5	1	6.4
3022/_r_at			AI057455	1.5	9.0	6.4

Figure 13XX

46371 at	hypothetical protein FLJ10895		N36090	12	6.4	7 9
/01/3_at			AI808579	25		100
65837 at	hypothetical protein MGC5306		W93232	201	3.0	4.0
44667_at			A1422758	510	0	0.4
52062_f_at			HQRIOS	2 71	0 00	4.0
46845_at			A10275A5	20.5	6.23	P.4
53666 at			MIU4/340	0.5	3.1	6.4
42513 at	ATPase Na+/K+ transporting beta 3 polypentide	C . C . C	AA114900	9.9	3.8	6.4
18997 24	anishor mile, pera o polybebride	AIFIBS	AA151771	8.1	4.7	6.4
44561 r 2+			AA435933	4.4	4.2	6.4
57100 f ot			AI096866	8.9	9.6	6.4
51500 at			AI802804	1.6	9.0	6.4
72406 t at			2945576	5.2	2.2	6.4
1,5430			AA552962	1	40	6.4
41830 at	KIAA0494 gene product		AB007963	6	200	1 0
35/89_at	KIAA1042 protein		AB028965	9	2	t v
39163_at	likely homolog of rat kinase D-interacting substance of 220 kDa; KIAA1250 protein		W27233	5.4	0.2	6.4
48860_at	CGI-99 protein		A1342336	7.1	7.0	
59721_at	clone FLB4739		A1972147	1 4	7.7	6.4
51002_s_at	cargo selection protein (mannose 6 phosphate receptor binding		AI380317	2.2	1.2	6.4
	Dioteil)		_	_		
, ,			A1970054	7	7 /	
43839 f at		GLS	AI982852	900	1 0 0	0.4
50244_at	nucleotide binding protein 2 (E.coli MinD like)	NUBP2	AA552351	4 8	5.5	4.0 A.A.
27007 at			AI970788	1.2	6.0	6.4
37114 at	n phosphate), member 1	SLC17A1	D28532	1.1	0	6.3
37770 24	forthood her On	ATBF1	L32832	6.1	1.1	6.3
30777 of		FOX03A	AF032886	6.6	3.5	6.3
1102 of			AF075587	0.4	4.8	6.3
33399 at	ribosomal profess See RIA, subunit 3, 77kD CS	CSTF3	U15782	5.9	4.6	6.3
39124 r at	toution observed 1	RPS6	AA142942	0	1.1	6.3
39609 21	Potential challer 1	I RPC1	X89066	0.3	1.7	6.3
20040 at	organista indiriotog z	SIM2	U80457	0.4	0.2	6.3
32240_at			AL080094	6.0	0	6.3

Figure 13YY

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	Superfamily)	CD83	211697	10.7	8.3	6.3
1461_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NFKBIA	M69043	17	4.9	6.3
51831_s_at	-		AWOO1EOE	,	0	
54914 at			COCTOOMS	1.4	3.9	6.3
56401 at	Zinc finger protein 22 (KOX 15)	741700	A1740938	0.5	m	6.3
	iein El 1104EE	ZNF 22	AI951311	7.8	4.7	6.3
47443 at			AI379622	9.0	3.1	6.3
17778 24			AI268054	0.5	0.8	6.3
66770 at			R37637	3.9	0.3	6.3
52050 at			AA970080	1.5	2.2	6.3
52000 at			AI221328	æ	2.1	6.3
23100 at			AI138596	2.4	1.8	6.3
02270 at			AI590337	2.3	1.3	6.3
00000			T54678	8.3	33	6.3
27009 at			T65381	1.6	0	63
10007	1		AI817150	-	0.3	6.3
000/2_41	Tibrinogen domain-containing) 3 (Hakata	FCN3	AI652910	3.8	4.7	6.3
63817_at	DKFZP434B203 protein		AAOGGGOA	α ν	20	
52634_at			AWO25596	p; c	6.0	6.0
45478_at			AW009224	2 0	2.0	0.3
43931_at	hypothetical protein FLJ11269		417/152/	2.3	C.2.	6.3
65839_at	PC3-96 protein		770707WV	4.4	1.9	6.3
50122_at			W87467	3.7	4.4	6.3
59076_at			VIZO1407	3.5	3.7	6.3
46869_at			10700	٥.٤	1.3	6.3
74680 r at	FLN29 gene product		C89501	9.9	1.1	6.3
47840 at			AW002527	4.7	7	6.3
46678 at			K42863	1.2	2.7	6.3
51949 at			AI734922	1.7	4.5	6.3
46706 at			AI982758	2.9	3.7	6.3
70198 4 at			AA149518	0.9	4.4	6.3
82253 1 24			AI821980	1.2	0.3	6.3
10 1 CC770			AA663583	1.3	0	6.3
86/60_r_at			AI096457	0	0.5	6.3

1300			A1985333	3.6		6.3
	transforming growth factor, beta-induced, 68kD	TGFBI	M77349		7 4	
3/591_at	uncoupling protein 2 (mitochondrial, proton carrier)	11CP2	1194592		0.0	0.3
33777_at	50, subfamily		D34625	6.6	6.5	6.3
46664_at	apoptosis-associated speck-like protein containing a CADD		0.00			
55525_at			A1148558	5.7	5.1	6.3
39868 at	poly(rC):binding protein 3	0000	AI9/2498	6.2	5.5	.9
39695 at	ng factor for complement (ODEE O	rcars	AL046394	2	e.0	6.2
	is factor for complement (CD33, Cromer blood	DAF	M31516	9.9	1.1	6.2
32106_at	ysteine) proteinase inhibitor, clade A (alpha-1 ase, antitrypsin), member 4	SERPINA4	L28101	0.5	0.5	6.2
40539_at		MYOGR	1140001			
2039_s_at	FYN oncogene related to SRC, FGR, YES	EVA	042391	1	0.7	6.2
41196_at	ortin) beta 1	KDND1	IM14333	0	1.6	6.2
740 g at	pecific membrane antigen) 1	בטו ועם	L38951	0	0	6.2
41234_at	molog. subfamily B. member 6	100 P	M9948/	2	9.0	6.2
33349 at		UNAJBO	AI540318	5.4	6.0	6.2
33175_at			AL049378	1.8	0	6.2
35220 at	Plutamyl aminopentidase (aminopontidase A)		AA156237	0.9	0	6.2
34970 r at	description of the second of t	ENPEP	L12468	2.2	0.5	6.2
40289 at			AI655458	1.9	0.3	6.2
35829 at	sometime factor attachment protein, gamma	NAPG	U78107	3.4	1.5	62
38466 at	nodysostosis)	IGSF4	AL080181	0.5	0	6.2
56817 at	(20000000000000000000000000000000000000	CLSK	X82153	3.2	ō	62
55729 at			AA576941	8.8	2.7	62
63623 at			AA476783	1.1	1.3	6.2
315 at	ornithine decarboxylase antizyme 1		AI694297	7.7	0	9.9
65065_at		UAZI	D78361	2.8	1.9	6.2
51716 r at	complement component 5		AA926703	3.6	6.0	6.2
50062 at		3	T71645	0.2	0.1	6.2
46943 at			AA622412	9.0	0.2	6 2
62008 at			AI733124	1.5	0.5	6.2
18961 at			A1935871	0.8	0.2	6.2
4			N58188	6.0	0.5	6.2
2000						

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Figure 13AAA

74033 at turnor flectosis factor, alpha-induced protein 2	TNFAIP2	A1986430	53.5	15.5	6.1
42270 dt		W24320	4.7	1.5	6.1
at		AA827798	1.8	2.4	6 1
/606/_at IUNA fragmentation factor, 45 kD, alpha polypeptide	tide DFFA	AI671302	1.7		6.1
SOUTUR at		AA451732	0.5	0.2	6 1
61905 at		H19232	1	6.0	6.1
01000 at		AI634650	0.2	0	6.1
S/OSI_dl		AA167704	10.2	9.4	6.1
9035/_at		AA195804	4.3	6.0	6.1
91434 at		AI221300	6.0	1.2	6.1
04131_dt		AI808593	0	6.0	6.1
4,2022_dl		AA020957	2.2	3.8	9
00091_at		AI989354	5.3	5.6	6.1
		AI921708	2.4	1.5	19
43104 at collagen, type I, alpha 2	COL1A2	AI610692	2.8	9.0	6.1
34029 3 dt		AA147881	0	1.6	6.1
30333 at		AA399009	2.9	2.6	6
96017 at		A1973024	1.6	m	6.1
63801 24		AF150371	1.2		6.1
		AA195855	0.4	1.6	6 1
44320_at hypothetical protein MGC548/		AA905113	4.4	2	6.1
44502 at		AA417797	4.7	3.8	6.1
04552 at		R42005	-	1.2	6.1
10003 at		H03627	9.0	1.6	6.1
20377 at 80613 at		R77480	1.6	9.0	6.1
53408 at		AI221511	1.4	2.6	6.1
50500 at		AA464480	9.6	7	6.1
47034 at		AI307109	7	2.3	6.1
38747 at CD34 antigen		AI653240	1.5	2	6.1
3 6	CD34	M81945	0.7	0.2	6.1
56769 at B7.H1 protein		AI652861	0	2.7	6.1
+		AA292201	25.6	8	6.1
Q2138 at		R09516	4	0.1	6.1
76033 -t		AI345255	0.3	0	6.1
13332 at		N33374	6.0	2.1	6.1

thyrothetical prot thyroid hormone death receptor 6 proteasome (pros tubiquitin C tumor protein p5 KIAA0958 protein HZB histone fami ubiquitin specific plastin 1 (i isofon ring finger protein at dermatopontin CD8 antigen, alpt carboxypeptidase guanylate cyclase DnaJ (Hsp40) hor	ciated protein, 240 kDa subunit ain) subunit, alpha type, 2 i syndrome)		AA904413	5.6	3.5	0.1
hypothetical prot thyroid hormone death receptor 6 proteasome (pros ubiquitin C turnor protein p5 KIAA0958 protein H2B histone fami ubiquitin specific plastin 1 (1 isofor ring finger protein at dermatopontin CD8 antigen, alpt carboxypeptidase guanylate cyclase DnaJ (Hsp40) hor tt	subunit 2		101010	5	-	
thyroid hormone death receptor 6 proteasome (proz ubiquitin C tumor protein p5 KIAA0958 protein H2B histone fami ubiquitin specific plastin 1 (i isoforning finger protein at dermatopontin CD8 antigen, alpt carboxypeptidase guanylate cyclase DnaJ (Hsp40) hor tri	subunit 2			1	5, 0	7 0
death receptor 6 proteasome (pro ubiquitin C tumor protein p5 KIAA0958 protein HZB histone fam ubiquitin specific plastin 1 (i isofor ring finger protein the dermatopontin CD8 antigen, alp carboxypeptidass guanylate cyclass DnaJ (Hsp40) ho tt	2		AB011165	3.3	1.9	9.1
proteasome (pro ubiquitin C tumor protein p5 KIAA0958 protein H2B histone fam ubiquitin specific plastin 1 (i sofor ring finger protein the dermatopontin CD8 antigen, alp carboxypeptidass guanylate cyclass DnaJ (Hsp40) ho tt	2					
ubiquitin C tumor protein p5 KIAA0958 protein H2B histone fam ubiquitin specific plastin 1 (i sofor ring finger protein the dermatopontin CD8 antigen, alp carboxypeptidass guanylate cyclass DnaJ (Hsp40) ho tt	1	DOMAG	Ar068868	5.9	2.1	9
	i syndrome)	SIMPE	AA//2359		4.5	9
# # # # # # # # # # # # # # # # # # #		UBC	M26880	3.2	2.2	9
# ## ##		1753	X02469	0.7	0	9
# 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			AB023175	2.3	0.1	9
t t t		H2BFR	X00088	3.5	0.8	9
# ## ##		USP19	AB020698	0	0.3	9
# 11 11		PLS1	L20826	1.9	0.7	9
		RNF15	U90547	7.2	1.1	9
22 1		DPT	222865	0.2	1.5	C
22 1	032)	CD8A	M12824	2.4	0.7	2
22 2		CPA2	U19977	9.7	6.2	٧
1 1 1 1		GUCA1A	L36861	2.9	0.7	9
t KIAAO117	1	DNAJA1	F08069	8.2	5.2	2
t KIAA0117			AA743565	5.5	1.3	9
t KIAA0117			AI627708	1.4	0.7	9
t KIAA0117			AI694231	9.0	0	9
at KIAA0117 f at KIAA0117 at at			AA285069	4.4	2.7	9
f at KIAA0117 at at at			AA424339	0	9.0	9
at at			AL037805	2.8	2.4	9
48435_at 55396_at			AI656542	5.4	2.8	9
55396 at			AA086015	9.0	1.2	9
20000			AI796988	0	0.8	9
14×4×4			N55264	5.8	2.5	9
50531 at			AI200546	3.2	2	9
76008 - 24			AA019613	1.5	2.6	9
66724 at hypothotical protein [11142	11170		AI304317	7.3	10	9
at higherinetical prot	711145		A1698705	1.7	6.0	9
47227 at			AA430014	1.8	1.9	9
22007 at 1			C14838	9.9	1.4	9

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52390 g at			7 VOCOW)	000		
16017 24			W9294/	7.8	L .	9
4001/ 41			AA013349	1.2		9
58622 at			AA463374	3.5	5.3	9
65108_at			Al346432	0.2		0
43485_s_at	hypothetical protein FLJ21343		AI633875	5.9	0.4	2
55353_at			AA760977	33.6	0 0	
48737_at			A1831738	200		D
51381_at			A1480091		t C	0
36181_at	LIM and SH3 protein 1	I ASP1	X82456	0 0	5 -	
36940_at	TGFB1-induced anti-apoptotic factor 1	TIAF1	D86970	7.5	10	O U
32562_at	endoglin (Osler-Rendu-Weber syndrome 1)	ENG	X72012	2.5	7 /	0
41619_at	adenosine A2b receptor pseudogene	ADORA2BP	AI 022398	0 - 0	t u	0 0
31727_at	ectonucleoside triphosphate diphosphohydrolase 2	ENTPD2	U91510	1.5	900	0 0
41689_at	plasmolipin		R16035	2.4	1.4	0
40487_at			W26634	C		3 4
40862 i_at	creatine kinase, brain	CKB	X15334	11 6	2 4	, r
41304_at		NRP2	AF016098	10.8	5.7	0
	karyopherin alpha 5 (importin alpha 6)	KPNA5	AF005361	1.2	c	200
			D86982	2.4	c	0 4
34231_at	histone acetyltransferase		AF074606	0	0 7	0 4
34/06 at	Max-interacting protein		AB011090	-	1 2	0.5
31961 r_at			AF070579	1.3	0.6	0 4
39976_at	hypothetical protein from EUROIMAGE 783647		AL050087	9.4	4 1	0.00
363/1_at	microfibrillar-associated protein 3	MFAP3	L35251	2		0 4
35348_at		PRKAB1	AF022116	10.8	m	200
38014_at	adenosine deaminase, RNA specific	ADAR	X79448	7.8	7.4	9 5
3/5/6 at	Ψı	PCP4	U52969	0.3	0.4	200
	signal transducer and activator of transcription 4	STAT4	L78440	54.6	10.3	0 5
58/59 at	1		AA481476	9.0	2.8	5.9
4/059_at	Splicing factor, arginine/serine-rich 11	SFRS11	AI002238	0	0	200
3/301_at			AI914124	7.6	12.8	20
66568 at			AA873121	1.3	1.4	5.9
90036 r at			AI692681	2.5	0.8	5.9
//54/_at			AA045155	1 4	D 0	0 4

Figure 13EEE

66294_at	decay accelerating factor for complement (CD55, Cromer blood DA group system)	DAF	AI888485	8	8.0	5.9
91023_f_at			F03144	2.6	1.2	20
42721_at			AI261490	17.5	4.3	5.9
84053_at			AI419969	4.5	2.4	
45522 at			R41958		40	
87285_at			AA679812	3.5		
43588_at			H69543	3.7	0.7	5.9
69464_at			AI655655	2.1	200	5.9
69558_s_at			AA431588	2.1	1.2	5.9
71278_at			AI912743	1.7	8.	5.9
42875_r_at			T97225	2.3	3.1	5.9
73781_at			A1669763	1.8	3.8	5.9
44/82 at			AA258063	8.2	4.3	5.9
45583_at			AA602585	13.1	6.0	5.9
68996 f at			A1681967	6.2	2.2	5.9
881// t at			AI492518	0.8	0.4	5.9
5//14_at			AA429113	0	0.8	5.9
45612_at			AI744560	4.9	3.7	5.9
62165_at	x 006 protein		W72231	4.8	3.2	5.9
435/6 at	hypothetical protein		AI348427	9.0	5.4	5.9
54463 at			AI356895	1.6	4.6	5.9
46639 at			AA398558	1.5		5.9
64306_at		FGG	AI568934	1.5	1.5	9
74932 at	ubiquitin conjugating enzyme E2B (RAD6 homolog)	UBE2B	AW002331	2.3	2.2	5.9
87195_at			AA191742	0.3		7.9
31816_at	glucosidase, alpha; acid (Pompe disease, glycogen storage GA disease type II)	GAA	X55079	5.2		5.9
39801_at		PLOD3	AF046889	Ľ.	2.1	0 4
1637_at	ed protein kinase-activated protein kinase 3	MAPKAPK3	U09578	r.	0	0.00
		VASP	246389	5.7	2.6	5.9
34481_at	vav 1 oncogene	VAV1	AF030227	4.5		5.9
49003_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, NDUFB10 PDSW)	DUFB10	AA195976	5.9		5.9
49389 at			AI262504	4	8	5.9

Figure 13FFF

5.9	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8
m	4.8	1.1	1.6	0.4	9.0	0.4	2.7	1.1	1.2	-	24.7	0.5	9.9	8.5	8.6	9.1	4.2	2.8	2.9	11.9	2.7	1.5	6.0	1.4	2.9	2.1	3.4
4.6	50.6	0	4.3	0.2	0.4	1.2	5.3	0	0	2.9	54.9	0	2.7	16.9	14.2	33.5	12.3	3.9	0.3	27.6	1.7	0.1	0.7	1.4	7	5.3	6.9
AA034095	AL109695	AF014794	M17754	X51602	X59350	N58318	AB014563	AL031282	AL096858	U36341	AF005775	AF009314	X87344	D11466	AI653621	H38110	AI732773	R18374	AA404273	AI634721	AI138886	AI215674	AI350227	AA703170	AA035377	N63911	R63071
		TNFRSF10C	BN51T	FLT1	CD22			GNB1		SLC6A8	CFLAR		PSMB9	PIGA	TXN		HLA.F										
		tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	BN51 (BHK21) temperature sensitivity complementing	rosine kinase 1 (vascular endothelial growth ir permeability factor receptor)		d in metastasis	KIAA0663 gene product	ing protein (G protein), beta polypeptide	NIAA0929 protein Msx2 interacting nuclear target (MINT) homolog	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	I FADD-like apoptosis regulator		proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)	phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria)	thioredoxin		major histocompatibility complex, class I, F			KIAA0477 gene product						hypothetical protein FLJ11058	
45758_at	37451_at	34493_at	41694_at		38521 at	at	at	33300_at	32172_at	40926_at	1867_at	36061_at	41184_s_at	39993_at	36992_at	46760_r_at	55400_at	75996_at	57682_at	57273_s_at	51275_f_at	79757_at	52686_at	62851_g_at	48565_at	45247_at	63083_r_at

			1796363	2.1	0	5.8
68133 r at			AI817762	1.4	2.2	5.8
4428/ at			H61057	1.5	0	5.8
72244 1 at			A1299404	1.4	0.8	5.8
74422_at			H05961	1.3	5	5.8
53209 at			T91952	0.2	0.1	5.8
86831_at			N24028	0.5	1.8	5.8
64185_at			AA009833	0	0	5.8
86865_at			A1089920	0.4	2.1	5.8
47130 at		FOXC1	AW022802	2.8	2.3	5.8
61298_at	Torknead box C1		R66534	4.8	1.5	5.8
50134_at			AL119305	2.7	2.7	5.8
42982_at			AL 044906	8.5	2.3	5.8
71106 Lat			R60655	1.8	1.6	5.8
50102_at	I٤		A1680350	41.7	5.3	5.8
42363_r_at	STAL induced STAL inhibitor 3		AA191741	3.4	m	5.8
44526_at			AA831034	6	9:0	5.8
52714_at			AA166624	1.7	1.6	5.8
58541_s_at			AI024369	1.5	1.7	5.8
			99069N	3.3	3.5	5.8
45071_at			AI671126	1.4	1.6	5.8
456/5 at	UKF2F4341210 protein		N99610	1.1	1.1	5.8
54039_at			AI572226	3.2	4	5.8
5//44 at	HOPCO/2 protein		AW007845	1.5	0	5.8
5/396 g at			D16154	9.0	0.4	5.8
20000			AA780435	1.7	9.0	5.8
38920 at			AA913861	1.3	1.4	5.8
24747	human hamalag of Drosophila Scribble		D63481	2.9	3.2	5.8
34/43 at	FIGURE HOLIONOR	KHSRP	AA628946	ry ox	2.8	5.8
38828 s at	KIAA15/15 profes		H17730	4.9	5.9	5.8
56546 at	NIAA1343 piote		AL044098	6.1	5.1	
53881_5_at	\neg	C200RF3	H09341	4.2	2.7	5.8
48829 s at	chromosome 20	C110RF24	AA065185	5.6	2.1	5.8
52164 at			N36986	5.5	4.2	5.8
44693_at	Inypotnetical protein ruli 1937		22221			

63971_s_at	sirtuin (silent mating type information regulation 2, S.cerevisiae,	SIRT2	AI984394	3.6	2.4	5.8
	homolog) 2					
54152_at	eukaryotic translation initiation factor 4E binding protein 1	EIF4EBP1	AI026669	5.8	5.2	5.8
524_at	postmeiotic segregation increased (S. cerevisiae) 1	PMS1	U13695	6.0	0.7	5.7
39790_at	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATP2A2	M23115	0.1	0.5	5.7
40146_at		RAP1B	AL080212	9.7	4.3	5.7
31921_at	mber 1	OR2F1	U56421	0	2.8	5.7
1184_at	proteasome (prosome, macropain) activator subunit 2 (PA28	PSME2	D45248	9.3	10.3	5.7
32364 at	sine oculis homeobox (Drosophila) homolog 6	SIX6	A (011785	-	000	7.7
32850_at	nucleoporin 153kD	NUP153	Z25535	1.6	2.1	5.7
34172_s_at	_	DAYS155E	M99578	1.2	1.4	5.7
(sednence					
33359_at	KIAA0768 protein		AB018311	0.8	0.1	5.7
34256_at	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha 2,3.	SIAT9	AB018356	0	7.8	5.7
	sialyltransferase; GM3 synthase)					
32405_at	KIAA0707 protein		AB014607	I	0	5.7
33684_at	wingless-type MMTV integration site family, member 2B	WNT2B	271621	3.8	0	5.7
35166_at	Down syndrome critical region gene 3	DSCR3	D87343	4.6	7.1	5.7
41329 at	hypothetical protein LOC57147		AI458463	7.6	8.1	5.7
33515_at	t-complex 10 (a murine tcp homolog)	TCP10	003399	0	0	5.7
1856_at	v-rel avian reticuloendotheliosis viral oncogene homolog	REL	X75042	5.6	4.1	5.7
36323_at	gamma aminobutyric acid (GABA) A receptor, alpha 1	GABRA1	X14766	1.1	9.0	5.7
39199_at			W28661	0.1	0	5.7
36536_at	schwannomin interacting protein 1		AF070614	10.9	0.2	5.7
31536_at	reticulon 4	RTN4	AB020693	1.5	2.6	5.7
36175_s_at	36175_s_at human immunodeficiency virus type I enhancer-binding protein 2	HIVEP2	AL023584	24.2	7	5.7
37248_at	carboxypeptidase Z	CPZ	U83411	80	9.0	5.7
37687_i_at	Fc fragment of IgG, low affinity IIa, receptor for (CD32)	FCGR2A	M31932	1.8	9.0	5.7
752_s_at	DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1	D85429	0	0.1	5.7
41018_at	DKFZP5640243 protein		AL050015	0.7	8.0	5.7
722_at	rcd1 (required for cell differentiation, S.pombe) homolog 1	RQCD1	D87957	1.2	0	5.7
42301 at			AA44100	0.3	9.0	5.7
66550_at			AA972106	0.2	0	5.7

Figure 13III

E0970 at			AI675751	0.1	1.6	2.7
30079 at			AI002236	8.5	0.1	5.7
75077 at			A1276680	9.0	1	5.7
E40944 at			AA903287	14	5	5.7
34004 at			AA142842	12	11.9	5.7
6101/at			A1792916	2	1.1	5.7
61976 at			H00945	2.4	1.2	5.7
03250 at			A1588981	0.2	1.6	5.7
50050 at	sin 3. associated polypentide 18kD	SAP18	AW006285	2.1	1.3	5.7
13865 at			R49396	1	3.1	5.7
45721 at	endothelin converting enzyme 1	ECE1	AL039866	12.6	4.3	5.7
164552 at			H04794	2.3	0.8	5.7
64221 at			H27234	0	0	5.7
70428 at			A1685341	10.9	2.3	5.7
13384 at			AW000990	0	2.6	5.7
56008 at			AA284288	0.3	1.7	5.7
54604 at	hyalironan synthase 3	HAS3	A1338972	4.2	2.9	5.7
18269 at			AA218544	1.3	0.8	5.7
60981 at			AI554853	6.0	1.7	5.7
56759 at			AI914936	3.7	0.4	5.7
48148 r at			AI168326	4.2	1.9	5.7
62391 f at			AA592983	0	0.3	5.7
51038 at			AA005354	1.2	0.7	5.7
51588 at			2933319	6.4	0.2	5.7
39443 s at	cytochrome c oxidase subunit Vb	COX5B	M19961	4.7	2.3	5.7
40120 at	hydroxyacyl gluta	HAGH	66606X	5.7	2.9	5.7
33833 at	1 (alpha-fodrin)	SPTAN1	J05243	5.1		5.7
37320 at		PTDSS1	D14694	5.3	2.2	5.7
45521 c at	roduct		A1967955	5.4	5.5	5.7
65737 r at	ш		AI701293	5	2.7	5.7
39542 at	ectodermal neural cortex (with BTB-like domain)	ENC1	AF059611	1.5	0.7	5.6
1713_s_at	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CDKN2A	U26727	4.7	0	5.6
33010_at	solute carrier family 5 (neutral amino acid transporters, system A) member 4	SLC5A4	AL008723	0	0.4	5.6
	1.0, 1110111					

40267 s at	IKIAA1036 protein		0.000000	000	-	ľ
10.00			A1000040	7.7	Ö	9.0
at	forkhead box F1	FOXF1	U13219	8.4	0.7	5.6
at	thyroid hormone receptor binding protein		D80003	2.5	1.8	5.6
1448_at	proteasome (prosome, macropain) subunit, alpha type, 3	PSMA3	D00762	4.3	4	5.6
41237_at	major histocompatibility complex, class I, A	HLA-A	D32129	14.9	9.7	5.6
a	sphingosine.1.phosphate lyase 1	SGPL1	AI128825	1.5	0.4	5.6
at	telomeric repeat binding factor (NIMA-interacting) 1	TERF1	U40705	0		5.6
2047_s_at	junction plakoglobin	JUP	M23410	0.1	1.1	5.6
넒	estrogen responsive B box protein		AF096870	1.7	4.1	5.6
35214_at	UDP-glucose dehydrogenase	UGDH	AF061016	3.7	2	5.6
35230_at	hypothetical protein, clone 24751		AF070530	17.3	5.7	5.6
34371_at	protein phosphatase 4, regulatory subunit 1	PPP4R1	U79267	1.5	1.6	5.6
33080_s_at	_	RAP1GA1	AB007943	1	0.7	5.6
36785_at	heat shock 27kD protein 1	HSPB1	223090	1.2	0.7	5.6
37603_at	interleukin 1 receptor antagonist	ILIRN	X52015	8.9	5.9	5.6
40724_at	zinc finger protein 200	ZNF200	Y14443	2.5	6.0	5.6
1022_f_at		IFNA14	V00542	0.1	0	5.6
84981_r_at	collagen, type III, alpha 1 (Ehlers-Danios syndrome type IV, autosomal dominant)	COL3A1	T54146	5.1	8.6	5.6
60835_at			AI831561	30.1	6	5.6
			AI080388	6	4.4	5.6
61557_at			AI074020	0	3.3	5.6
62371 g at	hypothetical protein FLJ13153		AI221377	9.9	2.9	5.6
578_at	recombination activating gene 2	RAG2	M94633	1.3	0.5	5.6
91669_at			AA491645	8.4	6.2	5.6
60635_at	hypothetical protein FLJ23282		W61076	1.7	2.5	5.6
6/515_at			AI479011	1.9	2.4	5.6
65360_at			R45940	2.3	2.2	5.6
86405_at			238166	0	0.4	5.6
86822_at			AI621229	3.4	2.8	5.6
68047_at			AA936632	10.3	14	5.6
43620_at			AA774785	3.7	2.1	5.6
70814_at			AI833139	9.0	1.7	5.6
44097_at	DKFZP586C1324 protein		A1928466	0.7	1.3	5.6
42848_at			C20550	9.0	3	5.6

32923_r_at	synapsin I	SYN1	M58378	1.5	0.5	5.6
65546_at			N78362	0	3.1	5.6
56228_r_at			N54910	3.2	2.1	5.6
72961_i_at			AI950023	1.8	1.4	5.6
56028_at			AI768884	0.8	2	5.6
42740_at			AI243610	1.5	1.9	5.6
53655_at			AI300574	9.0	2.1	5.6
57497_at			AA419263	2	1.9	5.6
58944_s_at	ribosomal protein	RPS6KC1	AA670286	30	7	5.6
34572 at	carbonic anhydrase VII	CA7	M76424	1	6.0	5.6
46391 i at			AI761712	0.2	-	5.6
51055_r_at			AA962343	0.7	2.6	5.6
53068_at			AI738621	1.9	2.3	5.6
57660_r_at			R43504	4.1	3.4	5.6
46103 at	MEK partner 1		AI335267	0.2	9.0	5.6
64749_r_at			AA535979	1.8	0	5.6
51854 at	KIAA1128 protein		AA424126	14.4	6.3	5.6
54355_at			AI523391	2.5	12	20
32704_at	dedicator of cyto-kinesis 2	DOCK2	D86964	9	2.6	5.6
34864_at	hypothetical protein		AF070638	4.9	9 0	5.6
49390_at			AA999858	5.6	5.6	9 6
51056_at	hypothetical protein DKFZp434D0412		AW025176	3.6	88	5.6
61291_at	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	SDHA	AI348006	2.7	1.3	5.6
58945_f_at	hypothetical protein FLJ11773		T55569	4.5	er er	7
47787_at			AA045461		1.5	7
32460_at	gamma-aminobutyric acid (GABA) A receptor, beta 2	GABRB2	867368	0	0	5 2
39386_at	gene predicted from cDNA with a complete coding sequence		D14811	4.2	1.7	5.5
31812_at	guanosine monophosphate reductase	GMPR	M24470	1.1	9.3	, r.
31586_f_at	immunoglobulin kappa constant	IGKC	X72475	0	60	5 5
162_at	ubiquitin specific protease 11	USP11	U44839	2.9	280	7
40582_at	protein tyrosine phosphatase, receptor type, J	PTPRJ	AI806482			5.5
32706_at	HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A	HIRA	X89887	0	1.6	5.5
33284_at	myeloperoxidase	MPO	M19507	1.3	0.8	r.

Figure 13LLL

		OMG	M63623	2		5 1
35903 at	otein	TDAC1	1119261	33.5	9.9	5.5
978 at	ciated factor 1	I LANGE TO SECOND	1102461	10.5	12.9	5.5
040	v 31 (copper transporters), member 2	SLC31A2	U83401	0.00	9 9	5.5
34/49 at		RAD9	U53174	2.2	000	14
32158_at			AA160708	6.8	8.2	0 1
32203_at	HBV associated factor	SIATAA	L13972	1.4	6.0	ر. م.ت
40291_r_at						1
	sialytransferase)		AF070571	1.7		0 0
41575_at		TRIP13	U96131	0	0.3	5.5
36813_at	thyroid hormone receptor interactor 13	PIP5K1B	X92493	1.3	O	5.5
37253_at	phosphatidylinositol-4-phosphate 5-Kinase, type 1, Deta	11.BF21	AL031714	0.1	0.7	5.5
33136_at	ubiquitin-conjugating enzyme EZI (nomologous to yeast ODO)					rt rt
			AA165208	2.3	7	2 1
46780_at			AA621324	0.7	1.4	2.0
42467_at			AA912180	2.3	1.5	5.5
66521_at			A1131053	6.0	9.0	5.5
91081_at			AI796514	2.4	0	5.5
80444 at			A1989733	2.3	3	5.5
43378 at		-	A1435504	1.4	1.4	5.5
82122_at			AI 043172	0.7	4	5.5
42813_at			A1792919	4.7	1.3	5.5
50608_r_at	putative brain nu	00×54	A1857509	1.2	0.1	5.5
73621 at	cytochrome c oxidase subunit Va	2500	AA133355	1.3	0.7	5.5
59022 at	DKFZP566F2124 protein		AA287372	1.1	1.5	5.5
87820 at			44262084	9.9	2.9	5.5
43793_at			AA992185	4.1	2.4	5.5
48655_r_at	at	-	AI862887	21.3	17.7	5.5
44092 at			N34402	1.6	2.2	5.5
53256_at			AI307778	1.7	1.8	5.5
50125_r_at	at		AA828830	0.1	0.4	5.5
67369_at		-	T81819	0	8.9	5.5
66084_at			AIR57594	3.4	3.2	5.5
45769 g at		CIT1	A1887641	4.8	2.8	5.5
44066_s_at	at G protein-coupled receptor kinase interactor i	5	N36861	4.7	2.1	5.5
60174 at			AA461205	7.8	5	5.5
45055_at						

51112 04			AA019836	0.6	a c	u
31113_at		GALNT1	AW021000	0.2	0.5	5.5
62941_r_at	Т	RARRES1	A1669229	6.3		
18316 at	V-ets avian erythroblastosis virus E26 oncogene homolog 2	ETS2	AI870399	3.0	4 0	
70013 at			AA286940	42		0 1
58336 at	hypothetical protein FLJ23033		AI653719	3.4	t 0	0.0
43665 r at	Sec23 interacting		AA405686	2.4	2.4	7.7
32007 at	1		AI332962	2.7	3.7	200
62328 at			W29045	5.4	0.5	j (C
45751 g at			T92565	0	0	7.
32218 at			AA528592	2.6	1.2	2 2
35787 at	dynein. cytonlasmic intermediate polymostida 2		AF034176	8.1	8.1	, r.
44078 at	2 applied bolypeptide 2	DNC/2	A1986201	1.3	1.4	2 4
51628 at			W95017	4.1	5.1	7
58501 at	KIAA0876 protein		AA009692	2.8	2.6	7
44080 at			AA524529	2.9	27	0 4
46247 at			W68180	6.3	5.2) r
47083 at	page, or committee, alpha subunit	SUCLG1	AA826261	4.1	3.3	2 4
56224 at	Chloride channel publicatide centition 14		AI280108	S	4.9	2 4
37415 at	type 10R	CLNS1A	N32865	2.2	1.4	3 5
41469 at	or 3 skin-derived (SKA) D	ATP10B	AB018258	0.3	0	5.4
2048 s at	100000000000000000000000000000000000000	PI3	L10343	12.9	0.4	12.0
1 00000	ei yuli oblastic leukemla	HKB	M26747	1.6	0.4	5.4
41690 at	glyceronephosphate O-acyltransferase	GNPAT	AJ002190	0.5		4
40556 at			AL049471	10.7	3.5	T C
894 g at	critain calciuri birding domain	RCN1	D42073	14.7	9.7	5 4
149 at			M91670	5.9	7.8	1 0
33779 at			U90426	1.4	13	7 7
33799 at	ynaptobrevin I)	VAMP1	AF060538	3.4	0 1	1 4
40819 at	Social Horrison 2	SIAH2	U76248	7.7	36	7
	hydroxysternid (17.heta) dehydrogenaso 2		AA161065	1.1		1.5
36845 at	r - Detay deliyatogetidae a	HSD17B3	005659	2.3	1.7	5.4
			D50926	7.2	5.1	5.4
					14.5	F .

Figure 13NNN

	viral (v.erb.a) oncogene homolog)		concey	J	1.3	t.
t at	heat shock 70kD protein 2	HSPA2	L26336	0	0.2	5.4
		UBE2B	M74525	0.8	1	5.4
П	frizzled (Drosophila) homolog 1	FZD1	AB017363	0.1	0	5.4
		SCYA22	U83171	6.9	5	5.4
46788 at			AI632740	4.2	0.1	5.4
	chromosome 11 open reading frame 15	C110RF15	AI188389	0.8	1.4	5.4
66625_at			AA890177	2	0	5.4
62393_at			AI277415	1.7	1.2	5.4
62425_at			AA921956	1.3	1.8	5.4
42761_at			W45259	1.1	1.3	5.4
91727 at			AI651474	1.5	0.4	5.4
82746 r at			AI743571	1.9	1.2	5.4
┰	glucose phosphate isomerase	GPI	AI248811	2.8	9.0	5.4
65510_f_at			AA034458	0.4	0.4	5.4
59814 at			AA628524	1.2	2.9	5.4
	ribosomal protein S11	RPS11	AA603467	2.9	1.9	5.4
54860_at			AI797678	2.3	2.4	5.4
ŧ	adaptor-related protein complex 1, mu 2 subunit	AP1M2	W92449	1	1.1	5.4
87801_at			AA604144	4.1	2.4	5.4
43177_at			AI732470	0.3	0.1	5.4
88280_r_at			AA703174	3.7	6.0	5.4
69345_at			N95633	2.2	0	5.4
71549_r_at			AA699538	3.6	2.2	5.4
52384_s_at			AI984780	15.6	1.9	5.4
50266_at			AI741178	7.7	6.5	5.4
49302_at H	HBV associated factor		AI971817	13.9	9.1	5.4
64183_r_at			R55749	1.1	1.2	5.4
85971_at			N54973	1.7	3.2	5.4
42804_at			W86160	3.7	5.1	5.4
56845_at R	Ras homolog enriched in brain 2	RHEB2	AA056145	0	2.3	5.4
44951_r_at			AI732184	2	2.7	5.4
44393_at h	hypothetical protein		AA604681	1.6	1.4	5.4
44572_g_at			AI765278	1.1	1.4	5.4

50952 at			1170204			
1100 24			N/0394	5.5	6.0	5.4
01128 at			AI338787	1.5	3.5	5.4
45/8/at			N29695	2	2.3	5.4
36707_s_at	serine/threonine kinase 9	STK9	X89059	1.8	2.3	5.4
41895_at			W93764	6.0	1.5	5.4
48859_f_at	HMP19 protein		A1968989		0 6	5.4
46042_at			N98235	3.7	4	5.4
52731_at	hypothetical protein FLJ20294		AI359466		23	5.4
56755_at			AI802568	1	0.5	5.4
41976_at			T11500	8	0	5.4
53032_at			3145395	100	1 7	200
82137 f at			AA876935	200	1.5	i u
91067_i_at			AI681736	0.5	0.0	7.00
39738_at	lypeptide 9, non-muscle	МҮН9	Z82215	0.5	1.5	5.4
39774_at	oxidase (cytochrome c) assembly 1-like	OXA1L	X80695	3.2	3.1	5.4
56351_at			A1436023	2.5	2.5	5 4
51089_at	KIAA1140 protein		AL042799	6.5	4.5	5.4
53848_at			A1422099	4.2	3.7	5.4
57079_at			AA503073	3.1	6	5.4
54912_at	translocase of inner mitochondrial membrane 13 (yeast) homolog TIMM13B	TIMM13B	AL035821	5.2	3.4	5.4
64901_at	P-ribosylation factor-like 1	ARL1	AI357567	6	3.4	7
65603_at	epeat-containing 6	BIRC6	AA886981	5.1	29	5.4
35109_at	KIAA0756 protein		AB018299	0	4.0	5.3
	KIAA0984 protein		AB023201	1.7	1.1	53
31731_at	olog 4 (Drosophila Pc class)	CBX4	AF013956	2.5	0	5.3
40156 at	KIAA0040 gene product		299715	1.6	2.7	5.3
32641_at	androgen induced prostate proliferative shutoff associated protein		AB023196	2.2	2.9	5.3
148_at			U88629	6.4	1.4	5.3
33652_at	metalloproteinase domain 20	ADAM20	AF029899	1.7	6.0	. L
34178_at	zinc finger protein 297	ZNF297	AI884738	9	3.4	20.00
41559_at			AA434319	7.1	2	5
33896_at		EP300	U01877	6.0	0	2
38757_at	PDGFA associated protein 1	PDAP1	U41745	29	α.	5 2

35227_at	اعا	RBBP8	072066	7.1	000	[
1330 g at	Dreast cancer 2, early onset	BRCA2	U43746	27		0 0
40332 at	- 1		AF109134	0.0		5.0
3//32_at		RYBP	A1 049940	1 t.0	4.7	5.3
1505 at	thymidylate synthetase	TYMS	DODESE	10.1	0.1	5.3
66170_at			700000		I.5	5.3
76032_at			1,32337	0.1		5.3
76206_at			AI3/0844	0.7	1.3	5.3
66402 at			AA/31738	1.6	6.0	5.3
66899 at			AA748556	0	1.2	77
51079 at	ATP-hinding cassatta suh family A (ADC1)		AI733062	3.2	0.8	200
59166 at	Commission of the cassons, subjusting A (ABCL), member /	ABCA7	AI668632	1.7	0.8	7.3
58530 r at			AI091214	4	9.0	2 2
61829 at			166185	3.4	2.5	2 2
47513 at			AA007461	2	1.1	5 2
82053 at			AA679424	9	4.2	0 0
92147 at			AI471845	2.6		2 0
50030			N92830		0	200
40202 at			A1967991	100	0 0	5.0
49292 s at		RREB1	A1097330	10	0.7	5.3
189 S at	plasminogen activator, urokinase receptor	PLALIR	700001		0.1	5.3
86470_at		10.11	0.0993/	18.8	3.3	5.3
88607_at			AA884313	0.1	0	5.3
64001 s at	Seven in absentia (Drosophila) homolog 2		AI660692	6.0	0.2	5.3
69842 f at	Solo Holl Children Co. Co.	SIAH2	AW008929	11.6	4.2	2 6
89412 at			AI766478	2	0.7	7.2
70151 at			AI804386	8.3	3.5	5 4
59671 at			AI805522	8.6	6.3	, L
72686 at			AI798769	0	1.5	7.2
74218 at			Ai093728	2	0.3	5 2
66144 at			A1990680	9.0	1.5	7.2
60527 at	Rho GTPase activation protein E		AA872556	1.1	12	7 3
89121 at		ARHGAP5	AI768264	3.2	3.1	0 4
71848 at			AI740879	0	4.3	n u
45159 r at			N74103	2.3	2.1	7
10100 1000 1000			H71807	0.3	0.4	i u
4303/_at	Jaimetnylarginine dimethylaminohydrolase 1	DDAH1	AI309320	2.1	2.1	5 4
				1	£:4	0.0

Figure 13QQQ

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at at at at at at at at at at at at at a		-	A1743307			
at at			1	1		
at at			A11 A6300	7	6.0	5.
t t			A1140322	1.9	1.4	5.3
t t	CGI:14 protein		A1565/05		0	5.3
18749 at 28827 at 34519 r at 31502 at 11668 f at 19556 at			AI814761	3.3	2.6	5.3
38827_at 54519_r_at 31502_at 31668_f_at 19956_at			K32893	0.2	0.4	5.3
31502 at 31688 f at 19956 at			D11630	2	5.7	5.3
31502 at 31668 f at 19956 at			AI992368	3.8	4.2	5.3
31668 f at 19956 at			AA976211	2.4	2.5	5.3
19956 at			W27953	3.5	2.1	5.3
ייטטט מו			W28193	0.8	0.1	5
60073 f at			AI080164	1.7	0.7	5.3
1			AA525753	2.1	6.0	5.3
86188 + 2+			AA743794	0.3	2.9	5
1	The section of the se		AI733033	9.0	9.0	5.3
Τ	Essed III activated 17 LAN lymphocytes		AB002405	4.3	1.1	
T	May occor	RANBP16	AB018288	4.8	2.5	2
Ţ	_I.		AB014520	4.1	4 3	2 4
40302_at guanif	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	GNA15	M63904	0.3	1.5	5.3
at	biliverdin reductase B (flavin reductase (NADPH))	BLVRB	D32143	5.2	000	
at			41952120	3.6	0 10	5.3
57152_at WAS	WAS protein family, member 2	WASES	14701167	0.4	5.5	5.3
s_at		3 1001	W/2145	7	0.4	5.3
52012 at			AI81068/	4.9	2.7	5.3
g at	fetal hypothetical protein		A1659020	5.2	3.5	5.3
_	. I		U84971	0.7	1.5	5.2
T	lymphocyte adaptor protein	SYNJI	AB020717	0	0	5.2
T	HOA history family, mamping D		AF055581	0.4	0.3	5.2
i to	ly, mermer D	HZAFD	298744	2.4	2.6	5.2
T	oo-like prospriotyrosine protein, 1-STAR		AF051321	3.7	2.4	5.0
T	Illillibitor of growth family, member 3	ING3	AC004537	1.1	0.0	5.0
T	2,3 cyclic nucleotide 3 phosphodiesterase	CNP	M19650	8.3	3.9	5.2
ğ		PTPN1	M31724	12.9	5.3	5.2
7	Simila (suppressor of mit two 3, yeast) homolog 2	SMT3H2	AI971724	3.4	27	2.2

27-10 9	DADO OTDOS ACTIVIDADES		AL049951	0.6	80	ď
100000	MADO GITASE ACTIVATING PROJEIN		AL096752	5.6	7.2	5 4
30032 at	omolog, subtamily B, member 5	DNAJB5	AF088982	2.0	2.,	n u
3381/_at	heterogeneous nuclear protein similar to rat helix destabilizing protein		\$63912	0	0.3	5.2
39274_at	nucleoporin 62kD	NIIDEO	VEOF21			
35950 at	X breakpoint 4	20 104	170001	8.9	2.5	5.
34145_at		2074	090841	0	1.1	5.2
34943 at			AI184/10	2.1	0.5	5.
34560_at	S100 calcium binding profein A5	1004	AF063564	1.2	1.5	5.2
35719_at	n: SCN Circadian Oscillatory Protein (SCOP)	STOUAS	218954	1.6	0.7	5.2
40362_at	kappa light polypeptide gene enhancer in B-cells	NFKB2	X61498	29	11.4	5.2
37015_at	/drogenase 1, soluble	AI DU1	00000			
1402_at	lated oncogene homolog	7.07.	N03000	Σ.	e e	5.2
38478_at		SFRSR	M16038	10.4	7.2	5.2
				7	٠. م.ت	5.
3/9/4 at		MSL3L1	AI 050178			
15/8_g_at	androgen receptor (dibydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	AR	M23263	2.8	1.5	5.2
55757_at			10000			
57997_at			C977/M	2.5	2.2	5.
58010 at			K37682	2.2	0.3	5.
48048_at	solute carrier family 34 (sodium phosphate), member 2	CI (73/142)	R27299	0	8:0	5.2
89821_at		1	A1057531	0.4	2.2	5.
76458 s_at			A1000331	0.7	0	5
58115_at			AI023195		0.0	5.
58287 at			AA806110	0.6	0.5	5.3
77328 at			AA872454	1	2.1	5
90623 at			AI223339	0	0.7	5
65434 at			AI655380	1.2	6.2	5
80861 at			N73778	3.9	1	2
59756 at			AA424811	0.7	0	5.2
43098 at			AI089319	1.7	1.4	5,
2000						

Figure 13SSS

48164 at			172557	5.1	4.1	5.2
50275 24			AA632138	0	0	5.2
14733 at	ilypoinetical protein		AL043154	1.7	2.5	5.2
444233 al			D61961	0.3	2.5	5.2
51121 at			AI458975	6.5	9.0	5.2
13785 i at			R45590	88	4.6	5.2
50060			Z39990	1.6	1.8	5.2
45449 at			A1090586	2.3	3.6	5.2
75734 4 at			R40373	2.4	2.7	5.2
59175 34			AI239473	3.1	1.5	5.2
71554 at			AA700040	2.1	2.2	5.2
46929 at			H64589	9.5	3.8	5.2
65553 24	Col 10 protein		N70317	0	0	5.2
60676 at	note in a protein		W07150	3.3	9.0	5.2
44908 at			AI093876	2.5	3.8	5.2
56200 at			H38046	2.2	1.1	5.2
50200 at			AI363050	1.4	1.4	5.2
50930 at			AI792455	1.4	1.5	5.2
47425 at			AI796010	0	O	5.2
47.423 at	paricreatitis-associated protein	PAP	AI621017	2.7	2.3	5.5
53661 34			N26892	1.5		5.2
46005 at			AL038450	16.2	2	5.2
50147	1 2 2 2 2 2 2		N81145	m	1 9	5.2
46580 at	KIAA1305 protein	MAT2B	AI344107	2.1	17	5.2
43478 at	hypothetical protein El 190373		AA411382	2.7	8.0	5.2
50186 s at	old insurance ()		AW021103	17.4	9.0	5.2
44058 at			AA143060	0.7	1.2	5.2
54969 at			W60953	3.9	2	5.2
40651 s at	40651 s at continuitropia releasing houses.		AI829724	0	6.0	5.2
42193 r at	company of the property of the	CKHK1	AF039523	2	0.5	5.2
48354 at			AA434246	0.4	0.2	5.2
32658 at	ring finger protein 1		AI929033	3.4	2.6	5.2
2035 s at	MYC promoter hinding protein 1	RING1	AL031228	2.8	1.9	5.2
יייי טיייייייייייייייייייייייייייייייי		MPB1	M55914	0	0	5.2
41540_at	protein phosphatase 1, regulatory subunit 7	PPP1R7	250749	5.2	2.0	5.7

Figure 13TTT

53708_at	cation chloride cotransporter interacting protein		AI467928	6.1	5.6	5.2
56575_at	CGI-108 protein		AW025521	3.8		5.2
81045_at	zinc finger protein 24 (KOX 17)	ZNF24	AA134771	2.4	2.7	5.2
59136_at			AA779895	5.2	5.1	5.2
45255 at	CGI-69 protein		AI354351	S	3.5	5.2
45808_at	anaphase promoting complex subunit 7		AA131793	5	2.4	5.2
55567_at			AA147933	5.3	5.3	5.2
41388_at	Meis (mouse) homolog 2	MEIS2	AF017418	1.3	0	5.1
34467 g at	5-hydroxytryptamine (serotonin) receptor 4	HTR4	Y12505	9.0	0.4	5.1
	sperm associated antigen 9	SPAG9	AB011088	4	1.6	5.1
40187_at			AW016815	0.7	1.4	5.1
31832_at	KIAA0286 protein		AB006624	41.3	5	5.1
40067_at	E74-like factor 1 (ets domain transcription factor)	ELF1	M82882	0.5	0.5	5.1
38181_at	matrix metalloproteinase 11 (stromelysin 3)	MMP11	X57766	2	0.1	5.1
40468_at	KIAA0554 protein		AB011126	8.3	6	5.1
38512_r_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu-antigen C)	ELAVL3	D26158	4	1.5	5.1
35459_at	regulator of G-protein signalling 13	RGS13	AF030107	0.5	0	5.1
32165_at	splicing factor, arginine/serine-rich 7 (35kD)	SFRS7	L41887	0	1.2	5.1
32010_at	hypothetical protein		282180	0	6.0	5.1
33447_at	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)		X54304	1.5	2.7	5.1
32980 f at	H2B histone family, member L	H2BFL	AI688098	1.5	0.7	5.1
282_at	M-phase phosphoprotein 1	MPHOSPH1	L16782	0.7	0	5.1
33924_at	KiAA1091 protein		AB029014	24.9	10.8	5.1
-1	immunoglobulin kappa variable 1/0R15 118	OR15-118	M20812	1.1	0	5.1
32271_at	FOS-like antigen-1	FOSL1	X16707	0	0	5.1
33842_at	Fanconi anemia, complementation group G	FANCG	AC004472	0	0	5.1
36818_at			AF052100	1.7	0.5	5.1
36937_s_at	401	PDLIM1	828060	1.6	0.1	5.1
38114_at	RAD21 (S. pombe) homolog	RAD21	D38551	7.4	5.2	5.1
37976_at	lg superfamily protein		AL034397	0.7	0.5	5.1
41028_at	ryanodine receptor 3	RYR3	AJ001515	0.5	0.1	5.1
43459 at	KIAA0680 gene product		A1472209	0	5.3	5.1
48034_at	eukaryotic translation initiation factor 2-alpha kinase 3	EIF2AK3	AA534710	3.4	2.6	5.1
42326_at			AW003808	2.7	0.7	5.1

		AADU8964	0.7	0.0	
		AI990713	1.3	1.5	5.1
zinc-binding protein Rbcc728		D59325	2.5	1.4	5.
		AA700460	0.4	2.4	5.1
hypothetical protein FLJ12903		AI807668	5.4	2.5	5.1
		AA922110	4	4.2	5.
		H19417	1.9	3.5	5.3
		AI889332	2.6	2.2	5.
		R06436	13	9.0	5.1
		N67792	1.1	1.1	5.
HSPC030 protein		AA203505	8.5	2.4	5.
		AI659354	1.4	0.1	5.
		AI972712	0	0.7	5.
		AI804384	5.5	2.6	5.7
		N24412	6.0	1.7	5.
		AI222957	3.5	0.8	5
KIAA1105 protein		AW003305	1.4	2.5	5.
nuclear pore complex protein		AA521256	8.0	1.2	5.
hairy/enhancer-of-split related with YRPW motif-like	HEYL	AL040197	4.4	3.2	5.1
		AI863402	8.1	1.2	5.
		R49368	1.6	2.2	S
		R54026	4.2	4.4	5.
hypothetical protein FLJ10737		W87554	0.1	0.2	5.
		H45282	2.5	1.9	5.
		N30160	1.7	2.2	5.1
		AI822115	1.8	2.1	5.
desmin	DES	AA527080	9.0	0	5.
		AA603472	2.7	1.3	5.
		Н66807	O	2.2	Ġ
		AA146979	5.9	3.2	5
		R44595	0.2	6.0	5.
		AA993031	0	2	5.
		AA813190	2.5	1.3	5.1
		AA662107	2.3	2.4	.5
		00001144	0 0	,	u

Figure 13VVV

E0130 at			AI675130	1.2	1.4	τc
, , , , , ,			AI823497	3.3		عا اذ
22228 at SKY (Sex determining region	ining region Y)-box 22	S0X22	AA700909		1 6	i r
			AI082535	60	2.1	i u
5/60/_at solute carrier family 30 (zin	mily 30 (zinc transporter), member 1	SLC30A1	AI553933	4	13	7
400/9_dl			W63785	10	9	0
0,000			AA044626	3	3.1	, u
30100_at NIAAU94Z protein			AI073412	17.4	00	5 1
T			AI632224	0.7		
calumenin		CALU	AA234047	C	0 0	2 4
4/080_at hypothetical protein			AW005818	9.0	1.7	7
52555 at			AI762208	6.4	2.2	5
			AW008207	2.2	2.2	5.1
aldehyde dehydr	المراجعة المراجعة المراجعة المراجعة		AI094933	4.1	3.8	5.1
voltage, depende	of anion change 3	ALDH10	N46689	5.3	3.9	5.1
Τ	(180kD)	VDAC3	AF038962	4	0.3	5.1
at vinculin	a (TOOKE)	110P2B	X68060	3.6	2.7	5.1
100		ACL.	M33308	5.5	4.6	5.1
1 10		SLA	D89077	3.5	3.7	5.1
at acidic protein ric	30	KPL1/	X53777	2.1	1.8	5.1
at	0.0		Y07969	4.4	2.9	5.1
68339 at Iransforming growth factor beta industry	hets induced 68kB		T65761	5.3	1.5	5.1
at	Deta-Hiduced, boxD	IGFBI	AI624028	5.1	2.2	5.1
at	in propried	HEXA	M16424	5	1.5	5.1
53857 at			AA773816	5.1	5.1	5.1
84122 at			H09392	1.8	4.9	5.1
49450 at mitogen activated protein kinase kinase kinase 13	nace Linear Linear 13		AI939453	2.8	4.2	5.1
Γ	mase Alliase 13	MAP3K13	W72274	2.1	3.9	5.1
at vaciolar protein	(veet) subutilit, alpha type, /	PSMA7	AA877820	4.2	3.4	7
at vacuolar protein	Sorting 11 (yeast normolog)	VPS11	AW007365	3.8	1.6	7.
two-nore channe	(yeast normolog)	VPS35	AI961227	2.7	2.9	5.1
1.	<u>a</u> a		AL048491	5.4	5.2	5.1
Nedd. A. like uhio	(c c c c c c c c c c c c c c c c c c c		AI952279	3.2	2.3	5.1
	I Igasc		AI668780	3.9		5.1
			00.010.4			

inventors:	ran naconen, er ar

31402 at	atibili		AF103884		0.4	
38241_at	butyrophilin, subfamily 3, member A3	BTN3A3	U90548	3.4	200	
10/6_at	interleukin 1, alpha	11 1A	M28082	7	† C	0
296_at	tubulin, beta polypeptide	TIBB	V70575	0.1	0.2	5
33716 at		000	V/ 9030	91	12.7	5
40957 at	KIAA0160 protein		N95443	0	0	5
	protein tyrosine kinase 2 hota	KIAA0160	D63881	14.6	17.7	5
30348 at	HMT1 (hpbNp mothultanes)	PTK2B	U43522	14.6	13.4	r.
2102E 2 24	חואון ז רוווין דו אינו	HRMT1L1	X99209	2.4	3.5	7
31333_s_at	DEAD/ n (ASP-GIU-Ala-ASP/HIS) box polypeptide 11 (S.cerevisiae CHL1-like helicase)	DDX11	U75968	8.0	0	2
33480_at	motilin	N I N	0001.7			
34562 at	Zinc finger protein with interaction domain	INICIA	A15393	5.4	1.8	5
1030 s at	topoisomerase (DNA) I		X82018	2.7	0	2
41601 at		IOPI	908200	6.7	2.8	5
41792 at	ATP-hinding contests and family 0 (ATP-hinding		AA142964	2.1	3.7	IC.
36812 at	breast capar actions sub-latinity C (CF I K/MKP), member 8	ABCC8	L78207	6.0	9.0	100
40357 24	inhibition to the Anti-Estingen resistance 3	BCAR3	U92715	9.0	3.1	0 4
37221 at		INHBA	J03634	38.6	4 9) L
27552 64	protein kinase, camp dependent, regulatory, type II, beta	PRKAR2B	M31158	9	46) 4
3/333 at	1	TESK1	D50863	17	3,5) u
20102 at	ets domain	ELF2	U43189	2.5	0.0	0 4
· •] ·	epithelial membrane protein 3	EMP3	1187947	8 7	2.7	١
49409 r at			AA910006		0.0	0
63580_at	serologically defined colon cancer antigen 43	SPOCACAS	277700014		5	5
53827_at		200000	AI0324//	8.0	0.9	5
79503 at			AA/811/6	3.7	2	5
84194 at			AL036462	0.9	2.8	5
			T52159	3.1	1.3	5
63397 at	Photoscociated coiled coiled in the second		AA503172	1.3	1.4	ת
48363 at	associated, concorred to the protein Kinase 1	ROCK1	AI872948	2.5	2.6	ı.
64222 6 24			AA651889	m	~) (
_	pyropriospriatase (morganic)	РР	AW009649	39.9	10 0	מו
	rrizui protein		AA668732	3.4	2.27	
10904 at			AIG78606			ווי
59745 r at			NO9174		5 (C)
63566_at			A100EC27	2.7	2.2	5
44207 at			/70000H	1.3	2.3	2
			A1422986	18.5	5.7	ŭ

73947_at			A1986440	4.1	1.6	5
50218_at			AI816806	2.3	1.5	S
78017_at			AI638269	6.0	1.4	5
44839_s_at			AW006891	9	2	5
78252_r_at			AA034137	2.8	1.5	5
75252_at			AI379494	2.5	2.3	5
47773_at			AA836114	1.5	1.5	5
1017_at	mutS (E. coli) homolog 6	MSH6	U73737	0	2	2
43450_at			R50504	1.4	3.4	5
65887_at	transducer of ERBB2, 2	T0B2	A1830948	4	3.4	5
60924_i_at			H63111	0	0	5
33966_at	interleukin 7	IL7	M29053	8.0	1.7	2
55988_at	G5b protein		AI446559	7.3	3.5	2
70228 r at	70228_r_at protein kinase, cAMP-dependent, regulatory, type II, beta	PRKAR2B	AI792179	5.3	9.7	5
65938_at	MADS box transcription enhancer factor 2, polypeptide C	MEF2C	AL118637	0	ō	2
	(myocyte enhancer factor 2C)					
48287_at			AA233912	2.3	1.5	5
48329_at			AA876002	0.7	0.7	5
61433_at			AI887923	5	3.1	5
47644 at			AI963632	2.4	1.3	5
1813_at				1.3	0	5
42295_at			Ai150454	3.1	2.2	5
48889_at			T51931	0	1.1	5
51250 f at			H17134	1.3	1.5	5
53017_at			3144516	0	0	2
74926 <u>r_</u> at			AI252805	1	0.5	5
84962 f at			R42423	2.8	9.0	5
86300_at			AA342715	0.1	1.8	5
41603 at	transducin (beta) like 3	TBL3	005609	4.8	3.8	2
1583_at		TNFRSF1B	M32315	0	1.6	5
35170_at		MAN2C1	AF044414	4	2.8)
35247_at	small nuclear RNA activating complex, polypeptide 5, 19kD		AI557062	5.5	2.9	5
1447_at	proteasome (prosome, macropain) subunit, beta type, 1	PSMB1	D00761	0.2	0.4	5
65130 at			AI749588	4.8	0.5	5
45577_s_at			AI471038	3.4	4.9	5

lnv	ento	rs:

48811_at	N-acetylglucosamine-1-phosphodiester alpha-N-		AW007594	5.2	4	2
	acetylglucosaminidase					
49488_at	DKFZP434F1735 protein		AW005775	4.9	3.5	5
45815_at	hypothetical protein		AL048939	4	2.9	2
54479_at			AA214559	5.8	3.9	2
39503 s_at	dihydropyrimidinase-like 4	DPYSL4	AB006713	1.9	0.2	4.9
37140_s_at	ectodermal dysplasia 1, anhidrotic	ED1	AF061193	0.5	0.7	4.9
33011_at	neurotensin receptor 2	NTSR2	Y10148	9.0	0	4.9
37839_at			AL109700	1.6	0	4.9
31861_at	immunoglobulin mu binding protein 2	IGHMBP2	L14754	3.9	1.4	4.9
31890_s_at	zinc finger protein 143 (clone pHZ·1)	ZNF143	AF071771	9.0	0	4.9
38173_at	KIAA1076 protein		AB028999	1.4	1.6	4.9
40141_at	cullin 4B	CUL4B	AB014595	0	1.3	4.9
41208_at	S164 protein		L40392	8.0	1.5	4.9
35438_at	SEX gene		X87852	1.5	6.0	4.9
33360_at	f-box and leucine-rich repeat protein 11	FBXL11	AB023221	9	3.5	4.9
34151_at	DKFZP586M1019 protein		AL050284	1.9	2.5	4.9
41026_f_at	glycophorin E	GYPE	U05255	3.1	1.1	4.9
884_at	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3	ITGA3	M59911	2.1	2.5	4.9
	receptor)					
33555 at	immunoglobulin-like transcript 7		AF041261	1.5	0.2	4.9
39986_at	DKFZP586D0919 protein		AL050100	16.5	4.2	4.9
1584_at	cell division cycle 25C	CDC25C	M34065	3.1	1.8	4.9
36859_at	non-metastatic cells 5, protein expressed in (nucleoside-	NMES	AF067724	3.8	0.1	4.9
37270 at	ATPase, Na+/K+ transporting, beta 2 polypeptide	ATP1B2	AF007876	1.3	0.8	4.9
37746_r_at	suppression of tumorigenicity 5	ST5	U15131	0.8	0.1	4.9
37561_at	nuclear transcription factor Y, alpha	NFYA	AL031778	1.3	1.8	4.9
418_at	antigen identified by monoclonal antibody Ki-67	MKI67	X65550	0.4	0	4.9
320_at	peroxisomal biogenesis factor 6	PEX6	D83703	0	9.0	4.9
38281_at	caspase 7, apoptosis related cysteine protease	CASP7	067319	22.7	14.4	4.9
38842_at	Leman coiled-coil protein		AB023206	3.1	3.1	4.9
38318_at			AL050128	1.2	1.2	4.9
63309_at	CGI-15 protein		A1241474	4.1	0.4	4.9
56341_at			AI123450	2	1.8	4.9

89795 at			AL040892	3.2	2.1	4.9
65135 at			A1916853	6.9	3.6	4.9
76200 r at			A1095270	2.3	2.4	4.9
57576 r at			AA780978	1.2	1.7	4.9
49536 at			AI733696	2.4	1.8	4.9
90922 at			A1608696	0.5	0.2	4.9
50475 at			AI679625	ō	0	4.9
62418 i at			AA908810	0.5	1.2	4.9
56258 f at			AI370094	-	0.2	4.9
54626 at			AI301188	2.2	3.4	4.9
67087 at			AI351909	10.3	4.9	4.9
62174_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	SMARCB1	N63449	14.3	1.9	4.9
42773 at			T67520	0.8	1.2	4.9
67336 at			AA525014	2	1.3	4.9
59365 at			D59637	32.9	6.9	4.9
51183 at	transcriptional intermediary factor 1 gamma		N98658	7.5	4.9	4.9
83046_r_at			AI459177	2.7	1.7	4.9
47988_at			AA028166	1.9	1.1	4.9
92163_at			AA504454	8.0	0	4.9
59020_at			AI492162	1.5	0.7	4.9
42690_at			AA034063	3.3	2.3	4.9
64334_at	chromosome 1 open reading frame 2	C10RF2	A1961216	2.6	1.9	4.9
69668_at			A1744371	0.3	0.8	4.9
43050_at			AI613413	2	2.5	4.9
64601_at			AI763164	1.3	1.3	4.9
43065_at	DNA (cytosine-5-)-methyltransferase 3 alpha	DNMT3A	N26002	0.3	1.2	4.9
50376_at	hypothetical protein FLJ11137		AI278629	2.5	3.5	4.9
48205_at			N34861	2	2.8	4.9
65405 at			H67680	0	1	6.4
48867_at			AA527919	8.1	4.4	4.9
60214_at			AA227861	1.8	1.9	4.9
64216_at			H09657	1.3	1.2	4.9
51254 at			AI090139	3.3	3.6	4.9
45975 at			N55070	1	2.3	4.9

53151_at	sex comb on midleg homolog 1		AIREODOS		Č	
62740_at			177560	1.4	7,	4.9
46234_at	CGI-148 protein		9907/1	0.5	0.4	4.9
55959 at			AA043242	4.5	4	4.9
64743 at			AA148929	3.7	5.7	4.9
64342 24			N66336	1.7	0.5	
04342 al	e growth factor	CTGF	AW008273	6	200	n c
40220 at	hypothetical protein FLJ105/9		WEDGD3	000	100	1,0
60968_at			41990212	4.70	χ. α.	
47134_at			21205610	25.3	8.3	4.9
1630_s_at	spleen tyrosine kinase	200	A1935/66	0	1.3	4.9
37737 at	Sartate (D. senartate) O methyltzaneterse	01N	729630	5.1	3.9	4.9
38011 at		PCM 1	D25547	1.9	0.5	4.9
38789 at	Protection Remarkable and the second of the		AB006572	5.3	2	4.9
57545 at	childre to sandil syndrome)	TKT	L12711	4.6	3.3	4 9
18750 24			AA706499	3.6	17	
10/30	Class I cylokine receptor		A1983115	5 2		1
44/05 at	hypothetical protein		AA133356			4.9
64309_t_at	amyloid beta (A4) precursor protein (protease nexin II Alzhaimer APB	day	000000	1	3.5	4.9
	\neg	-	A1625555	0.1	8.0	4.9
45276 g at	protein x 0001		2000011			
51123_at			W30943	3.4	3	4.9
57156 at	HSPC023 protein		H11724	5.2	5	4.9
52044 at			W92964	3.4	3.2	4.0
	SPC22/23	FLJ22649	AI801545	0.4	3.8	4.9
44079_at	general transcription factor IIIA	CTESA				
46719_at		2010	AA166851	4.5	3.9	4.9
47093_at			AI499694	0.3	0.1	4.9
38659 at	Suppressor of clear C. elegans, homological		AA527178	5.4	4.5	4.9
41662 at	DKFZP566B183 protein		AB020669	3.5	3.3	4 8
39723 at			AL050272	1.4	2.2	4
4046 24		CUL1	AF062536	16		2
40443_at	E/4-ilke factor 3 (ets domain transcription factor, epithelial specific)	ELF3	AF017307	8.0		4 4 8
1420_s_at		FIF4A2	Dance			
440_at	ctor)	NEIO	U30033	3.3	2.4	4.8
33387 at		2000	75555	2:1	0	4.8
420 at	Prentor (adrenocortiontronic bound	2H3/	AB00/854	0	0	4.8
, , , , , , , , , , , , , , , , , , ,	Interaction of the profit (autenocorticotropic normone)	MC2R	X65633	1.1	C	0 0

Figure 13BBBB

30616 24						
70000	000		ALUSUZZ/	18.5	0	4.8
32624_at	III 238	ZNF238	AJ223321	1.5	1.1	4.8
430_at	nucleoside phosphorylase	Nρ	X00737	8.6	0.1	4 8
1289_at	glutathione S-transferase M5	GSTM5	L02321	2		4 8
438_at	protein kinase, cAMP-dependent, catalytic, alpha	PRKACA	X07767	1.5	1.2	4 8
37334_at		HNRPA0	U23803	0	0.1	4 8
197_at		NME3	U29656	0.8	0	4
40749_at	membrane-spanning 4-domains, subfamily A, member 2 (Fc	MS4A2	X07203	2.6	0	4 8
)
48782_at	putative nuclear protein		AL040705	0	1.1	4.8
50795_at			AI693592	0.5	0	4 8
67002_at			AI025553	1.9	2	4.8
49415_at			AI027972	0.7	0.8	4.8
78715_at			AI379702	2.3	E	4.8
58052_at			W90549	1.3	0.5	4 8
59210_at			179178	2.7	3	4.8
55556_at			AA968469	1.6	2.8	4 8
62066_at			AI919146	1.4		4 8
65268_at			AA526937	0.4	9.0	4 8
55194_at			AI638607	7.9	4.1	4.8
58302_at			AA971619	1.4	2.4	4.8
84320_at			AA602573	3.2	3.5	4.8
59344_at			AA017033	6.9	m	4.8
88673 f at	hypothetical protein DKFZp434H247		T41344	0.8	1.2	4
43225 i at			AA001052	9.5	4	4.8
43231_at			N70008	4.6	2.8	4.8
59054 at			AA489100	4.1	6.6	4.8
55343_at			AI557402	m	3.6	4.8
4434/at			N53347	3.8	1.3	4.8
/2264_at			AI948563	0	9.0	4.8
56319_at	cofactor required for Sp1 transcriptional activation, subunit 6 (77kD)	CRSP6	C05931	4.3	2.7	4.8
59667_at			AW016310	1 6	7.0	8 7
60860_f_at			A1086805	0	1.2	4 4
43103_at			AA394147	0.5	6.0	4

			R66718	0.8	6.0	4
48921_at			W85737	0.5	23	2 4
52744_at			T70610	0.5	22	4 8
	aquaporin 5	AQP5	U46569	1.3		4
59574_at			AI807378	4	<u> </u>	4 8
54198_at			AA262451	0.4	0.7	4 8
45165_at			AI831506	7.8	3.2	4
54296_at			N35708	1.1	2.4	4.8
53156_at			D80679	3.2	1.1	4.8
45004_r_at			N46092	2.1	1.4	4.8
41886 r at			R85286	7.4	1.2	4.8
55309_at			W90521	0.2	1.3	4.8
_			AA127743	1.2	1.4	4.8
/5246_s_at s n	solute carrier family 1 (glial high affinity glutamate transporter), member 3	SLC1A3	W26838	43.1	7.2	4.8
42034_at			AA250845	6.	23	αV
43599_at			162955	α-	25	
70119_at			AI766259	1.5	1.4	0.4
70656 at			AI827487	0.5	0.8	4.8
/346/ f at			AI799544	9.0	0.7	4 8
T			AI652684	2.2	2.3	4.8
_		MARK3	M80359	2.9	1.9	4.8
닒		FLNA	AL050396	m	2.8	4.8
Т	hypothetical protein FLJ10815		AI963454	3.9	4.1	4.8
T	zinc finger protein homologous to Zfp 36 in mouse	ZFP36	N32721	3.9	2.8	4.8
Т			AA305994	2.5	1.3	4.8
Т	UNA polymerase epsilon p12 subunit		AI797479	5.4	3.7	4.8
_	nypotnetical protein LOC58481		AI335452	2.8	2.4	4.8
44823 s at			AA521476	4.7	4.4	4.8
T			AA233808	e	3.5	4.8
T	COP9 complex subunit /a		AI971871	3.4	2.9	4.8
a			N21131	4.9	4.9	4.8
, j		LYL1	M22637	4.8	3.5	4.8
T	nypothetical protein FLJ20442		AI681916	5.2	4.3	4.8
54878_at			AI 048421	0 <	C	

Figure 13DDDD

47077_at			A169/908	C.1	£.1	4.8
38624_at	solute carrier family 12 (potassium/chloride transporters),	SLC12A4	AF054506	=	Ō	4.7
	member 4					
39559 at	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	KMO	AF056032	4.2	1.3	4.7
38704_at			AB007934	3.8	3.6	4.7
l	t cross-linl					
41678 at	EphB2	EPHB2	AF025304	0.8	7.5	4.7
34940 at			AL080095	1	0	4.7
39701 at	paternally expressed 3	PEG3	AB006625	1.3	0	4.7
	retinal pigment epithelium-derived rhodopsin homolog	RRH	AF012270	0.4	0	4.7
40454 at	FAT tumor suppressor (Drosophila) homolog	FAT	X87241	0.2	1.3	4.7
40559 at			AL096727	1.2	0	4.7
41126_at	solute carrier family 1 (glutamate/neutral amino acid	SLC1A4	AA978353	5.7	7.9	4.7
	transporter), member 4					
32297 s at	+	KLRC2	AJ001684	0.2	0	4.7
40984 at	gamma tubulin ri		W28255	6.0	1	4.7
41331 at	KIAA0806 gene product		R93981	2	1.2	4.7
	xanthene dehydrogenase	XDH	U39487	1	9.0	4.7
38986 at	glucose regulated protein, 58kD	GRP58	Z49835	7.9	16.1	4.7
33493 at	erythroid differentiation and denucleation factor 1		AF048849	1.8	9.0	4.7
38216 at	thyroid hormone receptor interactor 8	TRIP8	L40411	1.1	9.0	4.7
36069 at			AB007925	0	3.7	4.7
36456 at	DKFZP5641052 protein		AL080063	10.7	6.9	4.7
40322 at	interleukin 1 receptor-like 1	IL1RL1	D12763	1.5	0.2	4.7
37308 at	KIAA1624 protein		AI888084	2.5	c	4.7
35847 at	ubiquitin specific protease 24	USP24	AB028980	3.7	3	4.7
121_at		PAX8	66969X	2	1.2	4.7
36872 at	cyclic AMP phosphoprotein, 19 kD		AL120559	13.9	12.3	4.7
36122 at	proteasome (prosome, macropain) subunit, alpha type, 6	PSMA6	X59417	7.7	3.3	4.7
36966 at	ankyrin 3, node of Ranvier (ankyrin G)	ANK3	U43965	1.8	0	4.7
37201_at	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein sensitive	ITIH4	D38535	0.6	5.9	4.7
	glycoprotein)					
41002_at	solute carrier family 16 (monocarboxylic acid transporters),	SLC16A5	U59299	9.0	0.3	4.7
	member 5					
39158 at	activating transcription factor 5	ATF5	AB021663	6.7	9.9	4.7

41075_at A kinas	A kinase (PRKA) anchor protein 3	AKAP3	AF087003	1.9	0.8	4.7
46462_at			AI822047	9.0	0.4	4.7
58008_at			AA521240	0.4	0.5	4.7
48088_at			AI300073	0	3.3	4.7
47174_r_at			AA285149	2.4	1.8	4.7
66352_at			AI003755	0.2	0.7	4.7
58030_at			AA845345	1.8	6.0	4.7
77208_at			AI732988	1.4	1.9	4.7
77298_at			AI675783	0.2	2.7	4.7
54069_at hypoth	hypothetical protein		AI431793	0.1	1.2	4.7
91011_at			A1668698	2.5	0	4.7
53456_at			T61326	1.6	0.2	4.7
	cadherin-like 24	CDH24	A1820755	1.9	1.7	4.7
at	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2		AA205994	10.7	5.1	4.7
42816_at			Z38762	4.2	1.2	4
58366_at			R71447	0	0	4
47961_at			AW013851	1.4	1.3	4.7
83066_r_at			AI536659	1	3.4	4.7
	aldehyde dehydrogenase 12		N70701	9.0	1.7	4.
51675_at			AI791859	1.6	1.6	4.
63074_at			AA570454	4	3.7	4.
69658_at			AI754641	9.0	0.5	4
42916_at			H53950	2.5	1.1	4
63900_at			R42022	0	1.6	4.
42866_s_at			AW003230	1.5	4.5	4.7
	hypothetical protein PRO2013		AW024795	0	2	4.7
45434_at			H05785	3.3	1.2	4.7
56681_at			AA628511	0	9.0	4.7
	hypothetical protein FLJ11159		AI954729	0	9.0	4.7
47805_at			AL046561	1.1	2.3	4
	ribosomal protein S19	RPS19	N91770	1.7	2.8	4
54820_at			AA203581	1	1.7	4.
54933_at			AI356461	11.3	8.8	4
45890 at			W21855	3	1.3	4.7

Figure 13FFFF

65265_r_at			190778	0	0.7	4.7
65795 r at			AL042362	9.4	8	4.7
59474_at			AI924028	0.5		4 7
60143 r at			H71532	2.2	1.2	4 7
59493_at			AA521317	1.3	2.5	4 7
45788_i_at	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N. acetylglucosaminyltransferase, isoenzyme B	MGAT4B	AI741591	2.2	2.6	4.7
46090_at			AA806216	or	a c	7
261_s_at	apolipoprotein B (including Ag(x) antigen)	APOB	M19828	200	400	4.7
63457 f at			AA022988	3.3	2.2	4 7
49213_s_at	KIAA1557 protein		AI692432	0.7	1.2	4.7
46025 at			AA040740	6.4	3.5	4.7
55829 at			AA058944	3.7	2.9	4.7
53975 at	KIAA1151 protein		Z78399	23.6	3.4	4.7
25869 at			R58910	1.6	1.8	4.7
4/8/2 at			AI417194	1.9	1.3	4.7
54985 at			AI346820	2.8	-	4.7
46997_at	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4		N74643	1.8	2.1	4.7
51028 at			AI218306	26	2 4	7 7
57452 at			AA451798	2 4	000	1
51667_f_at			N52088	0.0		1
32166_at	KIAA1027 protein		AB028950	2.3	0 6	7.7
32229 at	eukaryotic translation initiation factor 4E-like 3	EIF4EL3	AF038957	1.1	200	4.7
34368_at	histone deacetylase 2	HDAC2	U31814	4.4	2	4 7
32518 at	Zinc finger protein 259	ZNF259	AF019767	0.8	0	4.7
43422 at	CUZ/-binding (Siva) protein		AW025365	3.9	3.3	4.7
22004 at	т.		AA312905	4.9	3.9	4.7
33689 s at	U-dopachrome tautomerase	DDT	AF012434	4.5	1.8	4.7
42831 at			AI201843	4.7	4.2	4.7
45/12 at	SUMO: I activating enzyme subunit 1		H98166	3.3	2.6	4.7
65620_at	hypothetical protein FLJ14005		W52855	4.6	4.4	4.7
2414/ at	pyruvate dehydrogenase kinase, isoenzyme 4	PDK4	AI763378	0.3	3.7	4.7
3/842_at	II-mia domain-containing protein		AF054589	1.5	3.2	4.7

Figure 13GGGG

-	 	 	٠.,	41

	(myouth orbinost faster DD)	MERZU	L16/94	1:1	8.	4.6
39866 at	Inhightin specific protesse 22	00001	00000			
21200		U3F 22	AB028986	0.6	0.8	4.6
31309 r at			U50277	1.5	2.6	4.6
ro.	~		AB007874	4.6	2.2	4.6
	ADP-ribosylation factor GTPase activating protein 1	ARFGAP1	W26381	0	0.4	100
39696_at	KIAA1051 protein		AB028974	000		7
34951_at	putative chemokine receptor; GTP binding protein		D10923	2 9	200	7
1310_at	proteasome (prosome, macropain) subunit, beta type. 2	PSMB2	026599) L	12.5	1,0
40149_at	SH2-B homolog		AI 0.49924			0.4
31782_at	prostaglandin D2 receptor (DP)	PTGDR	1131000	100	5 0	0.4
38171 at			20100	0.1	0	4.6
1969 s at	kinase 7 (homolog of Yenopus MO15 calt	17.00	034/4/	4.5	1.2	4.6
	winds of Aeropus MOLD COK-	CUX	X///43	1.1	1.3	4.6
31594_at	keratin, hair, acidic,3A	KRTHA3A	Y16788	10		
32868 at	polypentide protein dutamine gamma	TOMAS	10000	7.7	1.0	4.0
	se)	ר פואוס מאוס	L10386	9. 9.	0.7	4.6
292_s_at		CLK1	M59287	7 -	1.5	0 4
32250_at	H factor 1 (complement)	HEI	X07522		1111	4.0
35186 at	PCAF associated factor 65 heta	1	220,00	۷.5	6.7	4.6
40631 at	280 1		AJ009770	1./	1	4.6
27770 24		TOB1	D38305	0	0.3	4.6
34773_91			R90942	1	0.1	4.6
	alpitaz,o siaiyitransterase					
35143 at	KIAA1031 protein		AI138605	50.6	24.1	7.6
3/358_at	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	UBE2E1	AI039880	4.8	1.7	4.6
37715_at	SKI-INTERACTING PROTEIN		AFOAS18A	0	0	
38442_at	microfibrillar-associated protein 2	MFAP2	1119718		0.0	0.4
40718_at	cathepsin W (lymphopain)	MOLO	AE013611	t (5 6	4.0
63307 at		2010	Ar013011	5.0	2.3	4.6
			AL041566	15.3	2.5	4.6
-1,			AI357616	1.6	1.3	4.6
40/30			AA421236	0.4	0.4	4.6
42333 at			AA449090	1.5	6.0	4.6
43022 at	Hypotnetical protein FLJZ2351		AA196189	4.1	2.1	4.6
52929 at			AI 044396	81	<u> </u>	

Figure 13HHHH

All Cittors.	Till Haconen, cr an.	

57537 at			AA001250	9.6	8.5	4.6
63399_at	E3 ubiquitin ligase SMURF1		AI126305	1.6	1.7	4.6
73870_at			A1700737	0.5	9.0	4.6
90776_at			AA781939	3.3	1.8	4.6
42564 at			W84667	5.1	2.9	4.6
76920_at			AA745592	4.1	3.6	4.6
35593_at	amine oxidase, copper containing 2 (retina specific)	AOC2	AB012943	0.4	6.0	4.6
61991_at			AI147060	1.4	2.6	4.6
84050_at			AI583750	9.0	1.3	4.6
62314 at			H04394	13.8	3.7	4.6
56433_s_at	56433_s_at KIAA0826 protein		AA463908	6.0	1.3	4.6
45471_s_at	aldehyde oxidase 1	AOX1	AI589531	2.3	2.1	4.6
48569_at	48569_at STRIN protein		AI608790	1.5	2.8	4.6
69448_i_at			AI700454	2.8	4.7	4.6
70246_at			AA630253	1	0.5	4.6
57139_at			AI341271	2.2	2	4.6
44804_s_at	hypothetical protein FLJ21313		AI982913	7.4	2.4	4.6
51131_at			AW007736	6.6	8.3	4.6
51872_r_at			AA890487	2.5	2.3	4.6
55549_s_at	Kruppel-type zinc finger protein		AI783578	4	1.2	4.6
75247_f_at			AA548037	3.4	6.5	4.6
62440_at			AI198946	6.3	3.6	4.6
58254_at	interleukin-1 receptor-associated kinase M		AI018069	1.4	2	4.6
60606_r_at			N68442	9.0	0.5	4.6
63718_at			N63823	0	2.1	4.6
43278_at			AA600721	1.1	1.6	4.6
50694_at	Carbonic anhydrase related protein 10		AI815895	4.2	3	4.6
47571_at	zinc finger protein 236	ZNF236	AA004757	6.0	1.3	4.6
52406_s_at			AI125673	0	1.7	4.6
42184_at			AA430269	4.4	1.4	4.6
43970_at			AA557271	6.0	1.1	4.6
49524_at	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	AMMECR1	AI032981	3.6	2.1	4.6
59468 at	SRY (sex determining region Y) box 11	SOX11	R44341	0.3	2.4	4.6
64326 r at			AI866358	0	2.7	4.6

45119 at			AIG38568	C	C	46
60129 f at			R92776	0.1	6.0	4.6
49816 at			H50751	1.5	0	4.6
50968 at			AA053842	1.6	1.5	4.6
81806_at	KIAA1681 protein		A1694702	3.7	4.7	4.6
44499 at			N67390	7.8	3.8	4.6
45590 at			AI673025	0.7		4.6
45080_at			103765	9.0	1.3	4.6
45700_at	KIAA1209 protein		AI816833	2.6	1.2	4.6
46183 at			AI810826	7	6.2	4.6
54506_at			AI289311	1.3	1.8	4.6
64883_at			AI744083	6.0	2.9	4.6
56005_at			AA044906	3.8	5.6	4.6
46308_at	rotease (reprolysin type) with	ADAMTS1	AI810627	1	9.0	4.6
	(thrombospondin type 1 motif, 1				-	
47152_at	hypothetical protein FLJ20291		N32572	2.1	8.0	4.6
57347_at			AA725801	0	8.0	4.6
49101_at			AI761058	4.1	1.8	4.6
47641_at			AI732810	1	3.1	4.6
1827_s_at			M13929	6.0	0	4.6
64832_at			AA113447	1	0.7	4.6
63121_at			T88970	4.2	1.3	4.6
54096_at			3149758	1.8	0.4	4.6
75380_at			AA099289	2.1	2.9	4.6
85307_at			AI469339	4.1	1.2	4.6
76239 r at			AA059247	2.6	3.9	4.6
824_at	glutathione. Stransferase like; glutathione transferase omega		U90313	0.4	0	4.6
38605_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, 10 MNLL)	NDUFB1	AI345944	3.5	2.1	4.6
40955_at	prostate tumor over expressed gene 1	PTOV1	U79287	5.2	2.6	4.6
33485_at	ribosomal protein L4	RPL4	D23660	3	1.9	4.6
39672_at	hosphatase, non-receptor type 7	PTPN7	M64322	3.2	4.4	4.6
34406_at	KIAA0602 protein		AB011174	4.9	2.7	4.6
34828_at	polymerase (RNA) II (DNA directed) polypeptide I (14.5kD)	POLRZI	AL037557	4	2.9	4.6
36639_at	adenylosuccinate lyase	ADSL	AF067853	4.6	m	4.6

7 7/1	227000 - ATR 11 11 11 11 11 11 11 11 11 11 11 11 11	CEBPA	Y11525	5.9	4.9	4
10-0-0-0	ATP synthase, IT+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	ATP50	X83218	4.1	2.2	4.6
48055_at			N66640	4	23	4.6
56906_at			AA193416	4.7		7
65578 at	cathepsin S	CTSS	AI817147	2.4	000	7 7
56225_at			A1744466	i	2.2	1
58780_s_at	hypothetical protein FLJ10357		DANAMO		0.0	4.0
43053 g at	-		AW025010		7.0	4.6
44085 at			AW025012	4.9	3.2	4.6
16,000			AL040188	4.4	4	4.6
16597 at	hypothetical protein El 190106		AA402192	0.4	1.2	4.6
54150 at	ilypotrietical protein Fuscotoo		AW014780	4.5	4.3	4.6
4136 at			AI453531	4.3	2.8	4.6
52313_at	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A	НАДНА	AI972144	3.9	2.4	4.6
	alpha subunit					
41113_at	KIAA0557 protein		41871306			
39080_at	KDEL (Lys.Asp.Glu.Leu) endoplasmic reticulum protein retention receptor 2	KDELR2	M88458	10	0.3	4.5
35527_at	calcium channel, voltage dependent, alpha 2/delta subunit 1	CACNAPP1	MZGEGO	C		
40204_at	chymotrypsin-like	CTRI	Y71877	0.0	4.6	4.5
192 at	TATA box binding protein (TRP) associated factor, BNA	TALAL	(V) 18/	C:1	5.1	4.5
		IAFZF	018062	1.4	1.2	4.5
40570 at	forkhead box O1A (rhabdomyosarcoma)	FOX01A	AF032885	6.1	٦	
40803_at			AL050161	6.6	3.6	4.0
41142 at		OXCT	U62961	23	2.0	4.0
41232_at	DKFZP564D116 protein		AI 050022	- 2	000	0.4
32227_at	proteoglycan 1, secretory granule	PRG1	X17042	7 10	200	4
32780_at	KIAA0728 protein		AR018271	0.71	4.0	4.5
32104_i_at	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CAMK2G	066063	1.3	0.5	4.5
34149_at	pleiotropic regulator 1 (PRL1, Arabidopsis homolog)	PI RG1	WOSEED			
34299_at	zinc finger protein 278	7NF278	0000014	1.1		4.5
38662 at			A1 04 7506	1.7	2.9	4.5
35321 at	thusted like kinase 2	0/1/14	ALO47330	٥	9.1	4.5
	ы	LKZ	AB004884	2 7	2 7	

35346 at	FEM·1 (C.elegans) homolog b	FEM1B	AB007856	0.8	1	4.5
195 s at	1 2	CASP4	U28014	11.6	8.7	4.5
1271_g_at	v-rel avian reticuloendotheliosis viral oncogene homolog A	RELA	٢١٩٥67	3.6	2.9	4.5
32439_at	ATPase, H+/K+ exchanging, beta polypeptide	ATP4B	M75110	0.7	0.7	4.5
38105_at	hypothetical protein FLJ11021 similar to splicing factor,		W26521	1.9	9.0	4.5
37645 at	=1~	CD69	722576	0 %	80	7 2
1064 at	protein tyrosine kinase 9	PTK9	089201	200	0 -	4.5
38440 s at	1-		AA015605	0.1	2.8	4.5
49880_at	_		R60061	2	1.6	4.5
56143_at			N32840	1.8	0.7	4.5
48158_at	transforming, acidic coiled-coil containing protein 3	TACC3	AA098825	1.1	1.1	4.5
56806_at			AI809891	1.5	3.3	4.5
50757_at			AA418074	3.3	1.3	4.5
54686_at	thyroid hormone receptor associated protein, 240 kDa subunit		AA122265	m	2.5	4.5
66519_at			AA845423	0.8	1.2	4.5
47460_at			N64794	9.4	2.7	4.5
48854 i at			AW025683	4	2.1	4.5
51367_at			A1189446	0.2	0.8	4.5
80256_at			A1167159	0	0.2	4.5
62081_at			AI209079	1.4	0	4.5
47144 at	ASB-1 protein		AI018173	5.7	4.1	4.5
61971_at			AI986197	1.5	0 4	4.5
57838_at	hypothetical protein FLJ10111		AA196477	2.3	2.4	4.5
82914_at			AI767564	1.9	2.4	4.5
65814_at			N95618	5.5	5.2	4.5
59566_at			AA705681	5.2	1.5	4.5
62147_at	hypothetical protein FLJ11155		A1265860	4.2	0.5	4.5
43784 r at	tumor necrosis factor receptor superfamily, member 7	TNFRSF7	H83425	0.5	1.7	4.5
60504_at			AI859849	13	3.8	4.5
65670_at			AA489239	1.7	0	4.5
44977 g at			AI972721	0	0.1	4.5

Figure 13LLLL

73705 at			AI991175	1.3	1.8	4.5
			R93729	2.8	2.5	4.5
56955 f at			Н95587	1.4	0.4	4.5
45739 at	hypothetical protein FLJ11210		AA056538	0	0	4.5
51680 at		MGP	AW023159	2.1	9.0	4.5
58618 at			AI741373	8.0	0.4	4.5
69126 at			AA470958	9.0	4.2	4.5
64086 at			AA004211	1.1	0.5	4.5
62712 r at			AI870532	1.8	1.3	4.5
63662 at			AI126468	12.6	4.9	4.5
45167 at	homeo box C9	НОХС9	AI332412	1.6	1.2	4.5
			N78361	0.1	6.0	4.5
45654 at			AI808746	1.6	1.6	4.5
52977 at	KIAA1634 protein		AI692181	0	2.6	4.5
			AA190571	6.0	4.3	4.5
88043 g at	keratin 18	KRT18	AI984261	1.1	2	4.5
55879 at	+		240682	0.3	6.0	4.5
46663 at			A1147033	2.2	1.7	4.5
64921 at	hypothetical protein FLJ10587		N29706	2.3	1.8	4.5
			AA460661	2	1.4	4.5
			AA243778	1.8	0.8	4.5
38990 at	F-box only protein 9	FBX09	AL031178	3.6	1.6	4.5
1228 s at	meningioma expressed antigen 6 (coiled-coil proline-rich)	MGEA6	U73682	2.6	2.3	4.5
36194_at	low density lipoprotein-related protein-associated protein 1 (alpha LRPAP)	_RPAP1	M63959	3.9	0.5	4.5
37730 at	EBNA.2 co-activator (100kD)		U22055	1.5	6.0	4.5
38050 at	KIAA0164 gene product		986610	3.4	1.7	4.5
38713 at	septin 3	03-Se	03.Sep 299716	4.9	1	4.5
53799 at	hypothetical protein similar to mouse Dnaji1		AA628434	0	0.4	4.5
43406 s at	-		AA890650	4.4	3.1	4.5
58410_at	cat eye syndrome chromosome region, candidate 1	CECR1	AI572068	3.7	3.4	4.5
49569 at			AI690893	5.1	4.2	4.5
63544_at			N33295	3.9	2.7	4.5
66112_at	translocase of inner mitochondrial membrane 17 (yeast) homolog		AA234191	3.3	1.4	4.5
	H					ı

Figure 13MMMM

56310_at	hypothetical protein FLJ10893		AIROANEA		-	
51163_at	hypothetical protein FLJ22405		AA115361	100	0.4	6.7
57031_at	ZYG homolog		A1001E7A	0.0	6.3	4.5
65762_at			410070014	0.7	2.1	4.5
65748 at			AI201/92	3.8	1.2	4.5
52596 f at			AA531437	2.9	1.6	4.5
64486 21			R52511	2.3	0.8	4.5
2007	hypothetical protein partp/02/100		AI341234	4	2.2	4 5
0440/ at			H16514	1.8		4.5
45115 at			AA909042	4.3	4.2	4.5
43404 at	Figure fastatic cells 3, protein expressed in	NME3	AW014797	3.2	3.1	4 5
40311 at	Cart 39 protein		AI525879	4	~	4 5
00120 at			AI769737	4.2	33	2 4
396/2_at	Cadnerin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog	CELSR1	AL031588	1.7		4.4
41856 at						-
20700			AL049370	6.0	0.3	4.4
18-00 / CC	signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	L29277	13.3	5.3	4.4
37887 at	protein kinase Chk2					
763 at	factor hota		AF086904	0	0	4.4
33072 24		GMFB	AB001106	0	1.3	4.4
10067 at	III) receptor 2	HCRTR2	AF041245	2.2	C	4.4
140237 at	10 528	RPS28	AI400011	С	0	
1456 s at	Interieron, gamma-inducible protein 16	IF116	M63838	0.4	2 2	t c
	triple runctiona	TRIO	AF091395		Pi C	
	MUKE-related gene X		D14812	0	-	1 4
3368/ at			AL049782	0.7	0.0	1 4
30242 dl	smail proline-rich protein 2C	SPRR2C	M21539	1.5	1 4	1 4
334/1 g at	+		AF052177	2.1	90	t v
32/39 at	NIAMIII/ protein		AA001791	0.8	0.7	1 0
41013 at			AL 080114	1 2		1
362/6 at	contactin 2 (axonal)	CNTN2	X67734	2 2		t
36294 at		STK4	1160207		4.00	4.4
37828_at			A1 050064		0 0	4.4
35978_at	proline-rich Gla (G-carboxyglutamic acid) polypeptide 1	PRECI	AE00004	0.4	1.2	4.4
1728 at		BM11	12003642	6.3	1.3	4.4
35317 at	pressed antigen E (hadingalidae)	DIVILI	L13089	4.1	4.0	4.4
20071	oressed antigen 5 (nyaluronidase)	MGEA5	AB014579	m	3.3	4.4

Figure 13NNNN

Aventors:	rair Haconen, er at.

20110	>1		AB014560	1.5	3.5	4 4
30118_at	coactivator 1	NCOA1	AJ000882	C.		
36641_at		CAPZA2	1103851		10	4.4
1519_at	v-ets avian erythroblastosis virus E26 oncogene homolog 2	ETS2	104102		0.0	4.4
46774 i_at	9	1	7000010		3.0	4.4
63056 r at	prostate cancer associated protein 1		A1888/95	0.3	0.5	4.4
76105 at	' 1	PCAINAP1	AI525303	1.3	0.8	4.4
66443 at			AA648486	0.2	1.8	4.4
66523 at			AA775536	0.3	0	4.4
501 Ap 24			AA829524	3.3	m	4.4
55829 at			AI733002	1.2	0.5	4.4
61002 at			AA987549	1.9	1.8	4.4
53880 at			A1147067	ō	0.4	4 4
48716 at	andonies mic retioning wide a state 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		AI285891	2.4	0.1	4.4
91364 at	chachiashing regending oxidoreductin 1-LDeta		AA001399	12.2	1.8	4.4
59274 at			AI928094	0.5	1.8	4.4
62923 at			R66045	11.7	2.9	4.4
84235 at	Dra B coll loubomin transceriation (1.1.1.1.1		AI312844	1.3	1.5	4.4
81168 at		PBX1	AW005924	9.0	0	4 4
58301 at			AA005089	2.6	6.0	4.4
			H12221	1.9	1.1	4 4
83874 at			AI768586	1.5	5.1	4.4
56066 at			AI024818	23.9	7.8	4.4
51942 at			AA923551	3.3	2.8	4.4
86613 at			AA142984	3.4	2.6	4.4
87506 at			R01897	2	1.2	4.4
63104 at			N80159	1	1.9	4.4
68969 at			H98113	o	8.0	4.4
80894 at	histone acetyltransferase		AI679892	4.2	2	4.4
49168 at	-1		AA553554	5.7	1.9	4.4
52522 at			AA151917	3.2	2.2	4.4
79405 at	noly(A) hinding protein afactories 1 11.		H06408	3.6	1.3	4.4
50100 at	Potent Strains Process, cytopiasissic 1-like		AA740146	1.5	1.1	4.4
87485 r at			AA845353	1.2	1.8	4.4
68299 24			T78883	2.5	2.5	4.4
ממלקטט			20000	1		

51033 2+			N54951	0	0	4.4
50001 at			AW023193	3.7	2	4.4
19301 dt			AW021543	5.1	c	47
64ZU1_at			AL044520	0.7	27	4.4
20/13 at			N65995	1.5	1 9	4.4
T			AI935521	0.8	C	44
64236 at wingless type Mi	e MM IV integration site family, member 4	WNT4	AI634496	0.5	0.4	4.4
23326 at			H08155	1.7		4 4
44397 at			H11252	5.1	4.3	44
3140 at			AI244908	61.5	3.8	4 4
01010 at			AI655467	64.4	21.6	4.4
15010 at			AA975060	0.1	0.8	4 4
65007 r at			AI796221	8.5	8.5	4.4
51714 at			AI421880	9.0	9.0	4.4
77703 24			AI830422	2.8	2.7	4.4
60504 at			AW002441	1.1	1.7	4.4
55079 at Beld accordated	ייסייותיים דיסיי		AI951932	2	3.8	4.4
T	-1		AI814271	5.8	1.2	4.4
57743 at			AI798863	3	2.8	4.4
20133 at			AI760013	4.5	2.5	4.4
38285 at covetallin mu			AA243840	6.0	0.5	4.4
T	3	CRYM	AF039397	1.1	9.0	4.4
49832 at			AI201001	3	1.5	4.4
32407 f at			AI147740	1.4	1.9	4.4
44162 r at 1			U92818	6.0	0.7	4.4
78852 at			R42278	1.1	1.6	4.4
86033 at			AI076830	3.8	1.7	4.4
89349 at			AI478597	0	0.2	4.4
T	-14		R08903	0	0.2	44
40890 at motovin 1	nne c synthase (cytochrome c heme-lyase)	HCCS	U36787	4.8	2.9	4 4
T		MTX1	U46920	2.9	2	44
T	otern		AB023199	4.3	2.7	4 4
Τ	0.1	CYC1	X06994	3.2	2.3	4 4
344UZ at IUNF-INTERACTING DI	ng protein		7000000	,		

Figure 13PPPP

34826_at	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	SDHA	L21936	3.6	0.8	4.4
39086_g_at	single-stranded DNA-binding protein	SSBP	AA768912	2.6	1.2	4.4
75026_s_at	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	MTHFD2	A1990317	0	9.0	4.4
54869_at			AA287799	3.9	3.7	4.4
63840_r_at	hypothetical protein FLJ22318		AA151600	2.1	2.4	4.4
51149_at			AA421991	6.0	3.8	4.4
45339_at	CGI-39 protein; cell death-regulatory protein GRIM19		AA181145	3.3	3.7	4.4
45335_at	CGI-28 protein		AI037884	4.1	2.7	4.4
44654_at			A1669655	3.4	4	4.4
51239_at	hypothetical protein FLJ23239		W67828	4.9	3.8	4.4
52159_at	HEMK homolog 7kb		W93807	2.4	1.7	4.4
50071_at			AL042592	3.3	3.1	4.4
65930_at	30S ribosomal protein S7 homolog		N78337	4.3	2.5	4.4
48731_at			AI948491	4.1	1.6	4.4
38973_at	KIAA1020 protein		AB028943	-	8.0	4.3
38149_at	KIAA0053 gene product		D29642	9.1	8.7	4.3
32673_at	butyrophilin, subfamily 2, member A1	BTN2A1	U90543	6.5	2.5	4.3
	kallikrein 3, (prostate specific antigen)	KLK3	X07730	1	0.7	4.3
41213 at	peroxiredoxin 1	PRDXI	X67951	0.4	1.9	4.3
<u>⊷</u> ا	KIAA0737 gene product		AB018280	1.5	1.5	4.3
	interferon, alpha 2	IFNA2	100207	6.0	0	4.3
	KIAA0197 protein		D83781	2.9	5.2	4.3
39508_at	N-myc downstream regulated gene 2	NDRG2	AI201607	2.9	1.8	4.3
36256 at	limbic system-associated membrane protein	LSAMP	U41901	1.7	1.5	4.3
38982_at	TRF2-interacting telomeric RAP1 protein		W28865	4.4	1.6	4.3
37383_f_at		HLA.B	X58536	4	2.7	4.3
32140_at	sortilin-related receptor, L(DLR class) A repeats-containing	SORL1	Y08110	1.1	0.7	4.3
35228_at	carnitine palmitoyltransferase I, muscle	CPT1B	Y08682	2.5	4.5	4.3
34575_f_at		MAGEA5	010689	m	0.4	4.3
35726_at	S100 calcium-bin	S100A2	AI539439	2.7	9.0	4.3
35987_g_at	member of MYST family histone acetyl transferases, homolog of Drosophila MOF		AL050395	0	0	4.3
40005_at	alkylation repair; alkB homolog		X91992	2.4	1.7	4.3

36/55_s_at	interleukin 5 rec	IL5RA	M75914	19.0	0.5	43
4033/_at	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)	FUT1	M35531	1.8		4.3
886_at	deoxycytidine kinase	DCK	M60527	0	, ,	
37340_at	methionine adenosyltransferase II, alpha	MATOA	14/270EA	200	C.2	4.3
40677_at	4	V-7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AE054004	000	1.1	4.3
37964 at	ring finger protein 3	DNES	AF034904	7.7	8.1	4.3
55747 at		CHINES	W25/93	6.0	2.2	4.3
			AA534565	2.3	1.6	4.3
50762 at			N39954	8.4	2.8	4.3
20340 K at			AI963304	4.4	3.6	4.3
30707 at			AA527219	3.7	3.8	4.3
42302 dt			AA628983	3.7	2.8	43
4/188 at			AA677561	1.3	2.4	43
77070 -1	ribulose-5-phosphate-3-epimerase	RPE	AA252480	0.8	1.9	4 3
1/8/9 at			AI024938	1.9	2.7	4.3
51243 at			R93374	0.3	1.4	2 4
46813 at	hairy/enhancer-of-split related with YRPW motif 2	HEY2	N46845	0.7	12	2 6
/9982_at			AI793177	000	α 0	5 6
61583 at			AI193207	0.5	1 4	i c
03188 at			AA948597	0	,	
83904_at			A1985614		7 0	24.
55253 at			AA621047	1 -	7 0 0	4.3
84746_at			0032000	10	0.0	4.3
84588_at			A1501020	5 0	9.0	4.3
42884 r at	hypothetical protein MGC2628		A1091017	y 4	2.9	4.3
64281 s at	upregulated by 1.25-dihydroxyvitamin D.3		AA01821/	2.8	1.3	4.3
86380 at			AW0266/2	0	0	4.3
			AI/18112	-	0.8	4.3
49234 c at	K14A1 389 protein		R67641	2.4	3.8	4.3
43754 at			AI436735	0.4	3.3	4.3
79392 at			AA194720	1.5	1.4	4.3
68697 at			AI200514	8.5	2.6	4.3
13628 24			AA883987	က	0.4	4.3
90400			H94876	2.8	2.6	4.3
50409 dl			AI652505	6.0	1.6	43
59629_at	putative G protein-coupled receptor 92		AA864327	1.9	2.8	43

45296_at	KIAA1631 protein		A1986035	12	13	4.3
63481_at			AA059478	18	7.	4 4
52204_at			AA894564	4 7	2	1
54675_at	inhibitor of kappa light polypeptide gene enhancer in B-cells,	IKBKB	AA521493	2.2	1.6	4.3
63729 f at	Milase Deta					
65403 at			N69123		0.2	4.3
67687 at	high mobility group (nonhistone obromosoma)) arotain 1	. 074	AAU30393	1.1	2.1	4.3
55372 at	otein OKEZOZKO CITOTO	ואום	A119122/		0	4.3
52576 s at	scellular matrix protein	CDONO	AI831481	4.0	1.4	4.3
53161 7 24		21014	AW00/426	5	J. 1	4.3
52790 at			AI826333	1.9	3.1	4.3
327.30 at			AI150158	2.8	3.1	4.3
44213 at			AI559696	2.6	3.9	4.3
/1542_at			AI191040	1.8	1.3	4.3
630//_at			AI733697	0.3	2.4	4.3
446/3 at			N53555	9.5	13.7	43
60712_at			AA394100	2	0.7	4 3
71544_at	KIAA0379 protein		AA852371	3.3	O	4.3
46366_at			179183	0.7	6.0	43
49598 at			H79046	4.2	2.1	4
52832_at			AA012862	1.8	3.5	4.3
54354 at			AA662774	0	1.3	4.3
46885_at			AI822096	0.3	0.4	43
4/5/0 at			AI741392	2.1	0.3	4.3
48243 at			AI857897	0.4	2.2	43
91324 at			AA149539	4.6	1-1	4.3
48300 at			AA713522	6.2	2.4	4.3
52922 at			AI214996	25.6	10	4.3
5/285 at			AA933717	1.9	2.2	4.3
51553 at			T90529	4.9	1.4	4.3
51613 T at			AI336271	2.9	3.1	4.3
493/8 t at			AI041389	9.7	2.8	4.3
52909_at			3096417	3.2	2.1	4.3
/3258_at			AI675987	1.3	1	4.3
87058_at			190289	0	6.0	4.3

39043_at	actin related protein 2/3 complex, subunit 1A (41 kD)	ARPC1B	AF006084	2.7	1.3	4.3
41865_at			AF052185	4.4	3.3	4.3
40266_at	KIAA1036 protein		AB028959	3.9	3.7	4.3
32622_at	dynamin 2	DNM2	L36983	4.5	0.1	4.3
40568_at	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta ATP6B2 polypeptide, 56/58kD, isoform 2	ATP6B2	L35249	3.2	1.8	4.3
32824_at	late infantile (Jansky.	CLN2	AF039704	8. 8.	8.0	4.3
35238 at	TNF receptor associated factor 5	TRAF5	AB000509	3.5	1.5	4.3
35688 g at		MTCP1	224459	5.3	2.6	4.3
36628_at	ralA binding protein 1	RALBP1	L42542	4.9	2	4.3
36635_at	ATPase, Class VI, type 11B	ATP11B	AB023173	3.8	1.2	4.3
38733_at	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)	XRCC5	M30938	4.8	1	4.3
37966_at	beta parvin		AA187563	2.9	9.0	4.3
39135_at	KIAA0767 protein		AB018310	4.5	3.7	4.3
39173_at	fibrillarin	FBL	X56597	e	3.1	4.3
56362_at	hypothetical protein FLJ20585		AA121624	1.1	1	4.3
56520_at	nudix (nucleoside diphosphate linked moiety X) type motif 5	NUDTS	AI188576	4.8	3.3	4.3
90610_at	leucine-rich neuronal protein	LRN	A1654857	3.3	2.5	4.3
53906_at	differentially expressed in FDCP (mouse homolog) 6	DEF6	AA523303	4.3	4.3	4.3
61668_at			A1963090	5	2.9	4.3
43798_s_at			AI347938	3.5	2.1	4.3
60863_s_at	hypothetical protein from EUROIMAGE 2021883		AA526910	3.9	2.8	4.3
58595 f at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	AA551303	2.6	3	4.3
49110_s_at			T48132	3.8	2.6	4.3
58528_s_at			AI760772	0	0.9	4.3
53354_at			AI668938	4.1	2.2	4.3
51984_at			AA148813	0.6	1.8	4.3
49210_s_at	_		AW023011	4.2	3.2	4.3
49914_at	hypothetical protein dJ511E16.2		AA147044	2.7	2.3	4.3
560 s at			M63589	4.3	4.3	4.3
38970_s_at	Nef-associated factor 1		AJ011896	26.4	7.6	4.2
41457_at	KIAA0423 protein		AB007883	1.5	3.9	4.2

34955_at	sette, sub-family C (CFTR/MRP), member 4	ABCC4	AF071202		2.1	(
40219 at			AI796944	7 2	100	4.7
36334_at	lymphocyte antigen 9	64	1 42621			7.7
1134_at	activated p21cdc42Hs kinase		113738	0.0	2.0	7.7
31888_s_at	tumor suppressing subtransferable candidate 3	TSSC3	AF001294	2.9	2.5	7.4
32119_at			AI 040423	0.5	2.0	7.4
40494_at	death effector domain-containing	DEDD	AF043733	1.0	0 0	4.2
40501 s_at	myosin-binding protein C, slow-type	MYBPC1	X73114		6.0	4.2
40791_at	directed) polypeptide A (220kD)	POI R2A	X63564	2 2	0	7.4
40831_at			AI 050190	0.0	3.5	4.2
33708_at		POV1	AF045584	2 2 2	0.1	4.4
35940_at	POU domain, class 4, transcription factor 1	POU4F1	X64624	0.0	0 0	1 0
33840_at		TPD52	U18914	1.7	1 0	100
33870_at	putative zinc finger protein		AB029005	24	7 -	4.6
31669_s_at	homeo box A11	HOXA11	AF039307	27	C	100
38138 at	nding protein A11 (calgizzarin)	S100A11	D38583	3.5	0 0	7 t
41032 at	n 151 (pHZ·67)	ZNF151	Y09723	13.8	5.4	4.2
39964 at	osa 2 (X-linked recessive)	RP2	AJ007590	3.4	6	100
	ctor, arginine/serine-rich 4	SFRS4	L14076		53	2.4
3/391_at	cathepsin L	CTSL	X12451	6.8	6 3	2.7
3/2/3 at			AF007153		0 0	1.5
38405_at	fragile X mental retardation, autosomal homolog 1	FXR1	U25165	0.7	0.40	4.6
38441_s_at	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-	MCP	X59408	2.9	4 1	7.1
				j		t.
553/6_at	MILI protein		N66625	3.3	2.3	4.2
75000 at			AI798874	3.6	9.0	4.2
1 3003 At			AL042660	0	0	4.2
22020 at			AI738556	1.5	0	4.2
1/0/0 at			AI949912	1.8	2.2	4.2
610EE at			A1124014	0.8		4.2
01233 at			N36377	0.1	0.1	4.2
47.221 dl			H58608	m	3.9	4.2
47898 at			A1566854	0	4	4
23896 at			AA147213	2.7	1.3	4.2
4/108_at	LIM protein (similar to rat protein kinase C-binding enigma)		AA196325	0	m	4.2

Figure 13UUUU

inventors:

48/5/ at	EH domain containing 1	EHD1	AI986040	53.8	2.9	4.2
02004 at			AA552150	3.8	2.5	4.2
6/3/5_at			A1829707	a c	0.00	
60421_at	RPA-binding trans-activator		N32669	5 -	1 7	4.6
48556_at	HIV TAT specific factor 1	HTATSF1	AA581365	7.7	1:4	4.6
62744_at	guanine nucleotide binding protein beta subunit 4		A1857502	10.4	4.0	4.2
85760 r at			VICOO 1	100	4.0	4.2
86062 r at			AIb8U3b2	9.0	0.8	4.2
62673 24			R91428	0	1.6	4.2
5020 A 2 21	S		N92444	2.3	2.4	4.2
30334 K at	KINA DINGING MOTH protein 3	RBM3	AI953114	3.6	1.4	4.2
62683 at			AA034014	1.2	2.1	4.2
4859/ at			AI871648	0	3.6	10 /
65676_at			AA115819	2.5	2 -	100
67713_r_at			A1986192	57 E	21.0	2.5
48172_at			D8/376	500		4.6
79179_at			0.0000	5 0	0.8	4.2
88595 at			Alooyazy	5	0	4.2
60416 24			AI653291	2.6	0.8	4.2
24204	┑		AI693716	0.8	0.2	4.2
34204_at	serna domain, immunogiobulin domain (Ig), short basic domain, (secreted, (semaphorin) 3E	SEMA3E	AL050043	0.4	3.1	4.2
52226_at			H16779	10.5	3.6	0
/4282_at			AW005199	-		2.5
80476_at			T16443	2.0	t c	4.0
56736_r_at	GRB2-associated binding protein 1	GAB1	AW022256	80	0 -	4.2
44955 1 at			N75945	3.9	0.1	4.0
51481 r at			N55558	2.5	6.0	4.2
52770_at	LIST-Interacting protein NUDE1, rat homolog		AI857685	3.9	4.3	4 2
24193 at			AA458742	1.9	0	4.2
/ 5044 r at			AI355014	3.7	0.4	4.2
01903_at	Vaniliold receptor-related osmotically activated channel; OTRPC4 protein		AI674479	0.7	9.0	4.2
51502_at			NE2096	4	7.	
50997_at			AI796264		1.7	4.4
80285_r_at			R98495	3.6	2.5	7.7
56441_at			W05842	000	j -	4.6
			1	5.5	1.0	4.4

-			H29258	3.2	10	01
92130 <u>r</u> at			H41107		1.0	4.4
58397_r_at			AA976373	000	0.1	4.6
63916_r_at			150788	0 0	0.00	4.6
55443_at			AA631027	4.3		7.7
52655_at			AI793179		\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	4.6
44392_at			HO7855	0.0	7.7	4.4
65043_at			AIR57698	i C	1.01	4.6
52446_at			A1281933	0	1.0	4.4
61704_i_at	hypothetical protein FLJ20036		AWO06276	0,0	0.0	4.4
44620_at			H97503	, c	2,0	4.6
46444_at			A1288239	500	2 6	4.6
60581_at			AA100715	, C		4.4
51595_at	protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum protein		W26575	1.5	0.0	4.2
47053_at			AI768650			
55359 at			VC0000 (NV	,	5	4.2
55384 g at			AAAE33024	ב. ביוני	1.4	4.2
47527 at			AA454036	7)	3.2	4.2
63013 at			AI632488	9.4	က	4.2
56735 at			AL120446	6.2	7.7	4.2
51510 1 24			AA262730	0.5	0.6	4.2
55168 + 3+			T92882	18.1	10.1	4.2
50100 at			AW024222	1.9	1.5	4.2
24302 at			AI765546	2.3	0.7	4.2
030/0 dt			AI027677	6.7	2.2	4.2
11334 st	000000000000000000000000000000000000000		AI760700	8.6	2.2	4.2
41624 at	П		AB018331	3.5	1.1	4.2
32//4_at	INADH denydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI)	NDUFB8	AI541050	2.9	1.3	4.2
37581_at	protein phosphatase 6, catalytic subunit	рррес	X92972	0		,
36637_at	annexin A11	ANXA11	119605	000	+ -	4.6
37306_at	KIAA0068 protein		D38549	200	101	4.6
38810_at	histone deacetylase 5	HDAC5	AF039241	42	w F	10.4
48014_at			N54957			4.7
44549_at			36600618	1		1

Figure 13WWWW

100300	4.46.28 at including the proprietable from 10.00 IV		AI244335	2.9	α.	
15517 c at	Misumi degrading enzyme	IDE	AA573292	5.2	26	
1001/ S at	NIAA1UZ/ protein		AIGERGGS	200	2 6	1
51906_at			7100011	6.3	2.3	4
51713_at			AISBOOLD	1.1	3.3	4.2
81574 at	Caspase recruitment domain protein 0		A1660536	4.2	3.8	4.2
51128 at	ממוויות אומניווי		AI307612	4.2	3.6	4.2
48042 at			AA166881	3.6	3.6	4.2
49071 at			AL119388	2.1	0.8	4.2
51188 at			AI541411	4.2	1.4	4.2
54765 at	yeroderma nigmentonim complete		AA454038	4.2	3.6	4.2
57828 at	Inhiguitin A 52 recidue discounting and a second control of the co	XPC	AL042673	3.8	2.8	0.4
57201 at	hypothetical profess El 1100co	UBA52	AI857945	2.5	2.5	4.2
46572 at			AI870481	4	2.5	4.2
65923 at			AI924230	4.3	2.3	4.2
55695 at	Plycine cleavage system protein H (aminomothy)		Al344311	3.7	3.2	4.2
55009 at		GCSH	AI890917	5.1	4.5	4.2
38694 at	KIAA0738 gene product		AI359000	2.4	1.7	4.2
32484 at	in 2		AB018281	0	9.0	4
32029 at	de dependent protein line 1	CCBP2	N94888	9.0	1.1	4
711 at	Shinding profess 1	PDPK1	AF017995	П	1.2	4
31528 f at	7	1P53BP1	U09477	4.8	3.1	4
33740 at		HZBFE	283738	1.7	1.4	4
38918 at	ning region VI box 12	CLK2	AF023268	1.1	1.3	4
34264 at	1.00v 1.3	SOX13	AF083105	က	0.8	4
33868 at	CGI-96 protein		AB026894	1.6	1.4	4
40937_at	KIAA1454 protein		293241	2.8	1.2	4
33556 at	Huntingtin interacting protein E		AA160056	3.3	2.3	4
33353_at			AF049611	1	3.7	4
34362 at	tated almoon transmission		W26466	1.9	2.1	4
		SLCZA5	M55531	3.5	2.6	4.1
35699_at	budding uninhibited by benzimidazoles 1 (yeast homolog), beta	BUB1B	AF053306	2.1	-	4.1
36075 at	ing protein similar to RAY/RAB1C		AL037167	0.3	0	A
0/10 at	cathelician antimicropial peptide	CANAD	720000			

Figure 13XXXX

40010_s_at	fragile X mental retardation 2	FMR2	L76569	0.4	1 1	-
35301_at			AL 049941		1 2	1,1
37234_at	kininogen	KNG	KOSEGE	-	7.7	1.1
37403_at	annexin A1	ANXA1	X05008	7.7	0	4.1
37264_at	zinc finger protein 131 (clone pHZ·10)	ZNF1.31	109410	1 -	6.7	4.1
37718_at	KIAA0096 protein		017500	1.0	5.1	4.1
32792_at	GCIP-interacting protein p29		043030	7.7	4.1	4.1
37629_at	casein kinase 2, alpha prime polypeptide	CONKODO	MEE960	2.1	3.2	4.1
1116 at		COINTENE	807CIMI	1.5	0.5	4.1
39174 at	Or coactivator A	CDIS	M28170	2.5	2.9	4.1
76657 at	1 000000	NCOA4	X77548	3.2	0.2	4.1
46793 at			AA058578	0.5	0	4
60115 at	hypothetical protein El 190523		AA421625	1.8	2.5	4.1
49991 at	Typotherical protein reactions		H23252	0.4	0.4	4.1
56945 24			AI872374	0	1.3	4
45332 7 24	d otot ototococ		AL043737	1.5	9.0	4 1
47459 21	Т	ASPH	AA156838	2.2	1.8	4 1
66578 at			AI290653	4.4	2.3	4 1
76825 at			AI732852	3.5	0.4	4 1
48916 24	7207		AA884474	2.1	3	4 1
82385 24	0000		AI028262	1.4	0.0	4 1
51007 at	Serine protease TADGIZ		AA534591	6.0	4.7	4.1
76473 at	2	CLCN2	AW003232	2.5	6.5	4.1
01176 24	enuation (iii S. pombe) I	ROD1	AA788925	2.8	4	1
79949 24			AI792991	9.0	0.5	4
53330 at			AI792635	1.2	1.6	4.1
81074 at			AI222203	3.3	0.8	4.1
59328 at			AA169554	9.0	0	4.1
65300 at			AI198875	2.3	1.4	4.1
82312 at			A1656358	1	1.1	4.1
59408 at			AI434767	2.9	1.2	4.1
84869 at			AA857437		1.8	4.1
47668 at			Al123917	2.9	1.9	4.1
59487 at			H94605	1.1	ĸ	4.1
45243 at			R70662	6.0	6.0	4.1
10,011			AI818209	0.5	~	4 1

Figure 13YYYY

71729_at			W90100	0.4	0.1	4.1
48601 at			AI225105	1.4	1.9	4.1
86447 at			AI525627	6.0	6.0	4 1
67812 at			AA504895	1.1	1.3	4.1
56835 at			AI018657	0.7	0.8	4.1
43708 at			T66877	1.3	3.1	4.1
68452 f at			R10307	4.3	0	4.1
43566 at			W87376	1.9	1.5	4.1
86737 at			AI674899	4.1	1.3	4.1
70089 at			H88330	10.2	9	4.1
70352 at			AI765926	0.5	0.3	4 1
70831 at			AI803691	0	6.0	4.1
63471 at			AI797620	0.3	0.2	4 1
71008 at			N92630	4.8	1.1	4 1
44245 at			AI863088	1.9	4.6	4
91162 at			H23230	1.3	0.8	4 1
51076 at			AI989878	1.5	1.6	4 1
74948 21	Pilops normalay interest		N49842	0.1	3.4	4
42256 at	nacioni por complex interacting protein	NPIP	AI991242	6.0	0	4 1
77228 at			R87972	1.2	1.9	4.1
66178 at			AI300953	0	0	4.1
55572 at			AA410395	0.5	9.0	4.1
88143 at			AA938267	2.2	3.4	4.1
65566 at	etonoside.indiced mBNA		AI253134	3.1	ĸ	4.1
51226 at			AI741005	0	9.0	4.1
45141 at			N53536	0.8	1.5	4.1
52072 at	hypothetical profein FI 110718		N51102	2.1	1.4	4.1
53197 g at	Suppression of fumorigenicity 16 (melanoma differentiation)	0.10	AA873182	5.1	0.8	4.1
7		5116	AI084226	3.2	2.6	4
51133 i at			AI128820	1.6	0.4	4.1
			AI334373	6.0	2.8	4.1
71884 f at			AA009648	4.5	က	4.1
91156 at			AI028732	1.4	0.5	4.1
78101 4 24			AI219949	0.2	0.4	4.1
10,101			AI468969	1.6	6.0	4.1

Figure 13ZZZZ

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79940 r at			0 0 0			
283 at	Inhighting orthograph or reduction and a second or inhighting		196976	2.6	1.3	4.1
10176 24	and die of the order of the protein i	UQCRC1	L16842	3.8	171	1
401/0 at		RFP	103407) Lu	, , ,	;
41749 at		C210RF33	1153003		0.1	4.1
32317_s_at	sulfotransferase	SULT1A2	U34804	4.5	3.1	4.1
41504_s_at	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene	MAF	AF055376	3.9	3.2	4.1
35331_at	catenin (cadherin-associated protein) alpha like 1	- 14 MINIST	1			
36537 at	Rho-specific guanine nucleotide exchange factor n114	CHAINALI	/90/60	4.1	3.3	4.1
32510_at	aldo-keto reductase family 7 member A2 (aflatoxin aldobuda	0,4,0,7,4	AB011093	3.3	1.7	4.1
	reductase)	AKK/AZ	AF026947	.5	2.1	4.1
32528_at	CIPP (caseinolytic protease, ATP-dependent, proteolytic subunit, E. coli) homolog	CLPP	Z50853	4.3	1.2	4.1
48833 at			A1749098	1	C	
52811_at	aryl hydrocarbon receptor nuclear translocator	ARNT	A1768497	100	3.5	4
43456 at	serine/threonine protein kinase MASK		A12000E2	3.1	2.1	4.1
52248_s_at			2066214	0 !	0.5	4.1
56404_at	CGI-109 protein		1107575	3./	3.1	4.1
46242_at			000760	7.7	1.1	4.1
50996_s_at	HSCARG protein		AAZ15/96	4.1	2.8	4.1
48094 at			AI080/01	2.1	0.7	4.1
50172 at			AA531025	4.4	3.8	4.1
43795_s_at	NADH dehydrogenase (uhiquinone) 1 alaha suhomalay 0 (1818)	041	AI377006	2.2	3.1	4.1
		NOLAS	AW005361	3.5	2.6	4.1
52908_at	hypothetical protein FLJ21324		44865610	0 ,		
54950_at			VI260501	4.6	3.9	4.1
42633 r at			AL/ 00001	3.5	3.2	4.1
45716_at	RAN, member RAS oncogene family	0.00	193591	0.5	2.1	4
39016_r_at	keratin 6A	V 0 1 0 1	W81244	0.6	2.1	4
1292_at	dual specificity phosphatase 2	2001	L42611	0.1	0.1	4
31993_f_at		DOSEZ	L11329	18.4	2.6	4
39916_r_at	ribosomal protein S15	00015	080/64	1.8	1.7	4
31687_f_at	hemoglobin, beta	HBB	JU2984	1.8	1.4	4
32068 at	noment 3a recentor 1	1000	&/ncziwi	C	1.4	4
	Solicili, Sa receptor 1	CSARI	1062027	٠. ٢.	C	_

Figure 13AAAAA

32128_at	small inducible cytokine subfamily A (Cys-Cys), member 18, pulmonary and activation-regulated	SCYA18	Y13710	7.8	7.9	4
38535_at	distal·less homeobox 4	DI X4	1173328	0	C	
41169 at	plasminogen activator, urokinase receptor	PI ALIR	V774030	0 0	0.8	4
1696_at	polymerase (DNA directed), beta	POLE	0.00013	χ	4.2	4
33668_at	ribosomal protein L12	RPI 12	053013 05037643	1.3	Σ.Ι	4
497_at	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer- Vogt disease)	CLN3	U32680	2.1	1.2	4 4
38928_r_at		TVP	1100			
32834_r_at	sudD (suppresso	SUDD	AF013501	1.4	0.4	4
34216_at			AA478904	1.0	0.0	4
41247_at			110001		0.3	4
38617_at	LIM domain kinase 2	I IMK2	DAE006	1.5	-	4
41488 at	hypothetical protein A-211C6.1	7	043300	27.3	4.4	4
38676_at	stress 70 protein chaperone, microsome associated 60kD	- 1010	AC002394	8.2	4.9	4
35221 at		מוכח	AA059408	7.6	3.8	4
32222 at	I R8 protein		X91648	2.3	0	4
36295 at	40,		AA152202	18.5	14.2	4
35762 at	KIAAAA83 gratein	ZNF134	U09412	1		A
35803 24	ran homolog man (mili		AB007952	ō	0.5	
52000 at	COO IN PRINCIPLE SERVING Member E	ARHE	S82240	6.0	12	1
36155 24		CLK2	129218	2.7	70	
36208 24	Komodomie		D87465	1.2		
38363 at	TVBO SCALES	BRD2	D42040	1.3	90	1
2005 2 24	Janus kinase 3 (2 costs to the	TYROBP	W60864	1.2	2.3	1
63867 at	lysyl oxidase	JAK3	U31317	1.1	1.2	4
56847 at		LOX	AI971709	2.4	2.1	4
58206 at			AI911070	0	0	4
75747 at			W63702	0	0.3	4
56460 at			AA626334	2.3	5	4
76055 at			AA809379	0	0	V
76905 at			AA707217	0.8	-	
77142 at			AI674760	3.4	0.7	
76710 at			AI640484	3.4	0	
/ 0/ 10_at	carulou opiiii-iike cytokine; neurotrophin-1/B-cell stimulating factor-3		AI040033	92.7	4.7	4
			_			

Figure 13BBBBB

59179_at			T89693	0	0	4
59200_at			T78626	1.4	2.8	4
52137_at			A1140767	1.3	1.4	4
52805_at			AI024348	8.0	0.7	4
53873_at			R67688	1.9	2.1	4
80872_at			AA533574	0	0.2	4
54757_at			N51283	1.5	2.7	4
63205_at			AA770196	2.9	3.4	4
67051_r_at			AI345851	1.4	2.6	4
81565_at			W85907	0.7	0.4	4
50631_at			AA843724	8.0	1.7	4
59000_at	x 010 protein	010	AA629304	9.9	4.8	4
51623_at	DKFZP434116 protein		AA203689	1.9	1.6	4
55656_at			AI651905	1.3	1.6	4
60502_at			AI743953	ō	0	4
43115_at			A1686303	1.5	2.8	4
42669_at	KIAA1304 protein		R00834	2.9	1.8	4
43573_at			AA251274	1.1	2	4
68403_at			AA781446	1.3	0	4
43646_at	zinc finger protein 14 (KOX 6)	ZNF14	AA599140	1.6	9.0	4
42475_at			T94540	2	m	4
69432_at			AI655716	1.2	11	4
79912_at			AA642419	1	2.2	4
43673_at			AI056293	1.5	2.3	4
89479_at	1000		AI810541	0.5	1.5	4
45308_at			AA114834	2.5	3.7	4
77927_i_at			AI743151	2	9.0	4
71619_at			A1936553	6.0	6.0	4
84510_at	interleukin 20 receptor, alpha	L20RA	A1800588	5.2	0.4	4
65541_at			AA628960	3.2	1.9	7
43038_r_at	KIAA1363 protein		AI769531	0	8.1	4
74131_at			AI989784	5.1	2	4
50354_at	FK506 binding protein precursor		N36303	2.5	3.9	4
77105 at	Fzr1 protein		AI732960	0.7	2.2	4
65416_i_at			R91398	2.2	1.2	4

74456 r_at			A1970474	6.5	7	
78720 at	hypothetical protein FLJ10335		AL036075	0.4		1
100000			AI939307	0.6	0	
90332 at			AA777061	1.6	0	1
491/9 al	NIAAU493 protein		AI675152	0.7	0.6	
003/4 4			H90328	22	200	
54583 at			H81933	17	100	1
54330 s at			AI827609	2,1	0.70	1
45624_at	core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase		A1967968	5.2	6.9	4 4
45993_at			N51961			
58569_r_at	niban protein		A1200107	1.1	7.7	4
46084_at			A1308197	16.7	5.9	4
91994 at	DEAD/H (Asp.Gli.Ala.Asn/His) hox polypopitide 17 (72).00	1.50	W/3092	2.1	1.6	4
59798 r at	polypeptide 17 (72KD)	DUX1/	AA461244	4.6	0.1	4
75024 at	adenosine deaminase DNA considio	ale.	AW025321	0.8	1.2	4
66122 at		ADAR	R49062	7.6	9.5	4
48327 at	planning 3, member AZ	BTN3A2	AA888172	2.5	3.7	4
51697 r at			AA831325	2.6	6.8	4
50457 at			AA649308	4.8	m	4
53077 at			AA425877	1.2	1 1	
75507 at			3147488	-	1 9	f
2027 at			AA778921	000	14.0	1
39341 at	tnyroid normone receptor interactor 6	TRIP6	AJ001902			4
41//1 g at	monoamine oxidase A	MAOA	AA420624	1 0	0.5	4
40848 g at	KIAAU/50 gene product		AB018293	4.3	1.9	4
33619 at	enase B	LDHB	X13794	3.5	7.6	4
33569 at	macrophage lectin 2 (calcium dependent)		D50532	2:0	t:3	4
30313_at	UDF-IN-acetylglucosamine-Z-epimerase/N-acetylmannosamine kinase		AJ238764	2.9	1.6	4
33121 g at	otein signalling 10	RGS10	AF0/15/20	0		
38424_at	KIAA0747 protein		AR018290	1.0	0.0	4
61259 at			W31042	1 0	2.3	4
80436_at			A1035C44	3.7		4
44713_at	HSPC009 protein		111 0006	3.4	3.3	4
56235 at	rrest deficient yeart homology like 2	0.000	018000	3.4	1.9	4
	car denoter, yeast, normong/like Z	MAD2L2	AA662845	1.2	2.6	4

Figure 13DDDDD

50926_s_at	50926_s_at [fatty acid hydroxylase		R54585	4	4		4
56875_at	tRNA selenocysteine associated protein		AA082704	1.1	0.7		4
48670_at	CGI-119 protein		AI189791	1.6	1.2		4
52090_at			AI198126	1.1	9.0		4
57210_at			AI862775	3.9	3.3		4
54061_at	hypothetical protein FLJ10595		AA088424	1.7	2		4
52841_at			AA731740	4.1	4		4
47057_at			D20714	3.5	3.4		4
47104_at			AI760368	4.5	3.4		4
47922_at			AA423837	2.6	0		4
38981_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12)	NDUFB3	AA203354	1.1	2.4		6 E
279_at	Inuclear receptor subfamily 4, group A, member 1	NR4A1	L13740	0.8	1.9		3.9
37491_at	TATA box binding protein (TBP) associated factor, RNA polymerase II, A, 250kD	TAF2A	090359	3.5	1.6		3.9
34539_at	olfactory receptor, family 7, subfamily E, member 12 pseudogene	OR7E12P	AF065854	8.0	0.5		3.9
39897_at	DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 16	DDX16	N36997	3.2	2.1		3.9
41852 at	rearranged L-myc fusion sequence	RLF	U22377	2.3	0.7		3.9
34544_at	zinc finger protein 267	ZNF267	X78925	4.3	2.9		3.9
39784_at			U26032	0	0.4		<u>ق</u>
40098 at	EH domain containing 1	EHD1	AF001434	28.1	9.0	i	3.9
40121_at	huntingtin interacting protein 2	HIP2	U58522	0.8	1.5		3.9
39459_at	ribosomal protein S13	RPS13	W28765	6.0			3.9
39290 f at	PAI-1 mRNA-binding protein		W28257	6.0	0		3.9
31342_at	UDP·N-acetyl-alpha-D-galactosamine:polypeptide N- acetylgalactosaminyltransferase 2 (GaINAc-T2)	GALNT2	X85019	4.4	1.3		3.9
32711_g_at	potassium voltage gated channel, shaker related subfamily, beta member 1	KCNAB1	X83127	1.6	0.8		3.9
33234_at	KIAA0117 protein		AA887480	2.7	3		3.9
41193_at	dual specificity phosphatase 6	9dSna	AB013382	11.5	2.5		3.9
33267_at			AF035315	4	1.5		3.9
33327_at	chromosome 11open reading frame 9	C110RF9	AB023171	0.1	0.7		3.9
40960_at	UDP-GalibetaGlcNAc beta 1,4· galactosyltransferase, polypeptide B4GALT1	B4GALT1	029805	16.7	4.9		3.9

Figure 13EEEEE

40988_at	YME1 (S.cerevisiae)-like 1	YME1L1	A1132637		cc	C
40997_at	Т	MAP3K12	AIGEOGES	2:0	4.3	ט ני
41279 f at	П	MAPK8IP1	AF007134		0.0	2.0
31671_at	RNA binding motif, single stranded interacting protein 1, pseudogene	RBMS1P	D82351	3.7	4.6	3.9
33479 g at	transition protei	TMP2	031000			
36270_at	CD86 antigen (C	2000	207007	1.4	1.2	3.9
37438_at	KIAA0419 gene product	2000	004343	6.4	13.2	3.9
33835 at			AB00/8/9	1.5	2.1	3.9
36298 at	Deripherin		AB018264	3.4	9.0	3.9
41595 at	KIAA0947 protein	РКРН	L14565	1.2	Ö	3.9
36821 at			AB023164	1.6	2.1	3.9
36753 24	la de la company		AL050367	0	Ô	3 6
00 / 00 - al	reductive initiation of the receptor, subfamily B (with TM and ITIM domains), member 4	LILRB4	AF072099	8.1	8.9	3.9
35799_at	DnaJ (Hsp40) homolog, subfamily B, member 9	DNA IRO	1000001	-		
36754_at	adenylate cyclase activating polypeptide 1 (pituitary)	ADCVAD1	VEO 43E	5.1	1.3	3.9
36110_at	RAS oncogene family	1 10000	A00433	0.4	0.3	3.9
36203 at		RABDA 000:	M28215	2.4	3.6	3.9
37212 at	Sn2 transcription factor	ODC1	X16277	1	0.3	3.9
508 34	-17	SP2	D28588	6.0	1.1	3.9
37915 at	lacent to zinc tinger domein	SUPT4H1	U43923	0	0.3	3.9
61865 at	Stationaria adjacent to tine iniger domain, ZB	BAZ2B	AL080173	8.9	3.4	3.9
56434 at			AI423165	7.3	4	3.9
90278 at			AA579598	0.3	0.8	3.9
50842 at			AA709455	6.0	0.7	3.9
76533 at			W92000	2.1	3.7	3.9
58132 at			AI660684	2.6	6.0	3.9
66742 at			AA807258	1.6	3.3	3.9
77647 at			AI681652	1.1	0.5	3.9
61771 at			AI131078	1.8	4	3.9
			AA886300	3.2	0.3	3.9
79240 at			AI425073	1.1		300
61543 at			AI435163	3	0	9.6
51343 r at			AI184720	3.6	1.6	3.6
52067 at			R62551	2.9		3.9
			A1220827	1.7	0.5	0 8
						,

Figure 13FFFFF

52664_at		AI263842	1.1	12	30
		AI420422	3.7	1 2	0.5
\neg		AW008847	-1	7 1	0.0
60906_r_at hypothetical protein FLJ10773		AA044181	4 4	2 4	0.0
80958_at		AA884148		2.0	300
83622_at		AI809213	12	0 1	000
42829 at		N58166	5.7	28	3.0
54/// at		H61899	0.1	0	3.9
79350 at		AA706315	0	0	3.9
75057		AI479376	5.3	1.1	3.9
/3300_at		AA555312	3.2	5.5	3.9
70700 24		AI608810	0.2	1.3	3.9
		AI690729	0.5	2.8	3.9
7703E 34	DNAJA2	AI560867	1.2	1.3	3.9
77332g at		AI939620	4.6	2.5	3.9
1		R44338	0	0.4	3.9
FOACS CALCALOS PROTEIN		AW008524	2.8	33	3.9
52422_at		AI741514	2.8	1.2	3.9
in location of		AA829939	0	0.3	3.9
AFAR7 at		AI689756	4.4	2	3.9
45050 at		R60981	0.2	0.1	3.9
42330_at		R85261	2.5	3.2	3.9
at NIV DENI 10 antig		W87368	0.5	-	3.9
1		AI425002	13.9	8.8	3.9
47554 at		W44959	1	0.5	3.9
81066 i at		AA226241	9.9	2.8	3.9
44528 at Invnothetical protein El 120004		AI285898	9.9	2.3	3.9
חול שבווים וויים היו		AI480121	0.7	0.7	3.9
acaser aisacilos		AL037445	1.3	6.0	3.9
		AI879238	6:0	0.7	3.9
47841_at		A1192897	0	1.0	0
		A1971552	1 7	2.1	3.9
51798_at hypothetical protein FLJ11000		AW006887	12,	13	2.0
49787_s_at KiAA1547 protein		A1291302	2 1		0.0

Figure 13GGGGG

at hypothetical prote at at at at at at at at at at at at at a	63911_at	phosphoglycerate dehydrogenase	PHGŪH	AI625116	2.8	3.5	3.0
hypothetical protein FL112484 hypothetical protein FL112484 6.2	45918_at			N53560	4.5	1.6	3.9
at t AAA59463 18 at t AAA55349 10 at at t NA2434 5 9 at t NA2434 5 9 at t AA557191 2 6 at t AA537272 3 6 at t AAA573727 3 6 at t AAA57372 3 7 at t AAA57372 3 3 at t AAA16835 3 4 at AAA16836 3 4 at AAA16836 3 4 at AAA16840 AAA18458 4 4 at AAA16840 AAA18458 4 4 at AAA16840	51962_at			W45523	6.2	2.7	3.9
AIA AIA	51058_at			AA459463	1.8	3.3	3.9
MAD (mothers against decapentaplegic, Drosophila) homolog 4 MADH4 S 9	50888_r_at			AI768349	0	2.9	3.9
Alternation Alternation Alternation Alternation	16826_at			N49233	2.1	1.4	3
1	16889_at			N74444	5.9	1.4	3.9
AAE73272 3.6	51830_at			AA557191		1	3.
at Inbosomal protein State of the part of t	33573_f_at			AA573272	3.6	2.7	Э.
at MAD (mothers against decapentaplegic, Drosophila) homolog 4 MADH4 AW021681 2 at MAD (mothers against decapentaplegic, Drosophila) homolog 4 MADH4 AW021681 2 at at epithelial membrane protein 3 AW005790 3.3 at a pithelial membrane protein 3 EMP3 AW005790 3.3 at a pithelial membrane protein 3 EMP3 AW005790 3.3 at a pithelial membrane protein 3 EMP3 AW005790 3.3 at builduinol-cytochrome c reductase core protein 11 UQCRC2 J04973 3.1 at Ubiquinol-cytochrome c reductase core protein 11 UQCRC2 J04973 3.1 at Ubiquinol-cytochrome c reductase core protein 11 UQCRC2 J04973 3.1 at Ubiquinol-cytochrome c reductase core protein 11 UQCRC2 J04973 3.1 at Ubiquinol-cytochrome c reductase core protein 11 UQCRC2 J04973 3.1 at Ubiquinol-cytochrome c reductase core protein 11 UQCRC2 J04973 3.1 at Ubiquinol-cytochrome c reductase core protein 11 UQCRC2 J04973 3.1 at Ubiquinol-cytochrome c reductase core protein 11 UQCRC2 J04973 3.1 at Ubiquinol-cytochrome c reductase core protein 11 UQCRC2 J04973 3.1 at Cathegora c reductase core protein 11 UQCRC2 J04973 3.1 at Cathegora c reductase core protein 11 UQCRC2 J04973 3.1 at Cathegora c reductase C reductase core protein 11 UQCRC2 J04973 3.1 at Cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at reductase core protein 11 UQCRC2 J04973 3.7 at reductase core protein 11 UQCRC2 J04973 3.7 at the cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at the cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at the cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at the cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at the cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at the cathegora c reductase core protein 11 UQCRC2 J04973 3.7 at the cathegora c reductase core protein 11 UQCRC2 J04973 3.7	33578_at			W70067	17.9	7.9	3
at MAD (mothers against decapentaplegic, Drosophila) homolog 4 MADH4 AL041224 2 at AAB (mothers against decapentaplegic, Drosophila) homolog 4 MADH4 AM021681 2 at AAB (mothers against decapentaplegic, Drosophila) homolog 4 AAB (ABSD 24) 2.3 3 at EMP3 AA416856 1.4 1.6 1.6 1.6 g at epithelial membrane protein 3 EMP3 AA4037529 6.8 1.4 r_at klAA0220 protein EMP3 AA515640 1.2 1.2 at Lubiquinol-cytochrome c reductase core protein 11 UQCRC2 JA4515640 1.2 1.2 at Ubiquinol-cytochrome c reductase core protein 11 UQCRC2 JA4515640 1.2 1.2 at N-acetylglucosamine-1-phosphodiester alpha-N- RAD23A D21235 0.4 1.1 acetylglucosamine-1-phosphodiester alpha-N- acetylglucosamine-1-phosphodiester alpha-N- RAD23A AF052111 4.1 acetylglucosamine-1-phosphodiester alpha-N- acetylglucosamine-1-phosphodiester alpha-N- ACRCAGORO ACR	16192 at			AI807693	1.7	0.8	3.9
MAD (mothers against decapentaplegic, Drosophila) homolog 4 MADH4 AW021681 2.3	5861_at			AL041224	2	2	3.9
epithelial membrane protein 3 EMP3 AA860344 2.3 T64805 1.6 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416856 1.4 AA416820 protein Ubiquinol-cytochrome c reductase core protein II UQCRC2 104973 3.1 AA515640 1.2 AA515	74813_at		MADH4	AW021681	2	2.3	3.9
epithelial membrane protein 3 EMP3 T64805 1.6 epithelial membrane protein 3 EMP3 AA416856 1.4 RAM0220 protein AA037529 6.8 1.4 KIAA0220 protein MA037629 6.8 1.4 KIAA0220 protein MA037629 6.8 1.2 RAD23 (S. cerevisiae) homolog A AA515640 1.2 N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase RAD23A D21235 0.4 aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde ALDH9 N34552 3.9 aldehydrogenase, E3 isozyme) ALDH9 N34552 3.9 cathepsin C CTSC AI28687 2.5 ribosomal protein S9 RPS9 AA194261 3.9 ribosomal protein S9 RPS9 AA194261 3.9 eukaryotic translation initiation factor 2, subunit 3 (gamma, E1F2S3 RRPS9 AA194261 3.7	1349 at			AA860344		1.1	3.
epithelial membrane protein 3 EMP3 AA416856 1.4 Repithelial membrane protein 3 EMP3 AA037529 6.8 KIAA0220 protein 1 R79063 1.2 RAD23 (S. cerevisiae) homolog A cetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase RAD23A D21235 0.4 N-acetylglucosaminidase aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme) ALDH9 U34252 3.9 ORF seven transmembrane domain protein Cathepsin C cathepsin C altrepsin C CTSC AI24687 4 Inbosomal protein S9 indosomal protein S9 eukaryotic translation initiation factor 2, subunit 3 (gamma, E1F2S3 RRFS9 AA194261 3.9 eukaryotic translation initiation factor 2, subunit 3 (gamma, E1F2S3 RRFS9 AA194261 3.7	34427_at			T64805	1.6	9.0	3.9
epithelial membrane protein 3 EMP3 AW005790 3.3 KIAA0220 protein R79063 1.4 KIAA0220 protein AA515640 1.2 BAD23 (S. cerevisiae) bromolog A AC003007 3.6 N-acetylglucosamined-robothorme c reductase core protein II UQCRC2 J04973 3.1 RAD23 (S. cerevisiae) bromolog A RAD23A D21235 0.4 N-acetylglucosaminidase Gamma-aminobutyraldehyde ALDH9 U34252 3.9 aldehydrogenase, E3 isozyme) ALDH9 U34252 3.9 dehydrogenase, E3 isozyme) ALDH9 U34252 3.9 ORF Seven transmembrane domain protein CTSC AI246687 4 cathepsin C CTSC AI246687 4 ribosomal protein S9 RPS9 AA194261 3.9 eukaryotic translation initiation factor 2, subunit 3 (gamma, E1F2S3 IN38902 3.7	7335 g at			AA416856	1.4	2.1	3
MAG220 protein R79063 1.4	74710_s_at	epithelial membrane protein	EMP3	AW005790	3.3	2.4	3
KIAA0220 protein R79063 1.4 MAA0220 protein AA515640 1.2 ubiguinoi-cytochrome c reductase core protein II UQCRC2 J04973 3.6 RAD23 (S. cerevisiae) homolog A acetylglucosaminidase RAD23A D21235 0.4 N-acetylglucosaminidase acetylglucosaminidase AF05211 4.1 aldehyde dehydrogenase (gamma-aminobutyraldehyde ALDH9 U34252 3.9 dehydrogenase, E3 isozyme) ALDH9 U34252 3.9 odry CTSC AI18007 3.7 seven transmembrane domain protein CTSC AI246687 4 cathepsin C CTSC AI246687 4 ribosomal protein S9 RPS9 AA194261 3.9 eukaryotic translation initiation factor 2, subunit 3 (gamma, BIF2S3 IN38902 3.7	79735_at			AA037529	8.9	3.7	3.9
KIAA0220 protein AA515640 1.2 ubiquinol-cytochrome c reductase core protein II UQCRC2 J04973 3.6 RAD23 (S. cerevisiae) homolog A acetylglucosamine 1-phosphodiester alpha-N. acetylglucosaminidase RAD23A D21235 0.4 N-acetylglucosaminidase acetylglucosaminidase adehydrogenase, E3 isozyme) ALDH9 N34252 3.9 Achydrogenase, E3 isozyme) ALDH9 N34252 3.9 odrydrogenase, E3 isozyme) CTSC Al246687 4 cathepsin C CTSC Al246687 4 ribosomal protein S9 RPS9 AA194261 3.9 eukaryotic translation initiation factor 2, subunit 3 (gamma, RFS3 RRPS3 N38902 3.7	35802_at			R79063	1.4	1.1	3.9
KIAA0220 protein KIAA0220 protein AC003007 3.6 ubiquinol-cytochrome c reductase core protein II UQCRC2 J04973 3.1 RAD23 (S. cerevisiae) homolog A RAD23A D21235 0.4 N-acetylglucosaminidase AF05211 4.1 acetylglucosaminidase AF05211 4.1 acetylglucosaminidase AF05211 4.1 aldehydrogenase 9 (gamma-aminobutyraldehyde ALDH9 U34252 3.9 aldehydrogenase, E3 isozyme) M68864 2.5 seven transmembrane domain protein CTSC AI246687 4 cathepsin C IN22262 3.8 ribosomal protein S9 RPS9 AA194261 3.9 eukaryotic translation initiation factor 2, subunit 3 (gamma, E1F2S3 IN38902 3.7	36858_r_at			AA515640	1.2	1.7	3
ubiquinol-cytochrome c reductase core protein II UQCRC2 J04973 3.1 RAD23 (S. cerevisiae) homolog A RAD23A D21235 0.4 N-acetylglucosamine-I-phosphodiester alpha-N-acetylglucosaminidase AF052111 4.1 aldehydrogenase (gamma-aminobutyraldehyde ALDH9 U34252 3.9 dehydrogenase, E3 isozyme) M68864 2.5 odehydrogenase, E3 isozyme) CTSC A18007 3.7 cathepsin C CTSC A1246687 4 ribosomal protein S9 RPS9 AA194261 3.9 at eukaryotic translation initiation factor 2, subunit 3 (gamma, E1F2S3 RRS9 AA194261 3.9	11733 at	KIAA0220 protein		AC003007		2	3.9
RAD23 (S. cerevisiae) homolog A RAD23A D21235 0.4 N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase AF052111 4.1 alcetylglucosaminidase ALDH9 U34252 3.9 aldehydrogenase (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme) M68864 2.5 ORF Seven transmembrane domain protein CTSC A1246687 4 cathepsin C Iribosomal protein S9 RPS9 AA194261 3.9 at eukaryotic translation initiation factor 2, subunit 3 (gamma, E1F2S3 E1F2S3 N38902 3.7	.0854_at	ubiquinol cytochrome c reductase core protein II	UQCRC2	J04973	3.1	1	33
N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase AF052111 4.1 acetylglucosaminidase ALDH9 U34252 3.9 aldehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme) M68864 2.5 cathepsin C CTSC A126067 3.7 cathepsin C CTSC A1246687 4 ribosomal protein S9 ribosomal protein S9 RPS9 AA194261 3.9 at eukaryotic translation initiation factor 2, subunit 3 (gamma, E1F2S3 E1F2S3 N38902 3.7	.1197_at	RAD23 (S. cerevisiae) homolog A	RAD23A	D21235	0.4	0	3.9
aldehyde dehydrogenase, E3 isozyme) ALDH9 U34252 3.9 dehydrogenase, E3 isozyme) (DRF (M68864 2.5 Seven transmembrane domain protein (CTSC) (A18007) 3.7 cathepsin C (TSC) (A1246687) 4 ribosomal protein S9 RPS9 AA194261 3.9 at eukaryotic translation initiation factor 2, subunit 3 (gamma, elekaryotic translation initiation factor 2, subunit 3 (gamma, elekaryotic translation factor 2, subunit	18956_at			AF052111	4.1	3.1	3.9
ORF M68864 2.5 seven transmembrane domain protein CTSC Y18007 3.7 cathepsin C A1246687 4 ribosomal protein S9 RPS9 AA194261 3.9 at eukaryotic translation initiation factor 2, subunit 3 (gamma, eukaryotic translation initiation factor 2, subunit 3 (gamma, eukaryotic translation factor 2) EIF2S3 N38902 3.7	13899_at	aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)	ALDH9	U34252	3.9	2.3	3.9
seven transmembrane domain protein Seven transmembrane domain protein 3.7 cathepsin C CTSC AI246687 4 ribosomal protein S9 RPS9 AA194261 3.9 at eukaryotic translation initiation factor 2, subunit 3 (gamma, eukaryotic translation initiation factor 2, subunit 3 (gamma, eukaryotic translation factor 2,	37376_at	ORF		M68864	2.5		er.
cathepsin C CTSC AI246687 4 ribosomal protein S9 RPS9 AA194261 3.9 at eukaryotic translation initiation factor 2, subunit 3 (gamma, eukaryotic translation initiation factor 2) EIF2S3 N38902 3.7	39088_at			Y18007		1.5	3.9
ribosomal protein S9 RPS9 AA194261 3.9 at leukaryotic translation initiation factor 2, subunit 3 (gamma, EIF2S3 RIF2S3 N38902 3.7	3866_at	cathepsin C	CTSC	A1246687		1.1	6
ribosomal protein S9 AA194261 3.9 at leukaryotic translation initiation factor 2, subunit 3 (gamma, EIF2S3 N38902 3.7	51126 at			N22262			33
tion initiation factor 2, subunit 3 (gamma, EIF2S3 N38902 3.7	54662_at		RPS9	AA194261			8
	14646_r_at	eukaryotic translation initiation factor 2, subunit 3 (gamma,	EIF2S3	N38902	3.7	3.4	E.